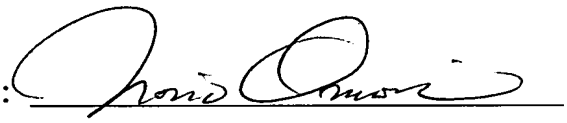
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VERIFICATION OF TRANSLATION

I, Norio Ohmori, registered Patent Attorney, having my business place at Fukuoka Building, 9th Floor 8-7, Yaesu 2-Chome, Chuo-ku, Tokyo 104-0028 Japan, do hereby declare that I am conversant in the Japanese and the English language and that I am the translator of the documents attached and certify that to the best of my knowledge and belief the following is a true and correct English translation of the specification contained in the Application No. JP2001-256862.

Signature : 

Norio Ohmori

This 24th day of June, 2005

日本国特許庁
JAPAN PATENT OFFICE

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This is to certify that the annexed is a true copy of the following application as filed with this Office.

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[Name of Document] SPECIFICATION

[Title of the Invention] METHOD OF DETECTING GENE POLYMORPHISM

[Scope of Claims]

1. A method for detecting a genetic polymorphism(s), comprising creating oligonucleotide probes and/or oligonucleotide primers so that the probes and/or primers contain a polymorphic site(s) present in a gene encoding a drug metabolizing enzyme or so that the polymorphic site(s) is/are contained in the amplified fragment when at least one of said gene encoding the drug metabolizing enzyme is amplified; and detecting at least one genetic polymorphism in a gene of a subject encoding the drug metabolizing enzyme using the resultant oligonucleotide probes and/or oligonucleotide primers.

2. The method according to claim 1, wherein the oligonucleotide probe and/or oligonucleotide primer containing a gene polymorphic site is created so that the nucleotide positioned at its 5' or 3' end or its central part is the polymorphic site.

3. The method according to claim 1, wherein the oligonucleotide probe containing a gene polymorphic site is composed of two fragments being linked to each other, one fragment being hybridizable to the gene encoding a drug metabolizing enzyme and the other fragment being not hybridizable thereto, and said polymorphic site is positioned at the 5' or 3' end of the hybridizable fragment.

4. The method according to claim 1, wherein the oligonucleotide probes and/or oligonucleotide primers containing a gene polymorphic site comprising an at least 13 nucleotide sequence within any of the nucleotide sequences as shown in SEQ ID NOS: 1 through 3360, said at least 13 nucleotide sequence containing the 21st nucleotide, or a sequence complementary to said at least 13 nucleotide sequence.

5. The method according to any one of claims 1 to 4 wherein the polymorphism is a single-nucleotide polymorphism, a polymorphism caused by deletion, substitution or insertion of a plurality of nucleotides, or a VNTR or microsatellite polymorphism.

6. A method for evaluating a drug, wherein the effectiveness and safety of a drug metabolized by the drug metabolizing enzyme are evaluated based on the results obtained by the detection method according to any one of claims 1 to 5.

7. A method for screening a drug, wherein the drug to be used is selected based on the results obtained in the evaluation method according to claim 6.

8. A method for screening a drug, wherein the genetic polymorphism data associated with the gene encoding a drug metabolizing enzyme in a control subject is compared to the genetic polymorphism data associated with the same gene in a test subject, and wherein a drug to be used is selected from the results of an analysis of the effectiveness

and/or safety of the drugs metabolized by the drug metabolizing enzyme.

9. The method according to any one of claims 1 to 8 wherein information of the polymorphic site is as shown in Table 1.

10. The method according to any one of claims 1 to 9, wherein the drug metabolizing enzyme is at least one selected from the group consisting of epoxide hydrolase, methyltransferase, N-acetyltransferase, sulfotransferase, quinone oxidereductase, glutathione S-transferase, UDP-glycosyltransferase, aldehyde dehydrogenase, alcohol dehydrogenase, esterase, NDUF, cytochrome P450 (CYP) and ATP-binding cassette.

11. An oligonucleotide selected from the group consisting of the nucleotide sequences as shown in SEQ ID NOS: 1 through 3360 and sequences complementary thereto.

12. An oligonucleotide created so that it contains information of the polymorphic site present in a gene encoding a drug metabolizing enzyme.

13. The oligonucleotide according to claim 12, which is created so that the nucleotide positioned at its 5' or 3' end or its central part is the polymorphic site.

14. The oligonucleotide according to claim 12, wherein the oligonucleotide containing a polymorphic site is composed of two fragments being linked to each other, one fragment being hybridizable to the gene encoding a drug metabolizing enzyme and the other fragment being not hybridizable thereto, and said polymorphic site is positioned at the 5' or 3' end of the hybridizable fragment.

15. The oligonucleotide according to any one of claims 12 to 14, wherein the oligonucleotide comprising an at least 13 nucleotide sequence within any of the nucleotide sequences as shown in SEQ ID NOS: 1 through 3360, said at least 13 nucleotide sequence containing the 21st nucleotide, or a sequence complementary to said at least 13 nucleotide sequence.

16. A genetic polymorphism detection kit comprising the oligonucleotide according to any one of claims 11 to 15.

[Detailed Description of the Invention]

[Technical Field to which the Invention Pertains]

The present invention relates to information on genetic polymorphisms; a method for detecting information on genetic polymorphisms; a method for evaluating drugs using genetic polymorphisms; and a method for screening for drugs.

[Background Art]

As physical appearances of human individuals vary infinitely, the human genetic code consisting of three billion (3,000,000,000) base pairs vary at a considerably large number of sites when compared among individuals. These differences in the genetic code

are called genetic polymorphisms, and single nucleotide polymorphism is known as a representative polymorphism.

Single nucleotide polymorphism (SNP) means a difference in one DNA letter among individuals. As faces and shapes of human individuals vary infinitely, nucleotide sequences (i.e. genetic code) of individuals vary at a considerably large number of sites. SNPs are classified into cSNP (coding SNP) and gSNP (genome SNP) depending on their locations; cSNP is further classified into sSNP (silent SNP), rSNP (regulatory SNP) and iSNP (intron SNP).

These SNPs are useful as polymorphic markers in searching for those genes which are associated in the development or worsening of diseases; finally, these SNPs directly relates to risk diagnosis of diseases or selection and use of therapeutic drugs in the clinical field. Also, drug development on the basis of evidence obtained using causative substances as target molecules has become the trend of the world. When a drug is administered to patients with the same disease, their responsiveness is diverse. Some patients show remarkable effect; some patients show low effect; and some patients show no effect. Thus, responsiveness to a drug varies greatly depending on the patient. Even if the conditions of patients are the same and diagnosed as the same disease, the routes which have caused that disease may be different; or the metabolizing rate of the drug may vary greatly among patients. Therefore, it is desired to select an appropriate drug and develop an appropriate therapeutic method against a target disease based on genetic polymorphisms such as SNPs (i.e. the so-called personalized medicine is desired).

In addition to responsiveness to drugs, the problem of strong side effect which sometimes might be lethal is also one of the major problems that medical staffs should address. Even if there is no excessive administration caused by prescription error or the like, unexpected, lethal side effect might occur. Therefore, with respect to responsiveness to a drug, it is desired that the metabolism and delivery of the drug, the responsiveness of the drug's receptor and the sensitivities of those receptors associated with side effect should be determined taking into account genetic polymorphisms such as SNPs.

[Problem to be Solved by the Invention]

It is an object of the present invention to provide a method for detecting information on genetic polymorphism; a method for evaluating the efficacy and safety of drugs based on the information; and a method for screening for drugs.

[Means for Solving Problem]

As a result of extensive and intensive researches toward the solution of the above problem, the present inventors have succeeded in establishing a method which comprises

detecting genetic polymorphisms in a gene encoding a drug metabolizing enzyme and evaluating with the resultant information the relationship between a drug and a disease. Thus, the present invention has been achieved.

The present invention is as described below.

(1) A method for detecting a genetic polymorphism(s), comprising creating oligonucleotide probes and/or oligonucleotide primers so that the probes and/or primers contain a gene polymorphic site(s) present in a gene encoding a drug metabolizing enzyme or so that the polymorphic site(s) is/are contained in the amplified fragment when at least one of said gene encoding the drug metabolizing enzyme is amplified; and detecting at least one genetic polymorphism in a gene of a subject encoding the drug metabolizing enzyme using the resultant oligonucleotide probes and/or oligonucleotide primers.

The oligonucleotide probe and/or oligonucleotide primer containing a gene polymorphic site is created so that the nucleotide positioned at its 5' or 3' end or its central part is the polymorphic site. The oligonucleotide probe containing a gene polymorphic site is composed of two fragments being linked to each other, one fragment being hybridizable to the gene encoding a drug metabolizing enzyme and the other fragment being not hybridizable thereto, and said polymorphic site is positioned at the 5' or 3' end of the hybridizable fragment. The oligonucleotide probes and/or oligonucleotide primers containing a gene polymorphic site include an oligonucleotide comprising an at least 13 nucleotide sequence within any of the nucleotide sequences as shown in SEQ ID NOS: 1 through 3360, said at least 13 nucleotide sequence containing the 21st nucleotide, or a sequence complementary to said at least 13 nucleotide sequence. The types of genetic polymorphisms include single-nucleotide polymorphism, polymorphism caused by deletion, substitution or insertion of a plurality of nucleotides, or VNTR or microsatellite polymorphism.

(2) A method for evaluating a drug, wherein the effectiveness and safety of a drug metabolized by the drug metabolizing enzyme are evaluated based on the results obtained by the detection method according to the above method.

(3) A method for screening a drug, wherein the drug to be used is selected based on the results obtained in the above evaluation method.

(4) A method for screening a drug, wherein the genetic polymorphism data associated with the gene encoding a drug metabolizing enzyme in a control subject is compared to the genetic polymorphism data associated with the same gene in a test subject, and wherein a drug to be used is selected from the results of an analysis of the effectiveness and/or safety of the drugs metabolized by the drug metabolizing enzyme.

In the above detecting method, evaluating method or screening method, information of the genetic polymorphism includes polymorphic site is as shown in Table 1. Example of the drug metabolizing enzyme includes at least one, selected from the group consisting of epoxide hydrolase, methyltransferase, N-acetyltransferase, sulfotransferase, quinone oxidereductase, glutathione S-transferase, UDP-glycosyltransferase, aldehyde dehydrogenase, alcohol dehydrogenase, esterase, NDUF, cytochrome P450 (CYP) and ATP-binding cassette.

(5) An oligonucleotide selected from the group consisting of the nucleotide sequences as shown in SEQ ID NOS: 1 through 3360 and sequences complementary thereto.

(6) An oligonucleotide created so that it contains information of the polymorphic site present in a gene encoding a drug metabolizing enzyme.

The above oligonucleotide is created so that the nucleotide positioned at its 5' or 3' end or its central part is the polymorphic site. The oligonucleotide is composed of two fragments being linked to each other, one fragment being hybridizable to the gene encoding a drug metabolizing enzyme and the other fragment being not hybridizable thereto, and said polymorphic site is positioned at the 5' or 3' end of the hybridizable fragment. Example of the oligonucleotide includes an oligonucleotide comprising an at least 13 nucleotide sequence within any of the nucleotide sequences as shown in SEQ ID NOS: 1 through 3360, said at least 13 nucleotide sequence containing the 21st nucleotide, or a sequence complementary to said at least 13 nucleotide sequence.

(7) A genetic polymorphism detection kit comprising the oligonucleotide described above.

[Mode for Carrying Out the Invention]

The present invention relates to a method for detecting a genetic polymorphism in a test subject using the genetic polymorphism data related to a drug metabolizing enzyme. The present invention analyzes the effectiveness, safety and strength of drugs metabolized by a drug metabolizing enzyme. The relationship between a disease and the drug to be evaluated is based on the results of the analysis. The genetic polymorphism data for the drug metabolizing enzyme is different for each patient with a given disease. Therefore, the effectiveness and safety of a specific drug depends on drug metabolism in the presence of certain genetic polymorphism data and the side effects in the presence of certain genetic polymorphism data. As a result, a physician can determine whether a certain drug should be used by a certain patient and can tailor drugs for use by a certain patient based on the genetic polymorphism data (so-called "made-to-order" treatments).

1. Genetic Polymorphism

Genetic polymorphism includes single nucleotide polymorphism, insertion/deletion polymorphism, and polymorphism caused by difference in the number of repetition of a nucleotide sequence. Generally, single nucleotide polymorphism (SNP) means a polymorphism caused by substitution of one specific nucleotide with other nucleotide in a gene or its complementary strand (complementary sequence) region. In the present invention, however, the term SNP also includes the polymorphism caused by substitution above as well as a polymorphism caused by deletion of the nucleotide and a polymorphism caused by addition of one more nucleotide to the nucleotide.

Insertion/deletion type polymorphism means a polymorphism caused by deletion or insertion of a plurality of nucleotides (e.g. two to several ten nucleotides). Sometimes, several hundred to several thousand nucleotides may be deleted or inserted. The polymorphism caused by difference in the number of repetition of a nucleotide sequence has repetition of a sequence of two to several ten nucleotides, and the number of this repetition varies among individuals. Those polymorphisms where the repeat unit consists of several to several ten nucleotides are called VNTR (variable number of tandem repeats) polymorphism, and those polymorphisms where the repeat unit consists of about two to four nucleotides are called microsatellite polymorphism. In VNTR or microsatellite polymorphisms, the number of such repetition is different among individuals' alleles, which results in acquisition of variation.

2. Drug Metabolizing Enzyme

"Drug metabolizing enzymes" refer to a group of enzymes that catalyze *in vivo* structural changes in exogenous materials including drugs. When used for clinical purposes, the group of metabolizing enzymes includes some endogenous materials. Because drug-metabolizing enzymes absorb, metabolize and secrete drugs, the polymorphism of an enzyme depends on the amount of enzyme expressed (transcription and translation) and the amount of activity. As a result, there are blood serum concentrations of both unchanged materials and metabolites.

Drug metabolizing enzymes expressed by the genes that are targeted for genetic polymorphism analysis in the present invention include, but are not limited to the following classes of enzymes:

Epoxide hydrolases

Methyltransferases

N-acetyltransferases

Sulfotransferases
Quinone oxidereductases
Glutathione S-transferases
UDP-glycosyltransferases
Aldehyde dehydrogenases
Alcohol dehydrogenases
Esterases
Ubiquinone dehydrogenases : NDUF
Cytochrome P450s (CYPs)
ATP-binding cassettes
ATP-binding cassettes
Other enzymes

(1) Epoxide hydrolases are enzymes that hydrolyze epoxide using a trans-cleavage mechanism to produce 1,2-glycol. Examples include microsomal epoxide hydrolase 1 and cytoplasmic epoxide hydrolase 2.

(2) Methyltransferases are enzymes that catalyze transmethylation in amino groups, hydroxyl groups and thiol groups. Examples include the following.

Catechol-O-methyltransferase
Histamin-N-methyltransferase
Phenylethanolamine-N-methyltransferase
Phosphatidylethanolamine-N-methyltransferase
Nicotinamide-N-methyltransferase
Guanidinoacetate-N- methyltransferase
Acetylserotonin-O-methyltransferase

(3) N-acetyltransferases are enzymes that catalyze transacetylation in amino groups, sulfonamide groups and hydrazine groups. Examples include the following.

Arylamine-N-acetyltransferase 1, 2
Arylalkylamine-N-acetyltransferase
N-acetyltransferase homologues of Saccharomyces cerevisiae
LI intracellular adhesion molecules

(4) Sulfotransferases are enzymes that contribute to sulfate conjugation and catalyzes trans-sulfonylation in phenols, steroids, arylamines and biliary acid. Examples include the following.

Sulfotransferase 1A1, 1A2, 1A3, 1C1, 1C2, 2A1, 2B1

Thyroid hormone sulfotransferase

Tyrosyl protein sulfotransferase 1, 2

Sulfotransferase-opening protein 3

Estrogen sulfotransferase

Cerebroside sulfotransferase

HNK-sulfotransferase 1

Carbohydrate sulfotransferase 2, 4, 5

(5) Quinone oxidereductases are enzymes that catalyze the reduction of quinones such as o-quinone and p-quinone. Examples include the following.

NAD(P)H: Quinone oxidereductase 1

NRH: Quinone oxidereductase 2

Quinone oxide transferase homologue

(6) Glutathione S-transferases are enzymes that catalyze the conjugation of glutathione. Examples include the following.

Glutathione S-transferase Mu1, Mu2, Mu3, Mu4, Mu5

Glutathione S-transferase Z (zeta)

Glutathione S-transferase Π (pi)

Glutathione S-transferase 1 Theta 1, Theta 2

Microsomal Glutathione S-transferase 1

Microsomal Glutathione S-transferase 1-like 1

Microsomal Glutathione S-transferase 2, 3

Glutathione S-transferase Ha subunit 1, 2

Glutathione S-transferase A3, A4

(7) UDP-glycosyltransferases are enzymes that catalyze the contribution of glucuronic acid to functional groups such as hydroxyl groups, carboxyl groups, amino groups and thiol groups after their introduction in the 1st drug metabolism route. Examples include the following.

UDP-glycosyltransferase 1

UDP-glycosyltransferase 2 Family Polypeptide A1, B7, B10, B4, B11, B15, B17

UDP-glycosyltransferase 8

Dolichyl-diphospho-oligosaccharide protein glycosyl transferase

(8) Aldehyde dehydrogenases are enzyme that converts aldehydes into carboxylic acids. Examples include Aldehyde dehydrogenase 1 through 10.

(9) Alcohol dehydrogenases are enzymes that convert alcohols into aldehydes or ketones. Examples include the following.

Alcohol dehydrogenase 1 through 7

Hydroxy-CoA-dehydrogenase

Short-chain alcohol dehydrogenase family genes

(10) Esterases are enzymes that hydrolyze some esters. Examples include the following.

Arylacetoamide deacetylase

Granzyme A

Granzyme B

Interleukin 17

Ubiquitin carboxyl-terminal esterase L1, 3

Carboxyl esterase 1

Lipase A

Esterase D-formylglutathione hydrolase

Carboxylester lipase

(11) Ubiquinone dehydrogenases (NDUF) are enzymes that support energy metabolism, *e.g.*, as in the mitochondrial respiratory chain. Examples include NADH-dehydrogenase 1α-subunit 1 through 10

(12) Cytochrome P450s (CYPs) are enzymes that regulate 1st drug metabolism and introduce oxygen atoms to the drug. Examples include following.

Cytochrome P450 (CYP) 1A1, CYP 1A2, CYP 2A6, CYP 2B6, CYP 2C8, CYP 2C18, CYP 2C9, CYP 2C19, CYP 2E1, CYP 2D6, CYP 2E1, CYP 2F1, CYP 3A3, CYP 3A4, CYP 3A7, CYP 3A43, CYP 4A11, CYP 4B1, CYP 4F2, CYP 4F3, CYP 4F8, CYP 11B1, 2, CYP 17, CYP 19, CYP 21A2, CYP 27.

(13) ATP-binding cassettes/transporter absorb the drug and adjust the interstitial concentration with a transporter. Examples include the following.

ATP-Binding Cassette Subfamily A Members 1 through 6 and 8

ATP-Binding Cassette Subfamily B Members 1 through 11

ATP-Binding Cassette Subfamily C Members 1 through 6 and 8 through 10

ATP-Binding Cassette Subfamily D Members 1 through 4

ATP-Binding Cassette Subfamily E Member 1

ATP-Binding Cassette Subfamily F Members 1 through 3

ATP-Binding Cassette Subfamily G Member 1

(14) Other enzymes include gamma glutamyl transferase 1 and transglutaminase 1.

3. Information on Genetic Polymorphisms

Genetic polymorphism data can be obtained using any general genetic polymorphism detection method. Examples include PCR methods hybridization methods using an allele-specific oligonucleotide matrix (e.g., TaqMan PCR method, Invader assay method), primer extension reaction methods, sequencing methods, MALDI-TOF/MS methods and the DNA chip methods, etc. PCR methods or sequencing methods are applicable to detection of any genetic polymorphisms and the other methods are applicable to detection of SNP.

TaqMan PCR is a method using PCR reaction with a fluorescence-labeled, allele-specific oligo(s) and Taq DNA polymerase (Livak, K.J. Genet. Anal. 14, 143 (1999); Morris T. et al., J. Clin. Microbiol. 34, 2933 (1996)). The invader method is a method in which the hybridization of two reporter probes specific to respective alleles of SNP and one invader probe to the template DNA is combined with DNA cleavage by an enzyme having a special endonuclease activity of cleaving upon recognition of DNA structure (for example, see Livak, K. J. Biomol. Eng. 14, 143-149 (1999); Morris T. et al., J. Clin. Microbiol. 34, 2933 (1996); Lyamichev, V. et al., Science, 260, 778-783 (1993)).

As methods using primer extension reaction, SniPer method may be employed, for example. The basic principle of SniPer method is a technique called RCA (rolling circle amplification) method in which DNA polymerase moves on a circular single-stranded DNA as a template to thereby synthesize a complementary strand thereto continuously. According to this method, SNP may be judged by detecting the presence or absence of a coloring reaction that occurs when DNA amplification takes place (Lizardi, P. M. et al., Nature Genet., 19, 225-232 (1998); Piated, A. S. et al., Nature Biotech., 16, 359-363 (1998)).

The sequencing method refers to methods in which polymorphism-containing areas are amplified by PCR and the DNA sequences of the amplified products are sequenced with Dye Terminator or the like to thereby analyze the frequency of genetic polymorphisms (especially SNPs).

MALDI-TOF/MS method is a method using a mass spectrometer. Basically, this is a method for SNP genotyping utilizing the difference in mass of different nucleotides. There are methods using PCR amplification and methods using multiplex (Haff, L.A., Smirnov, I.P., Genome Res., 7, 378- (1997); Little, D.P. et al. Eur. J. Clinica. Chem. Clin. Biochem., 35, 545- (1997); Ross, P., et al. Nat Biotechnol., 16, 1347- (1998)).

The DNA chip method is a method in which a large variety of DNA probes are aligned and immobilized on a baseboard such as glass; then, hybridization of a labeled DNA is performed thereon; and perfect match and one-nucleotide-mismatch are detected

discriminably by using a method of detecting the label signal (such as fluorescence) on the probe.

The information on genetic polymorphisms, in particular information on SNPs, which may be used in the method of the present invention is as shown in Table 1 below.

[Table 1]

In Table 1, the "Designation of Gene" column shows the designations of the genes encoding receptors. The nucleotides expressed with capital letters in the "Sequence" column are the SNP information. The two nucleotides on both sides of the mark "/" represent a homozygous or heterozygous SNP of the nucleotide. For example, "A/G" means that the allele is A/A or G/G homozygote or A/G heterozygote. The sequences in this Table basically represent 20 nucleotides each before and after the SNP. However, the nucleotide in parentheses [e.g. (T) in No. 26 of ABCB4] represents a polymorphism caused by insertion. The mark of open triangle (e.g. see No. 10 of NAT2) means a polymorphism caused by deletion of one nucleotide. In the nucleotide sequence in SEQ ID NO:674, n means VNTR and represents repeat sequence consisting of (cctgy)x (X represents integer of 1 to 50). The nucleotide in parentheses provided with a number means that the nucleotide in the parentheses is repeated that number of times. For example, "(T) 9-12" appearing in SEQ ID NO: 1552 (Table 1, No. 55 of ABCB11) means a sequence where T is repeated from 9 to 12 times.

The "Location" shows the location of SNP in the genome. The locations of SNPs in 5' flanking region, intron regions and 3' flanking region are counted taking the first nucleotide located immediately to the exon/intron junction as position 1 of the nucleotide sequence of the intron. The locations of SNPs in exon region are counted taking the first nucleotide located immediately to the exon/intron junction as position 1 of the nucleotide sequence of the exon. Numbers with "+" mark or without any mark mean that they are counted toward the 3' end of the gene; numbers with "-" mark mean that they are counted toward the 5' end of the gene. The numbers appearing in the "No." column correspond to the numbers appearing in respective gene maps (Figs. 9-141) which show the locations of SNPs.

4. Preparation of Oligonucleotide Probes or Oligonucleotide Primers

Oligonucleotides which are used in the detection method of the present invention as primers and/or probes may be prepared based on the nucleotide sequences described in Table 1 (SEQ ID NOS: 1-3360), for example, when SNPs are to be detected, and these sequences

per se may be synthesized, or primers and/or probes may be designed and synthesized so that they contain a part of these sequences. However, it should be noted here that the nucleotide sequences of such primers or probes must contain an SNP (the portion indicated in capital letters in the "Sequence" column in Table 1). The present invention also includes complementary strands to such sequences.

Taking SNP as an example for the purpose of illustration, a primer or probe is designed so that an SNP site is located at the 3' or 5' end of the nucleotide sequence of the primer or probe; or a primer or probe is designed so that an SNP site is located at the 3' or 5' end of the sequence complementary to its nucleotide sequence; or a primer or probe is designed so that an SNP site is located within four nucleotides, preferably two nucleotides, from the 3' or 5' end of its nucleotide sequence or the sequence complementary thereto. Alternatively, a primer or probe is designed so that an SNP site is located at the center of the full-length nucleotide sequence of the oligonucleotide. The "center" refers to a central region where the number of nucleotides counted from there toward the 5' end and the number of nucleotides counted from there toward the 3' end are almost equal. If the number of nucleotides of the oligonucleotide is an odd number, the "center" is the central five nucleotides, preferably the central three nucleotides, more preferably the single nucleotide at the very center. For example, if the oligonucleotide consists of 41 nucleotides, the "center" is from position 19 to position 23 nucleotides, preferably from position 20 to position 22 nucleotides, more preferably the nucleotide at position 21. If the number of nucleotides of the oligonucleotide is an even number, the "center" refers to the central four nucleotides, preferably the central two nucleotides. For example, if the oligonucleotide consists of 40 nucleotides, the "center" is from position 19 to position 22 nucleotides, preferably the nucleotide at position 20.

If the polymorphism consists of a plurality of bases, the probe/primer is designed so the full polymorphism sequence is contained in the probe/primer. In some preferred embodiments, it is designed so one of the bases 1 through 4 on the 5' end or 3' end complementing the primer DNA corresponds to the base at the very end of the polymorphism bases. (This is called the "corresponding base"; ideally, it is the base at the 5' or 3' end). For example, in the INVADER assay, if a probe and INVADER oligonucleotide are prepared to detect a genetic polymorphism (CAGAGGCT) in No. 12 of NDUFA7 in Table 1 (SEQ ID NO: 828), the position of the corresponding base in the probe in FIG 4a (a "T" base in the figure) is designed to become "C" at the far left of sequence CAGAGGCT, and the N base in the INVADER oligonucleotide shown in FIG 4b is designed to replace the "C" at the far left of CAGAGGCT with A, T, C or G). Conversely,

if designed so the position of the corresponding base in the INVADER oligonucleotide is the far right "T" in CAGAGGCT, the "N" base is such that the corresponding base in the probe is "T." Further, the corresponding base of the INVADER oligonucleotide and the allele probe can be set anywhere in the CAGAGGCT sequence.

The length of the nucleotide sequence is designed so that at least 13 nucleotides, preferably 13 to 60 nucleotides, more preferably 15 to 40 nucleotides, and most preferably 18-30 nucleotides are contained. This oligonucleotide sequence may be used as a probe for detecting a target gene, and it may be used as either a forward (sense) primer or a reverse (antisense) primer.

The oligonucleotide used in the invention may be an oligonucleotide composed of two regions connected in tandem, one region being hybridizable to the genomic DNA and the other region being not hybridizable thereto. The order of connection is not particularly limited; either region may be located upstream or downstream. The hybridizable region of this oligonucleotide is designed based on the information on SNP-containing sequences described in Table 1. The oligonucleotide is prepared so that the nucleotide located at the 5' or 3' utmost end of the region hybridizable to the genomic DNA corresponds to an SNP of interest. The region of the above oligonucleotide not hybridizable to the genomic DNA is designed at random so that it does not hybridize to the SNP-containing sequence described in Table 1. This oligonucleotide may be used as a probe mainly for detecting SNPs in the invader method.

Further, the primer used in the present invention is designed so that a nucleotide sequence given in Table 1 contains a SNP when amplified by PCR for the purposes of examining functional changes resulted from the SNP, judging the efficacy or non-efficacy, and examining the occurrence of side effect. The length of the primer is designed so that at least 15 nucleotides, preferably 15 to 30 nucleotides, more preferably 18 to 24 nucleotides are contained in the primer. The primer sequence is appropriately selected from the template DNA so that the amplified fragment has a length of 500 bp or less, preferably 100 to 300 bp, more preferably 100 to 150 bp.

The thus designed oligonucleotide primers or probes may be synthesized chemically according to known techniques. Usually, such primers or probes are synthesized with a commercial chemical synthesizer.

It is also possible to label probes with fluorescent substances (e.g. FAM, VIC, Cy3, etc.) in advance to thereby automate detection procedures.

The above-described oligonucleotide may be included in a genetic polymorphism detection kit together with polymerases (e.g. Taq polymerase), buffers (e.g. Tris buffer),

dNTPs and fluorescent dyes such as VIC, FAM.

5. Detection

Using the oligonucleotides prepared as described above as primers, a gene encoding a drug metabolizing enzyme (template DNA) is amplified with a DNA polymerase. Alternatively, the probe prepared as described above is hybridized to template DNAs to thereby detect those DNAs having the genetic polymorphism of interest. The template DNA may be prepared according to conventional methods, e.g. cesium chloride gradient centrifugation, the SDS lysis method, or phenol/chloroform extraction.

(1) Detection by PCR

Amplification may be performed by polymerase chain reaction (PCR). Specific examples of useful DNA polymerase include LA Taq DNA polymerase (Takara), Ex Taq polymerase (Takara), Gold Taq polymerase (Perkin Elmer), AmpliTaq (Perkin Elmer), Pfu DNA polymerase (Stratagene) and the like.

Amplification conditions are as follows. Denaturation step at 85-105°C for 10-40 seconds, preferably at 94°C for 20-30 seconds; annealing step at 50-72°C for 30 seconds to 1 minute, preferably at 60°C for 20 seconds to 1 minutes; and extension step at 65-75°C for 1-4 minutes, preferably at 72°C for 2-3 minutes constitute one cycle, and 30 to 40 cycles are performed. However, in order to denature the template DNA and the primers sufficiently, a denaturation step of at 95°C for 1-5 minutes [if Gold Taq polymerase (Perkin Elmer) is used, at least 8-15 minutes, preferably 10-12 minutes] may be added before the start of the above-described amplification cycles. Also, in order to extend the amplified DNA completely, an extension step of at 72°C for 1-10 minutes may be added after the above amplification cycles. Moreover, if the detection of the amplified product is not performed immediately, it is desirable to add a step of storing the amplified product at 4°C to avoid unspecific amplification. Thus, a gene encoding a receptor can be amplified.

Subsequently, the amplified product is subjected to agarose gel electrophoresis, followed by staining with ethidium bromide, SYBR Green solution or the like to thereby detect the amplified product as a band or two to three bands (DNA fragments). Thus, a part of a gene encoding a drug metabolizing enzyme, containing a genetic polymorphism can be detected as a DNA fragment. Instead of agarose gel electrophoresis, polyacrylamide gel electrophoresis or capillary electrophoresis may be performed. It is also possible to perform PCR using primers labeled in advance with a substance such as fluorescent dye and to detect the amplified product. A detection method which does not require electrophoresis may also be employed; in such a method, the amplified product is bound to a solid support

such as a microplate, and a DNA fragment of interest is detected by means of fluorescence, enzyme reaction, or the like.

(2) Detection by TaqMan PCR

TaqMan PCR is a method using PCR reaction with fluorescently labeled allele-specific oligos and Taq DNA polymerase. The allele-specific oligo used in TaqMan PCR (called "TaqMan probe") may be designed based on the SNP information described above. The 5' end of TaqMan probe is labeled with fluorescence reporter dye R (e.g. FAM or VIC), and at the same time, the 3' end thereof is labeled with quencher Q (quenching substance) (Fig. 1). Thus, under these conditions, fluorescence is not detectable since the quencher absorbs fluorescence energy. Since the 3' end of TaqMan probe is phosphorylated, no extension reaction occurs from TaqMan probe during PCR reaction (Fig. 1). However, when PCR reaction is performed using this TaqMan probe together with Taq DNA polymerase and primers designed so that an SNP-containing region is amplified, the reaction described below occurs.

First, a TaqMan probe hybridizes to a specific sequence in the template DNA (Fig. 2a), and at the same time, an extension reaction occurs from a PCR primer (Fig. 2b). At this time, Taq DNA polymerase having 5' nuclease activity cleaves the hybridized TaqMan probe as the extension reaction of PCR primer proceeds. When the TaqMan probe has been cleaved, the fluorescent dye becomes free from the influence of the quencher. Then, fluorescence can be detected (Fig. 2c).

For example, as shown in Fig. 3, two alleles are supposed: one allele has A at the SNP site (allele 1) and the other allele has G at the SNP site (allele 2). A TaqMan probe specific to allele 1 is labeled with FAM and another TaqMan probe specific to allele 2 is labeled with VIC (Fig. 3). These two allele specific oligos are added to PCR reagents, and then TaqMan PCR is performed with a template DNA whose SNP is to be detected. Subsequently, fluorescence intensities of FAM and VIC are determined with a fluorescence detector. When the SNP site of the allele is complementary to the site within TaqMan probe corresponding to the SNP, the probe hybridizes to the allele; and Taq polymerase cleaves the fluorescent dye of the probe, which becomes free form the influence of the quencher. As a result, fluorescence intensity is detected.

If the template is a homozygote of allele 1, strong fluorescence intensity of FAM is recognized but the fluorescence of VIC is hardly recognized. If the template is a heterozygote of allele 1 and allele 2, fluorescence of both FAM and VIC can be detected.

(3) SNP Detection by the Invader Method

The invader method is a method for detecting SNPs by hybridizing allele-specific

oligos to the template. In the invader method, two unlabeled oligos and one fluorescently labeled oligo are used. One of the two unlabeled oligos is called an "allele probe". The allele probe is composed of a region which hybridizes to the genomic DNA (template DNA) to form a complementary double strand, and a region (called "flap") which has a sequence entirely unrelated to the sequence of the template DNA and thus does not hybridize to the genomic DNA. A nucleotide located at the 5' or 3' utmost end of the hybridizable region corresponds to the SNP (Fig. 4a). The above-described flap sequence is an oligonucleotide having a sequence complementary to a FRET probe described later. The other oligo is called an "invader probe". This oligo is designed so that it hybridizes complementarily from the SNP site toward the 3' end of the genomic DNA (Fig. 4b). However, the nucleotide corresponding to the SNP ("N" in Fig. 4b) may be any nucleotide. Thus, when the genomic DNA (the template) is hybridized to the above-described two probes, one nucleotide (N) of the invader probe invades into the SNP position (Fig. 4c) forming a triple strand at the SNP site.

On the other hand, the fluorescently labeled oligo has a sequence completely unrelated to the allele. This sequence is common regardless of the types of SNPs. This probe is called a "FRET" probe (fluorescence resonance energy transfer probe) (Fig. 5). The nucleotide at the 5' end of FRET probe (reporter) is labeled with fluorescent dye R, while quencher Q is linked upstream of the reporter. Therefore, under these conditions, the quencher absorbs the fluorescent dye and no fluorescence is detectable. A certain region of the FRET probe starting from the 5' end reporter nucleotide (designated "region 1") is also designed so that it is complementary to a certain region of the probe located 3' to region 1 (designated "region 2") when region 1 and region 2 are faced with each other. Therefore, region 1 and region 2 form a complementary strand within the FRET probe (Fig. 5). Also, the region located toward 3' end of this complementary strand forming region is designed so that it hybridizes to the flap of the allele probe to thereby form a complementary strand (Fig. 5).

In the invader method, an enzyme called cleavase is used which is one of enzymes (5' nucleotidases) having a unique endonuclease activity of cleaving upon recognition of a special structure of DNA. Cleavase is an enzyme which cleaves the allele probe at a point immediately 3' to the SNP site when the genomic DNA, the allele probe and the invader probe form a triple strand at the SNP site. Therefore, when three nucleotides form a triple strand as shown in Fig. 4c, cleavase recognizes the 5' flap and cuts off this flap. As a result, the structure of this SNP site is recognized by cleavage (Fig. 6a), and the allele probe is cut at the site of its flap to liberate the flap (Fig. 6b). Subsequently, the flap liberated from the

allele probe complementarily binds to the FRET probe since it has a sequence complementary to the FRET probe (Fig. 6c). At this time, the SNP site of the flap invades into the portion of the FRET probe which has already formed a complementarily bound region. Cleavase again recognizes this structure and cuts off the nucleotide labeled with the fluorescent dye. The thus cleaved fluorescent dye becomes free from the influence of the quencher and emits fluorescence (Fig. 6d). When the SNP does not match the nucleotide corresponding to the SNP in the allele probe, a specific DNA structure recognizable by cleavase is not formed as seen in Fig. 7. Thus, the probe is not cleaved and no fluorescence is detected.

For example, when an SNP is T/C, an invader probe and an allele probe for T, and a FRET probe with a FAM-linked reporter corresponding to the SNP are prepared. Separately, an invader probe and an allele probe for C, and a FRET probe with a VIC-linked reporter corresponding to the SNP are also prepared. Then, all of them are mixed to carry out SNP detection. As a result, if the SNP is T/T homozygous, the fluorescence of FAM is emitted; if the SNP is C/C homozygous, the fluorescence of VIC is emitted; and if the SNP is T/C heterozygous, the fluorescence of both FAM and VIC is emitted. Since FAM and VIC have different fluorescent wavelengths, they can be discriminated.

(4) Detection by SniPer Method

In order to detect SNPs by SniPer method, it is possible to discriminate alleles by examining the presence or absence of amplification by RCA. Briefly, the genomic DNA to be used as a template is linearized. Then, a probe is hybridized to this genomic DNA. When the probe sequence and the sequence of the genomic DNA as a template are complementary to each other and form a complementary strand, the genomic DNA can be converted into a circular DNA through ligation reaction. As a result, RCA of the circular DNA proceeds. On the other hand, when the ends of the probe do not match with the genomic DNA, the DNA is not ligated to become a circular DNA. Thus, RCA reaction does not proceed. Therefore, in Sniper method, a single-stranded probe which anneals with the genomic DNA and is circularizable is designed. This single-stranded probe is called a padlock probe. The sequences of the two ends of this padlock probe are designed so that they correspond to the SNP to be detected. Then, this padlock probe and the genomic DNA are mixed for ligation. If the two ends of the padlock probe and the SNP site of the genomic DNA are complementary to each other, the two ends of the padlock probe are joined by ligation, yielding a circular probe. If the two ends of the padlock probe and the SNP site of the genomic DNA are not complementary to each other, the probe does not become circular. Therefore, only those padlock probes which are complementary to the

SNP to be detected become circular and are amplified by DNA polymerase. By detecting the presence or absence of this amplification, SNP may be detected. For the detection, synthetic oligonucleotides which have a fluorescent dye and a quencher at their respective ends and also have a hairpin structure are used.

(5) Detection by MALDI-TOF/MS Method

MALDI-TOF/MS (Matrix Assisted Laser Disorption-Time of Flight/Mass Spectrometry) is a method using a mass spectrometer in SNP typing. This method is composed of the following steps.

(i) PCR Amplification and Purification of SNP-Containing DNA Fragments

PCR primers are designed so that there is no overlapping between them and the nucleotides of SNP site. Then, DNA fragments are amplified. The amplified fragments are purified from the amplification reaction product by treatment with exonuclease, alkaline phosphatase, etc. to remove primers, dNTPs, etc.

(ii) Primer Extension (Thermal Cycling) and Purification

Ten-fold or more primers are added to the template of the target region (which is the PCR product), and primer extension is performed by thermal cycling. The primers used here are designed so that their 3' ends are adjacent to the nucleotide of the SNP site. The length of the primer is 15 to 30 nucleotides, preferably 20 to 25 nucleotides. When multiplex reaction is performed, a sequence not complementary to the template is added to the 5' end. Thermal cycling is performed between the two temperatures of at 85-105°C (preferably 94°C) and at 35-40°C (preferably 37°C) for 20 to 30 cycles (preferably 25 cycles). The resultant reaction products are purified with a purification kit or the like to make them fit for mass spectrometer.

(iii) Mass Spectrometry of DNA with Mass Spectrometer

The purified extension reaction product is applied to a mass spectrometer to determine the mass of the objective product. Briefly, the purified product is mixed with a matrix, and 0.5-1.0 μl of the mixture is spotted on MALDI plate. After drying the plate, laser light is applied to the sample to prepare spectrograms.

(6) Detection by DNA Sequencing Method

In the present invention, polymorphisms may be detected by using single nucleotide extension reactions. Briefly, four types of dideoxynucleotides labeled with different fluorescent compounds are added to a reaction system containing a gene of interest. Then, single nucleotide extension reactions are performed. In this case, the nucleotide to be extended is the polymorphic site. Also, two reactions of DNA synthesis termination and the fluorescent labeling of the 3' end of DNA molecules are operated. Four types of

reaction solutions are subjected to electrophoresis on the same lane of a sequencing gel or on capillary. Difference in the fluorescent dyes used for labeling is detected with a fluorescence detector to thereby sequence the DNA band. Alternatively, the one-nucleotide extended oligonucleotide is examined with a fluorescence detection system or a mass spectrometry system or the like to thereby determine which nucleotide was extended using the difference in the fluorescent dyes. Instead of fluorescently labeled dideoxynucleotides, primers may be fluorescently labeled and used with unlabeled dideoxynucleotides.

6. Evaluation of Drugs

In the present invention, it is possible to evaluate the efficacy and safety of a drug intermediated by the receptor, from the results of detection of SNP and like that obtained as described above.

Evaluation of drugs may be performed by typing system. Briefly, according to any one of the detection methods described above, allele frequencies between toxicity (side effect) occurrence group and non-occurrence group are compared. A polymorphism which brings about difference in allele frequencies between the two groups is selected as a marker for recognizing the occurrence of toxicity. As a statistical test, usually chi square test is carried out, but other statistical processing such as Fisher test may also be used. The active components (altered and metabolized drug components) in the drug will be reflected in blood and tissue concentrations. With respect to all genetic polymorphisms, the relation of cause and effect with the action or toxicity is examined. Then, only those genetic polymorphism sites that show correlation with the action or toxicity are selected. Allele pattern can be examined by preparing in advance all probes or primers for analyzing the genetic polymorphisms and reagents necessary for each technique in reaction plates, cards, glass baseboards or the like, and adding thereto the genomic DNA of a human subject for reaction. When the subject has a genetic polymorphism which has correlation with the toxicity, it is possible to predict whether the drug exhibits toxicity in that subject. The efficacy of a drug may be evaluated in a similar manner. Also, genetic polymorphisms which correlate with side effect or efficacy vary depending on drugs. Therefore, by conducting typing using correlating genetic polymorphisms for each drug, it becomes possible to predict the efficacy or side effect of the relevant drug.

Using this, the frequency of the relevant genetic polymorphism is compared with efficacy/non-efficacy or presence/absence of side effect. When there is difference in allele frequency, a judgment on the relevant drug can be made.

For example, if the results of analysis of an SNP in persons who showed toxicity

(side effect) upon administration of drug A have revealed statistically that 90% of those persons have T/T (e.g. fluorescence intensity of FAM was detected), and if the results of analysis of the SNP in persons who did not show toxicity (side effect) have revealed that only 10% of those persons have T/T and 90% of them have C/C, drug A can be evaluated that it should not be administered to persons with T/T.

7. Screening for Drugs.

In the present invention, the genetic polymorphism data obtained as described above is compared to genetic polymorphism data from genes encoding certain drug metabolizing enzymes to indicate the safety and effectiveness of drugs metabolized by these drug metabolizing enzymes. Therefore, the genetic polymorphism data obtained using the method of the present invention can be used to determine the likely effectiveness of certain drug therapies and to select the appropriate drug.

As a method, the evaluation method described in "5. Evaluation of Drugs" may be used. Genetic polymorphisms with correlations to side-effects and effectiveness are said to be influenced by the activation, transfer and translation of certain enzymes. The cause and effect relationship with the side-effect or effectiveness expression mechanism may be indirect. The metabolization of drugs is being studied by pharmaceutical companies in laboratory and clinical testing. If there are genetic polymorphisms in enzyme genes correlating with severe side-effects, they can be removed and used under different conditions. The same is true of effectiveness. Drugs can be screened, therefore, using side-effects and effectiveness data.

Further, by conducting genetic polymorphism frequency analysis on cases of volunteers with side effect occurrence and cases without side effect occurrence in clinical tests (from phase I to phase III tests), it becomes possible to detect new genetic polymorphisms other than the above-mentioned polymorphism which correlate with side effect or efficacy. By examining such polymorphisms in the same manner as described above, drug screening becomes possible.

[Examples]

Hereinbelow, the present invention will be described more specifically with reference to the following Example. However, the technical scope of the present invention is not limited to the Example.

[EXAMPLE 1] Obtaining SNP Information

(1) DNA Extraction

Blood samples were collected in the presence of EDTA from 48 individuals who have no kinship relation with one another. DNA extraction was carried as described below according to the method described in "Genome Analysis Laboratory Manual" (Yusuke Nakamura (ed.), Springer Verlag Tokyo).

Blood sample (10 ml) was transferred to a 50 ml Falcon tube and centrifuged at room temperature at 3000 rpm for 5 minutes. After removal of the supernatant (serum) with a pipette, 30 ml of RBC lysis buffer (10mM NH_4HCO_3, 144mM NH_3Cl) was added and mixed until the precipitate became loosened. Then, the mixture was left at room temperature for 20 minutes. After centrifugation at room temperature at 3000 rpm for 5 minutes, the supernatant (serum) was discarded with a pipette to obtain a pellet of white blood cells. RBC lysis buffer (30 ml) was added thereto, and the above-described operations were repeated twice. To the resultant white blood cell pellet, 4 ml of Proteinase K buffer (50mM Tris-HCl (pH7.4), 100mM NaCl, 1mM EDTA (pH8.0)), 200 μl of 10% SDS, and 200 μl of 10 mg/ml Proteinase K were added and mixed by inversion. The resultant mixture was left overnight stationery at 37°C. Subsequently, 4 ml of phenol was added to the mixture, which was then mixed slowly by inversion for 4 hours in a rotator (Rotator T-50, Taitec). After centrifugation at room temperature at 3000 rpm for 10 minutes, the resultant upper layer was collected into a fresh tube. Four milliliters of phenol/chloroform/isoamyl alcohol (25:24:1 in volume ratio) was added to the tube and mixed by inversion for 2 hours in the same manner as described above. Then, the mixture was centrifuged. The resultant upper layer was collected into a fresh tube, to which 4 ml of chloroform/isoamyl alcohol (24:1 in volume ratio) was added and mixed by inversion for 30b minutes in the same manner as described above. Then, the mixture was centrifuged. The resultant upper layer was collected into a fresh tube, to which 400 μl of 8M ammonium acetate and 4 ml of isopropanol were added and mixed by inversion. Thread-like white deposit (DNA) was recovered into a 2 ml tube, to which 70% ethanol (1 ml) was added and mixed by inversion. The DNA was recovered into a fresh 2 ml tube and air-dried. Then, 500 μl of TE solution (10mM Tris-HCl (pH7.4), 1mM EDTA (pH7.4)) was added for lysis, to thereby obtain a genomic DNA sample.

(2) PCR

Genomic sequences were obtained from GenBank DNA database. After removal of repeat sequences using RepMask computer program, PCR primers were designed so that PCR products have a length of about 1 kb. As genomic DNA, DNA samples obtained from 48 individuals who have no kinship relation with one another and prepared to have the same concentration were used. DNA samples derived from three individuals each were mixed in

a tube in equal amounts. Of this mixture, 60 ng was used in PCR. PCR was performed with Ex-Taq (2.5 U; Takara) using GeneAmp PCR System 9700 (PE Applied Biosystems). Following a reaction at 94°C for 2 minutes, 35 cycles of denaturation at 94°C for 30 seconds, annealing at 60°C or 55°C for 30 seconds and extension at 72°C for 1 minute were performed.

(3) Sequencing

PCR products were purified with Arraylt (Telechem) and subjected to sequencing reaction using BigDye Terminator RR Mix (PE Applied Biosystems). Briefly, following a reaction at 96°C for 2 minutes, 25 cycles of denaturation at 96°C for 20 seconds, annealing at 50°C for 30 seconds and extension at 60°C for 4 minutes were performed using GeneAmp PCR System 9700 (PE Applied Biosystems). After the sequencing reaction, sequences were analyzed with ABI PRISM 3700 DNA Analyzer.

(4) Detection of SNPs

PolyPhred computer program (Nickerson et al., 1997, Nucleic Acids Res., 25, 2745-2751) was used for the detection and analysis of SNPs.

(5) Results

The results as shown in Table 1 were obtained on SNPs. Figs. 9 to 141 show the designations, abbreviations and GenBank database Accession Nos. of the analyzed drug metabolizing enzyme, the structures of the genes encoding them, and the locations of SNPs. In Figs. 9 to 141, exons are indicated as open boxes or black lines on the relevant gene expressed as a horizontal line. The locations of SNPs are indicated above the gene with solid lines provided with numbers.

[Example 2]

Typing was performed on two different groups of patients using the INVADER assay. Results are shown in FIG. 142. In FIG 142, the x-axis (Allele 1) indicates the intensity of the FAM fluorescent light corresponding to T, and the x-axis (Allele 2) indicates the intensity of the VIC fluorescent light corresponding to C. The slanted line indicates the SNP pattern for T/T, the black circles denote the pattern for C/C, and the white circles denote the pattern for T/C. The black squares indicate the background values. The x marks indicate where the detection failed. The group of patients in the graph for panel A (top) had many C/C SNP patterns and the group of patients in the graph for panel B (bottom) had many T/T SNP patterns.

[Exmple 3] SNP Detection

Genome DNA was extracted from five unrelated people using the method described in Example 1, and the SNPs in three different drug metabolizing enzyme genes (EPHX1, ABCB2, AANAT) were detected using the INVADER assay method. The INVADER oligonucleotides and probes were designed using base sequence No. 3 (SEQ ID NO: 49) and No. 17 (SEQ ID NO: 63) in the case of EPHX1, base sequence No. 4 (SEQ ID NO: 4) and No. 11 (SEQ ID NO: 11) in the case of ABCB2, and base sequence No. 3 (SEQ ID NO: 561) in the case of AANAT. The positions of the SNPs are shown in Table 1.
The results are shown in Table 2.

Table 2

Drug Metabolizing Enzyme Gene	EPHX1		ABCB2		AANAT
	No. 3	No. 17	No. 4	No. 11	No. 3
	SEQ. ID No. 49	SEQ. ID No. 63	SEQ. ID No. 4	SEQ. ID No. 11	SEQ. ID No. 561
SNP	(T/G)	(A/G)	(G/T)	(G/A)	(T/A)
Subject I	T/T	A/G	T/T	G/A	T/T
Subject II	T/T	A/A	G/G	G/G	T/A
Subject III	T/G	A/A	G/G	A/A	T/T
Subject IV	G/G	A/G	G/T	G/G	T/T
Subject V	T/G	A/G	G/T	G/A	T/A

As shown in Table 2, the SNPs in the drug metabolizing genes of patients can be detected and the patterns determined using the method of the present invention.

[Effect of the Invention]

According to the present invention, methods for analyzing SNPs are provided. According to the methods of the invention, it becomes possible to select appropriate drugs for target diseases. Thus, the methods of the invention are extremely useful.

[SEQUENCE LISTING]

[SEQUENCE LISTING FREE TEXT]

SEQ ID NO 39 : n represents t (Location 21).

SEQ ID NO 64 : n represents c (Location 21).

SEQ ID NO 580 : n represents a or deletion (Location 21).

SEQ ID NO 634 : n represents a or deletion (Location 21).

SEQ ID NO 656 : n represents a or deletion (Location 21).

SEQ ID NO 658 : n represents c or deletion (Location 21).

SEQ ID NO 671 : n represents a or deletion (Location 21).
SEQ ID NO 672 : n represents g or deletion (Location 21).
SEQ ID NO 673 : n represents c or deletion (Location 21).
SEQ ID NO 674 : n represents $(cctgy)_X$ (Location 21).
SEQ ID NO 676 : n represents gaa or deletion (Location 21).
SEQ ID NO 677 : n represents ag or deletion (Location 21).
SEQ ID NO 785 : n represents ta (Location 21).
SEQ ID NO 797 : n represents acac (Location 21).
SEQ ID NO 806 : n represents gatttgtggtatccag (Location 21).
SEQ ID NO 808 : n represents ag or deletion (Location 21).
SEQ ID NO 809 : n represents ta or deletion (Location 21).
SEQ ID NO 815 : n represents t (Location 21).
SEQ ID NO 828 : n represents cagaggct (Location 21).
SEQ ID NO 830 : n represents ca or deletion (Location 21).
SEQ ID NO 831 : n represents ag or deletion (Location 21).
SEQ ID NO 843 : n represents gtaaa (Location 21).
SEQ ID NO 845 : n represents a (Location 21).
SEQ ID NO 888 : n represents tc (Location 21).
SEQ ID NO 890 : n represents t or deletion (Location 21).
SEQ ID NO 913 : n represents t or deletion (Location 21).
SEQ ID NO 932 : n represents t or deletion (Location 21).
SEQ ID NO 933 : n represents t or deletion (Location 21).
SEQ ID NO 955 : n represents at or deletion (Location 21).
SEQ ID NO 956 : n represents a or deletion (Location 21).
SEQ ID NO 957 : n represents c or deletion (Location 21).
SEQ ID NO 987 : n represents c (Location 21).
SEQ ID NO 999 : n represents gtt or deletion (Location 21).
SEQ ID NO 1164 : n represents at (Location 21).
SEQ ID NO 1166 : n represents c or deletion (Location 21).
SEQ ID NO 1167 : n represents t or deletion (Location 21).
SEQ ID NO 1168 : n represents t or deletion (Location 21).
SEQ ID NO 1169 : n represents g (Location 21).
SEQ ID NO 1171 : n represents c (Location 21).
SEQ ID NO 1173 : n represents t (Location 21).
SEQ ID NO 1175 : n represents c or deletion (Location 21).

SEQ ID NO 1200 : n represents a or deletion (Location 21).
SEQ ID NO 1204 : n represents a (Location 21).
SEQ ID NO 1207 : n represents tt (Location 21).
SEQ ID NO 1210 : n represents at (Location 21).
SEQ ID NO 1245 : n represents t (Location 21).
SEQ ID NO 1248 : n represents t or deletion (Location 21).
SEQ ID NO 1249 : n represents t (Location 21).
SEQ ID NO 1251 : n represents a or deletion (Location 21).
SEQ ID NO 1252 : n represents tgt or deletion (Location 21).
SEQ ID NO 1260 : n represents t or deletion (Location 21).
SEQ ID NO 1309 : n represents a or deletion (Location 21).
SEQ ID NO 1389 : n represents g or deletion (Location 21).
SEQ ID NO 1411 : n represents a or deletion (Location 21).
SEQ ID NO 1417 : n represents aaag (Location 21).
SEQ ID NO 1424 : n represents gtg or deletion (Location 21).
SEQ ID NO 1426 : n represents gg or tggtggggtgga (Location 21).
SEQ ID NO 1429 : n represents at or deletion (Location 21).
SEQ ID NO 1436 : n represents a (Location 21).
SEQ ID NO 1453 : n represents c or deletion (Location 21).
SEQ ID NO 1456 : n represents gg (Location 21).
SEQ ID NO 1465 : n represents gtc or deletion (Location 21).
SEQ ID NO 1487 : n represents t or deletion (Location 21).
SEQ ID NO 1494 : n represents tt (Location 21).
SEQ ID NO 1497 : n represents 9 to 12 repeats of t (Location 21).
SEQ ID NO 1499 : n represents a or deletion (Location 21).
SEQ ID NO 1501 : n represents 10 to 13 repeats of a (Location 21).
SEQ ID NO 1504 : n represents ct or deletion (Location 21).
SEQ ID NO 1507 : n represents cagatcttcttcagctaatttagaaatgt (Location 21).
SEQ ID NO 1533 : n represents a or deletion (Location 21).
SEQ ID NO 1540 : n represents c (Location 21).
SEQ ID NO 1545 : n represents t (Location 21).
SEQ ID NO 1552 : n represents 9 to 12 repeats or t (Location 21).
SEQ ID NO 1555 : n represents t (Location 21).
SEQ ID NO 1557 : n represents aaaaaaagaaaa (Location 21).
SEQ ID NO 1558 : n represents aaaaaaaaaaaa (Location 21).

SEQ ID NO 1559 : n represents aaaaaaaaaa (Location 21).
SEQ ID NO 1563 : n represents t or deletion (Location 21).
SEQ ID NO 1572 : n represents c (Location 21).
SEQ ID NO 1574 : n represents a or deletion (Location 21).
SEQ ID NO 1575 : n represents c or deletion (Location 21).
SEQ ID NO 1596 : n represents cct or deletion (Location 21).
SEQ ID NO 1598 : n represents tc (Location 21).
SEQ ID NO 1616 : n represents ca or deletion (Location 21).
SEQ ID NO 1638 : n represents g (Location 21).
SEQ ID NO 1661 : n represents t or deletion (Location 21).
SEQ ID NO 1690 : n represents gccag (Location 21).
SEQ ID NO 1718 : n represents t (Location 21).
SEQ ID NO 1723 : n represents c or deletion (Location 21).
SEQ ID NO 1729 : n represents tc or deletion (Location 21).
SEQ ID NO 1740 : n represents ct or deletion (Location 21).
SEQ ID NO 1771 : n represents a (Location 21).
SEQ ID NO 1781 : n represents a or deletion (Location 21).
SEQ ID NO 1787 : n represents t or deletion (Location 21).
SEQ ID NO 1791 : n represents t or deletion (Location 21).
SEQ ID NO 1792 : n represents g or deletion (Location 21).
SEQ ID NO 1800 : n represents t or deletion (Location 21).
SEQ ID NO 1801 : n represents t or deletion (Location 21).
SEQ ID NO 1802 : n represents a or deletion (Location 21).
SEQ ID NO 1815 : n represents a or deletion (Location 21).
SEQ ID NO 1819 : n represents ca or deletion (Location 21).
SEQ ID NO 1820 : n represents t or deletion (Location 21).
SEQ ID NO 1824 : n represents t or deletion (Location 21).
SEQ ID NO 1829 : n represents t or deletion (Location 21).
SEQ ID NO 1830 : n represents c or deletion (Location 21).
SEQ ID NO 1838 : n represents a or deletion (Location 21).
SEQ ID NO 1840 : n represents t or deletion (Location 21).
SEQ ID NO 1847 : n represents gatt or deletion (Location 21).
SEQ ID NO 1848 : n represents t (Location 21).
SEQ ID NO 1853 : n represents t or deletion (Location 21).
SEQ ID NO 1854 : n represents gt (Location 21).

SEQ ID NO 1857 : n represents a or deletion (Location 21).
SEQ ID NO 1858 : n represents a or deletion (Location 21).
SEQ ID NO 1862 : n represents t or deletion (Location 21).
SEQ ID NO 1865 : n represents at or deletion (Location 21).
SEQ ID NO 1871 : n represents a or deletion (Location 21).
SEQ ID NO 1874 : n represents t or deletion (Location 21).
SEQ ID NO 1877 : n represents at or deletion (Location 21).
SEQ ID NO 1878 : n represents a or deletion (Location 21).
SEQ ID NO 1879 : n represents 12 to 14 repeats of t (Location 21).
SEQ ID NO 1882 : n represents t or deletion (Location 21).
SEQ ID NO 1884 : n represents cac or deletion (Location 21).
SEQ ID NO 1891 : n represents cca (Location 21).
SEQ ID NO 1919 : n represents t or deletion (Location 21).
SEQ ID NO 1949 : n represents c or deletion (Location 21).
SEQ ID NO 1957 : n represents aaaa or deletion (Location 21).
SEQ ID NO 1970 : n represents c or deletion (Location 21).
SEQ ID NO 1980 : n represents 7 to 9 repeats of t (Location 21).
SEQ ID NO 1981 : n represents a or deletion (Location 21).
SEQ ID NO 1993 : n represents taac or deletion (Location 21).
SEQ ID NO 1994 : n represents ctcttt (Location 21).
SEQ ID NO 1995 : n represents ct (Location 21).
SEQ ID NO 2002 : n represents a or deletion (Location 21).
SEQ ID NO 2005 : n represents t or deletion (Location 21).
SEQ ID NO 2008 : n represents g or deletion (Location 21).
SEQ ID NO 2011 : n represents aattagaa or deletion (Location 21).
SEQ ID NO 2012 : n represents tttaaaa or ttttaa (Location 21).
SEQ ID NO 2015 : n represents t or deletion (Location 21).
SEQ ID NO 2020 : n represents t or deletion (Location 21).
SEQ ID NO 2024 : n represents g or deletion (Location 21).
SEQ ID NO 2025 : n represents t or deletion (Location 21).
SEQ ID NO 2030 : n represents aaa or deletion (Location 21).
SEQ ID NO 2031 : n represents a or deletion (Location 21).
SEQ ID NO 2042 : n represents c (Location 21).
SEQ ID NO 2072 : n represents a or deletion (Location 21).
SEQ ID NO 2074 : n represents a or deletion (Location 21).

SEQ ID NO 2243 : n represents 14 to 16 repeats of tca (Location 21).
SEQ ID NO 2244 : n represents 8 to 10 repeats of a (Location 21).
SEQ ID NO 2245 : n represents cacagtcat or deletion (Location 21).
SEQ ID NO 2246 : n represents tt or deletion (Location 21).
SEQ ID NO 2247 : n represents 10 to 12 repeats of a (Location 21).
SEQ ID NO 2248 : n represents c or deletion (Location 21).
SEQ ID NO 2249 : n represents 16 to 18 repeats of a (Location 21).
SEQ ID NO 2250 : n represents g (Location 21).
SEQ ID NO 2252 : n represents c or deletion (Location 21).
SEQ ID NO 2253 : n represents t or deletion (Location 21).
SEQ ID NO 2254 : n represents a or deletion (Location 21).
SEQ ID NO 2255 : n represents tg (Location 21).
SEQ ID NO 2257 : n represents 10 to 13 repeats of t (Location 21).
SEQ ID NO 2258 : n represents 11 to 13 repeats of gt (Location 21).
SEQ ID NO 2259 : n represents a or deletion (Location 21).
SEQ ID NO 2260 : n represents g or deletion (Location 21).
SEQ ID NO 2261 : n represents g or deletion (Location 21).
SEQ ID NO 2262 : n represents 9 to 11 repeats of t (Location 21).
SEQ ID NO 2263 : n represents g (Location 21).
SEQ ID NO 2265 : n represents tt or deletion (Location 21).
SEQ ID NO 2266 : n represents 7 to 9 repeats of a (Location 21).
SEQ ID NO 2267 : n represents 9 to 11 repeats of t (Location 21).
SEQ ID NO 2268 : n represents 9 to 10 repeats of a (Location 21).
SEQ ID NO 2269 : n represents gt or deletion (Location 21).
SEQ ID NO 2270 : n represents a or deletion (Location 21).
SEQ ID NO 2271 : n represents t (Location 21).
SEQ ID NO 2273 : n represents a or deletion (Location 21).
SEQ ID NO 2274 : n represents ct or deletion (Location 21).
SEQ ID NO 2275 : n represents g or deletion (Location 21).
SEQ ID NO 2276 : n represents a or deletion (Location 21).
SEQ ID NO 2277 : n represents a or deletion (Location 21).
SEQ ID NO 2278 : n represents a or deletion (Location 21).
SEQ ID NO 2279 : n represents c or deletion (Location 21).
SEQ ID NO 2280 : n represents aaag or deletion (Location 21).
SEQ ID NO 2348 : n represents 22 to 26 repeats of t (Location 21).

SEQ ID NO 2349 : n represents 8 to 10 repeats of g (Location 21).
SEQ ID NO 2350 : n represents 6 to 7 repeats of c (Location 21).
SEQ ID NO 2351 : n represents 12 to 14 repeats of a (Location 21).
SEQ ID NO 2427 : n represents caccaggcagcagactctgatgaggaggggaggggg (Location 21).
SEQ ID NO 2429 : n represents g (Location 21).
SEQ ID NO 2474 : n represents tcac or deletion (Location 21).
SEQ ID NO 2475 : n represents t or deletion (Location 21).
SEQ ID NO 2476 : n represents 9 to 11 repeats of t (Location 21).
SEQ ID NO 2477 : n represents 7 to 8 repeats of a (Location 21).
SEQ ID NO 2495 : n represents 13 to 16 repeats of t (Location 21).
SEQ ID NO 2496 : n represents 9 to 10 repeats of t (Location 21).
SEQ ID NO 2497 : n represents 14 to 16 repeats of t (Location 21).
SEQ ID NO 2498 : n represents 13 to 17 repeats of t (Location 21).
SEQ ID NO 2499 : n represents t (Location 21).
SEQ ID NO 2501 : n represents 8 to 9 repeats of a (Location 21).
SEQ ID NO 2502 : n represents 8 to 9 repeats of t (Location 21).
SEQ ID NO 2503 : n represents gcagtattactgtagt or deletion (Location 21).
SEQ ID NO 2504 : n represents 13 to 14 repeats of t (Location 21).
SEQ ID NO 2505 : n represents 9 to 10 repeats of t (Location 21).
SEQ ID NO 2506 : n represents 10 to 11 repeats of t (Location 21).
SEQ ID NO 2524 : n represents t or deletion (Location 21).
SEQ ID NO 2525 : n represents 12 to 15 repeats of t (Location 21).
SEQ ID NO 2586 : n represents a or deletion (Location 21).
SEQ ID NO 2587 : n represents at or deletion (Location 21).
SEQ ID NO 2594 : n represents t or deletion (Location 21).
SEQ ID NO 2595 : n represents ttc or deletion (Location 21).
SEQ ID NO 2606 : n represents ctt (Location 21).
SEQ ID NO 2651 : n represents 9 to 11 repeats of c (Location 21).
SEQ ID NO 2652 : n represents 15 to 21 repeats of a (Location 21).
SEQ ID NO 2653 : n represents ggggtggcggggtggg or deletion (Location 21).
SEQ ID NO 2654 : n represents t or deletion (Location 21).
SEQ ID NO 2655 : n represents a (Location 21).
SEQ ID NO 2657 : n represents a or deletion (Location 21).
SEQ ID NO 2658 : n represents 10 to 12 repeats of t (Location 21).
SEQ ID NO 2659 : n represents tt (Location 21).

SEQ ID NO 2661 : n represents tccctccttgaagctgatcgt or deletion (Location 21).
SEQ ID NO 2662 : n represents 12 to 18 repeats of ca (Location 21).
SEQ ID NO 2685 : n represents 18 to 20 repeats of a (Location 21).
SEQ ID NO 2686 : n represents aa (Location 21).
SEQ ID NO 2688 : n represents t or deletion (Location 21).
SEQ ID NO 2689 : n represents 9 to 13 repeats of t (Location 21).
SEQ ID NO 2690 : n represents aa or deletion (Location 21).
SEQ ID NO 2691 : n represents ttgaca or gtccaatat (Location 21).
SEQ ID NO 2692 : n represents cta or deletion (Location 21).
SEQ ID NO 2693 : n represents 9 to 10 repeats of t (Location 21).
SEQ ID NO 2694 : n represents gagatgttgtggctcacat (Location 21).
SEQ ID NO 2696 : n represents cc or deletion (Location 21).
SEQ ID NO 2697 : n represents act or deletion (Location 21).
SEQ ID NO 2755 : n represents tat or deletion (Location 21).
SEQ ID NO 2756 : n represents 14 to 17 repeats of ac (Location 21).
SEQ ID NO 2757 : n represents 16 to 27 repeats of a (Location 21).
SEQ ID NO 2758 : n represents t or deletion (Location 21).
SEQ ID NO 2759 : n represents 8 to 10 repeats of a (Location 21).
SEQ ID NO 2760 : n represents 9 to 11 repeats of gt (Location 21).
SEQ ID NO 2761 : n represents aa or deletion (Location 21).
SEQ ID NO 2762 : n represents t or deletion (Location 21).
SEQ ID NO 2763 : n represents 8 to 12 repeats of ac (Location 21).
SEQ ID NO 2764 : n represents a or deletion (Location 21).
SEQ ID NO 2810 : n represents a (Location 21).
SEQ ID NO 2812 : n represents aa or deletion (Location 21).
SEQ ID NO 2813 : n represents ca or deletion (Location 21).
SEQ ID NO 2814 : n represents t or deletion (Location 21).
SEQ ID NO 2815 : n represents tgtgtg or deletion (Location 21).
SEQ ID NO 2912 : n represents a (Location 21).
SEQ ID NO 2914 : n represents g (Location 21).
SEQ ID NO 2916 : n represents actt or deletion (Location 21).
SEQ ID NO 2917 : n represents ttta or deletion (Location 21).
SEQ ID NO 2918 : n represents 11 to 13 repeats of a (Location 21).
SEQ ID NO 2919 : n represents 8 to 10 repeats of t (Location 21).
SEQ ID NO 2920 : n represents 12 to 14 repeats of a (Location 21).

SEQ ID NO 2921 : n represents cttgta or deletion (Location 21).
SEQ ID NO 2922 : n represents 9 to 10 repeats of a (Location 21).
SEQ ID NO 2923 : n represents ctt or deletion (Location 21).
SEQ ID NO 2924 : n represents ctt (Location 21).
SEQ ID NO 2926 : n represents a or deletion (Location 21).
SEQ ID NO 2927 : n represents 9 to 11 repeats of a (Location 21).
SEQ ID NO 2928 : n represents tgt or deletion (Location 21).
SEQ ID NO 2929 : n represents 24 to 27 repeats of a (Location 21).
SEQ ID NO 2930 : n represents 10 to 21 repeats of ta (Location 21).
SEQ ID NO 2931 : n represents 8 to 10 repeats of a (Location 21).
SEQ ID NO 2932 : n represents 11 to 13 repeats of a (Location 21).
SEQ ID NO 2933 : n represents 8 to 10 repeats of a (Location 21).
SEQ ID NO 2999 : n represents tatc or deletion (Location 21).
SEQ ID NO 3000 : n represents atattcacttggtatctg or deletion (Location 21).
SEQ ID NO 3001 : n represents ttta or deletion (Location 21).
SEQ ID NO 3002 : n represents t (Location 21).
SEQ ID NO 3004 : n represents g or deletion (Location 21).
SEQ ID NO 3005 : n represents a or deletion (Location 21).
SEQ ID NO 3006 : n represents 9 to 11 repeats of a (Location 21).
SEQ ID NO 3007 : n represents g or deletion (Location 21).
SEQ ID NO 3008 : n represents 4 to 5 repeats of at (Location 21).
SEQ ID NO 3009 : n represents 7 to 8 repeats of t (Location 21).
SEQ ID NO 3010 : n represents 19 to 23 repeats of t (Location 21).
SEQ ID NO 3011 : n represents t or deletion (Location 21).
SEQ ID NO 3012 : n represents tgat or deletion (Location 21).
SEQ ID NO 3013 : n represents 8 to 10 repeats of t (Location 21).
SEQ ID NO 3014 : n represents a or deletion (Location 21).
SEQ ID NO 3021 : n represents 13 to 15 repeats of a (Location 21).
SEQ ID NO 3022 : n represents 12 to 15 repeats of t (Location 21).
SEQ ID NO 3042 : n represents g (Location 21).
SEQ ID NO 3044 : n represents a or deletion (Location 21).
SEQ ID NO 3046 : n represents g or deletion (Location 21).
SEQ ID NO 3047 : n represents 11 to 13 repeats of t (Location 21).
SEQ ID NO 3049 : n represents a or deletion (Location 21).
SEQ ID NO 3051 : n represents 9 to 11 repeats of t (Location 21).

SEQ ID NO 3054 : n represents t or deletion (Location 21).
SEQ ID NO 3056 : n represents t or deletion (Location 21).
SEQ ID NO 3060 : n represents t or deletion (Location 21).
SEQ ID NO 3065 : n represents aaga (Location 21).
SEQ ID NO 3069 : n represents aaaa or deletion (Location 21).
SEQ ID NO 3073 : n represents 9 to 11 repeats of t (Location 21).
SEQ ID NO 3081 : n represents a or deletion (Location 21).
SEQ ID NO 3103 : n represents 11 to 13 repeats of t (Location 21).
SEQ ID NO 3119 : n represents acta (Location 21).
SEQ ID NO 3125 : n represents gtg or deletion (Location 21).
SEQ ID NO 3130 : n represents 11 to 12 repeats of t (Location 21).
SEQ ID NO 3140 : n represents tta or deletion (Location 21).
SEQ ID NO 3154 : n represents g (Location 21).
SEQ ID NO 3156 : n represents a (Location 21).
SEQ ID NO 3158 : n represents cct or deletion (Location 21).
SEQ ID NO 3169 : n represents gga (Location 21).
SEQ ID NO 3179 : n represents 12 to 14 repeats of t (Location 21).
SEQ ID NO 3184 : n represents 16 to 17 repeats of t (Location 21).
SEQ ID NO 3196 : n represents g (Location 21).
SEQ ID NO 3273 : n represents ag (Location 21).
SEQ ID NO 3306 : n represents g (Location 21).
SEQ ID NO 3310 : n represents c (Location 21).
SEQ ID NO 3315 : n represents ct or deletion (Location 21).
SEQ ID NO 3317 : n represents gc or deletion (Location 21).
SEQ ID NO 3352 : n represents 8 to 11 repeats of t (Location 21).
SEQ ID NO 3355 : n represents a (Location 21).
SEQ ID NO 3358 : n represents t or deletion (Location 21).

[Brief Description of Drawings]

Figure 1 shows TaqMan probes.

Figure 2 represents an outline of the TaqMan PCR method.

Figure 3 shows probes labeled with fluorescent dyes.

Figure 4 shows an outline of the INVADER assay.

Figure 5 shows a FRET probe.

Figure 6 shows an outline of the INVADER assay.

Figure 7 shows a probe in which the allele does not match the probe.

Figure 8 shows one embodiment of allele identification using a ligation reaction.

Figure 9 shows a structure of ATP-binding cassette subfamily B member 2 (ABCB2) gene and the SNP location therein.

Figure 10 shows a structure of ATP-binding cassette subfamily B member 4 (ABCB4) gene and the SNP location therein.

Figure 11 shows a structure of microsomal epoxide hydrolase 1 (EPHX1) gene and the SNP location therein.

Figure 12 shows a structure of cytoplasmic epoxide hydrolase (EPHX2) gene and the SNP location therein.

Figure 13 shows a structure of guanidinoacetate N-methyl transferase (GAMT) gene and the SNP location therein.

Figure 14 shows a structure of nicotinamide N-methyl transferase (NNMT) gene and the SNP location therein.

Figure 15 shows a structure of phenyl ethanolamine N-methyl transferase (PNMT) gene and the SNP location therein.

Figure 16 shows a structure of phosphatidylethanolamine N-methyl transferase (PEMT) gene and the SNP location therein.

Figure 17 shows a structure of glutathione S transferase 3 (GSTM3) gene and the SNP location therein.

Figure 18 shows a structure of aldehyde dehydrogenase 5 (ALDH5) gene and the SNP location therein.

Figure 19 shows a structure of transglutaminase 1 (TGM1) gene and the SNP location therein.

Figure 20 shows a structure of gamma-glutamyl transferase 1 (GGT1) gene and the SNP location therein.

Figure 21 shows a structure of NAD (P)H: quinone oxidoreductase 1 (NQO1) gene and the SNP location therein.

Figure 22 shows a structure of p53-inducible gene 3 (PIG3) in a quinone oxidoreductase homolog and the SNP location therein.

Figure 23 shows a structure of NRH: quinone oxidoreductase 2 (NQO2) gene and the SNP location therein.

Figure 24 shows a structure of sulfotransferase 1A1 (SULT1A1/STP1) gene and the SNP location therein.

Figure 25 shows a structure of sulfotransferase 1A2 (SULT1A2/STP2) gene and the SNP location therein.

Figure 26 shows a structure of sulfotransferase-associated protein 3 (SULTX3) gene and the SNP location therein.

Figure 27 shows a structure of tyrosyl protein sulfotransferase 1 (TPST1) gene and the SNP location therein.

Figure 28 shows a structure of tyrosyl protein sulfotransferase 2 (TPST2) gene and the SNP location therein.

Figure 29 shows a structure of sulfotransferase 1A3 (SULT1A3/STM/HAST) gene and the SNP location therein.

Figure 30 shows a structure of cerebroside sulfotransferase (CST) gene and the SNP location therein.

Figure 31 shows a structure of sulfotransferase 1C1 (SULT1C1) gene and the SNP location therein.

Figure 32 shows a structure of sulfotransferase 1C2 (SULT1C2) gene and the SNP location therein.

Figure 33 shows a structure of thyroid hormone sulfotransferase (ST1B2) gene and the SNP location therein.

Figure 34 shows a structure of carbohydorate sulfotransferase 2 (CHST2) gene and the SNP location therein.

Figure 35 shows a structure of sulfotransferase 2A1 (SULT2A1) gene and the SNP location therein.

Figure 36 shows a structure of sulfotransferase 2B1 (SULT2B1) gene and the SNP location therein.

Figure 37 shows a structure of carbohydorate sulfotransferase 4 (CHST4) gene and the SNP location therein.

Figure 38 shows a structure of carbohydorate sulfotransferase 5 (CHST5) gene and the SNP location therein.

Figure 39 shows a structure of HNK-sulfotransferase (HNK-1ST) gene and the SNP location therein.

Figure 40 shows a structure of estrogen sulfotransferase (STE) gene and the SNP location therein.

Figure 41 shows a structure of alcohol dehydrogenase 1 (ADH1) gene and the SNP location therein.

Figure 42 shows a structure of alcohol dehydrogenase 2 (ADH2) gene and the SNP

location therein.

Figure 43 shows a structure of alcohol dehydrogenase 3 (ADH3) gene and the SNP location therein.

Figure 44 shows a structure of alcohol dehydrogenase 6 (ADH6) gene and the SNP location therein.

Figure 45 shows a structure of alcohol dehydrogenase 7 (ADH7) gene and the SNP location therein.

Figure 46 shows a structure of short-chain alcohol dehydrogenase family gene (HEP27) and the SNP location therein.

Figure 47 shows a structure of L1 cell adhesion molecule (L1CAM) gene and the SNP location therein.

Figure 48 shows a structure of arylalkylamine N-acetyltransferase (AANAT) gene and the SNP location therein.

Figure 49 shows a structure of N-acetyltransferase homolog (ARD1) gene of *Saccharomyces cerevisiae* and the SNP location therein.

Figure 50 shows a structure of N-acetyltransferase (NAT1) gene and the SNP location therein.

Figure 51 shows a structure of N-acetyltransferase 2 (NAT2) gene and the SNP location therein.

Figure 52 shows a structure of granzyme A (GZMA) gene and the SNP location therein.

Figure 53 shows a structure of granzyme B (GZMB) gene and the SNP location therein.

Figure 54 shows a structure of esterase D/formylglutathione hydrolase (ESD) gene and the SNP location therein.

Figure 55 shows a structure of dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST) gene and the SNP location therein.

Figure 56 shows a structure of microsomal glutathione S transferase 1 (MGST1) gene and the SNP location therein.

Figure 57 shows a structure of alcohol dehydrogenase 5 (ADH5) gene and the SNP location therein.

Figure 58 shows a structure of glutathione S transferase M1 (GSTM1) gene and the SNP location therein.

Figure 59 shows a structure of glutathione S transferase M2 (GSTM2) gene and the SNP location therein.

Figure 60 shows a structure of glutathione S transferase M4 (GSTM4) gene and the SNP location therein.

Figure 61 shows a structure of glutathione S transferase Z1 (GSTZ1) gene and the SNP location therein.

Figure 62 shows a structure of glutathione S transferase Pi (GSTPi) gene and the SNP location therein.

Figure 63 shows a structure of glutathione S transferase T1 (GSTT1) gene and the SNP location therein.

Figure 64 shows a structure of microsomal glutathione S transferase 1-like 1 (MGST1L1) gene and the SNP location therein.

Figure 65 shows a structure of microsomal glutathione S transferase T2 (MGST2) gene and the SNP location therein.

Figure 66 shows a structure of microsomal glutathione S transferase T3 (MGST3) gene and the SNP location therein.

Figure 67 shows a structure of glutathione S transferase A1 (GSTA1) gene and the SNP location therein.

Figure 68 shows a structure of glutathione S transferase A4 (GSTA4) gene and the SNP location therein.

Figure 69 shows a structure of NADH-ubiquinone oxidoreductase 1α-subcomplex 1 (NDUFA1) gene and the SNP location therein.

Figure 70 shows a structure of NADH-ubiquinone oxidoreductase 1α-subcomplex 2 (NDUFA2) gene and the SNP location therein.

Figure 71 shows a structure of NADH-ubiquinone oxidoreductase 1α-subcomplex 3 (NDUFA3) gene and the SNP location therein.

Figure 72 shows a structure of NADH-ubiquinone oxidoreductase 1α-subcomplex 5 (NDUFA5) gene and the SNP location therein.

Figure 73 shows a structure of NADH-ubiquinone oxidoreductase 1α-subcomplex 6 (NDUFA6) gene and the SNP location therein.

Figure 74 shows a structure of NADH-ubiquinone oxidoreductase 1α-subcomplex 7 (NDUFA7) gene and the SNP location therein.

Figure 75 shows a structure of NADH-ubiquinone oxidoreductase 1α-subcomplex 8 (NDUFA8) gene and the SNP location therein.

Figure 76 shows a structure of NADH-ubiquinone oxidoreductase 1α/β subcomplex 1 (NDUFAB1) gene and the SNP location therein.

Figure 77 shows a structure of NADH-ubiquinone oxidoreductase 1α-subcomplex 9

(NDUFA9) gene and the SNP location therein.

Figure 78 shows a structure of NADH-ubiquinone oxidoreductase Fe-S protein 1 (NDUFS1) gene and the SNP location therein.

Figure 79 shows a structure of NADH-ubiquinone oxidoreductase Fe-S protein 3 (NDUFS3) gene and the SNP location therein.

Figure 80 shows a structure of NADH-ubiquinone oxidoreductase Fe-S protein 4 (NDUFS4) gene and the SNP location therein.

Figure 81 shows a structure of NADH-ubiquinone oxidoreductase Fe-S protein 5 (NDUFS5) gene and the SNP location therein.

Figure 82 shows a structure of NADH-ubiquinone oxidoreductase Fe-S protein 6 (NDUFS6) gene and the SNP location therein.

Figure 83 shows a structure of NADH-ubiquinone oxidoreductase Fe-S protein 8 (NDUFS8) gene and the SNP location therein.

Figure 84 shows a structure of NADH-ubiquinone oxidoreductase 1β-subcomplex 3 (NDUFB3) gene and the SNP location therein.

Figure 85 shows a structure of NADH-ubiquinone oxidoreductase 1β-subcomplex 5 (NDUFB5) gene and the SNP location therein.

Figure 86 shows a structure of NADH-ubiquinone oxidoreductase 1β-subcomplex 7 (NDUFB7) gene and the SNP location therein.

Figure 87 shows a structure of ATP-binding cassette subfamily A member 1 (ABCA1) gene and the SNP location therein.

Figure 88 shows a structure of catechol-O-methyl transferase (COMT) gene and the SNP location therein.

Figure 89 shows a structure of histamine N-methyl transferase (HNMT) gene and the SNP location therein.

Figure 90 shows a structure of cytochrome P450 subfamily 1 (aromatic compound-inducible) polypeptide 1 (CYP1A1) gene and the SNP location therein.

Figure 91 shows a structure of cytochrome P450 subfamily 1 (aromatic compound-inducible) polypeptide 2 (CYP1A2) gene and the SNP location therein.

Figure 92 shows a structure of cytochrome P450 subfamily 1 (dioxin-inducible) polypeptide 1 (CYP1B1) gene and the SNP location therein.

Figure 93 shows a structure of allylacetamide deacetylase (AADAC) gene and the SNP location therein.

Figure 94 shows a structure of neuropathy target esterase (NTE) gene and the SNP location therein.

Figure 95 shows a structure of ATP-binding cassette subfamily C (CTFR/MRP) member 2 gene and the SNP location therein.

Figure 96 shows a structure of ATP-binding cassette subfamily B member 1 (ABCB1) gene and the SNP location therein.

Figure 97 shows a structure of ATP-binding cassette subfamily B member 3 (ABCB3) gene and the SNP location therein.

Figure 98 shows a structure of ATP-binding cassette subfamily B member 7 (ABCB7) gene and the SNP location therein.

Figure 99 shows a structure of ATP-binding cassette subfamily B member 8 (ABCB8) gene and the SNP location therein.

Figure 100 shows a structure of ATP-binding cassette subfamily B member 9 (ABCB9) gene and the SNP location therein.

Figure 101 shows a structure of ATP-binding cassette subfamily B member 10 (ABCB10) gene and the SNP location therein.

Figure 102 shows a structure of ATP-binding cassette subfamily B member 11 (ABCB11) gene and the SNP location therein.

Figure 103 shows a structure of cytochrome P450 subfamily IVB polypeptide 1 (CYP4B1) gene and the SNP location therein.

Figure 104 shows a structure of cytochrome P450 subfamily XXVIIA polypeptide 1 (CYP27A1) gene and the SNP location therein.

Figure 105 shows a structure of cytochrome P450 subfamily IVF polypeptide 2 (CYP4F2) gene and the SNP location therein.

Figure 106 shows a structure of cytochrome P450 subfamily 4F polypeptide 3 (CYP4F3) gene and the SNP location therein.

Figure 107 shows a structure of cytochrome P450 subfamily 4F polypeptide 8 (CYP4F8) gene and the SNP location therein.

Figure 108 shows a structure of aldehyde dehydrogenase 1 (ALDH1) gene and the SNP location therein.

Figure 109 shows a structure of aldehyde dehydrogenase 2 (ALDH2) gene and the SNP location therein.

Figure 110 shows a structure of aldehyde dehydrogenase 7 (ALDH7) gene and the SNP location therein.

Figure 111 shows a structure of aldehyde dehydrogenase 8 (ALDH8) gene and the SNP location therein.

Figure 112 shows a structure of aldehyde dehydrogenase 9 (ALDH9) gene and the

SNP location therein.

Figure 113 shows a structure of aldehyde dehydrogenase 10 (ALDH10) gene and the SNP location therein.

Figure 114 shows a structure of ATP-binding cassette subfamily C member 7 (ABCC7) gene and the SNP location therein.

Figure 115 shows a structure of ATP-binding cassette subfamily C member 8 (ABCC8) gene and the SNP location therein.

Figure 116 shows a structure of ATP-binding cassette subfamily C member 9 (ABCC9) gene and the SNP location therein.

Figure 117 shows a structure of carboxyl esterase 1 (CES1) gene and the SNP location therein

Figure 118 shows a structure of ATP-binding cassette subfamily A member 4 (ABCA4) gene and the SNP location therein.

Figure 119 shows a structure of ATP-binding cassette subfamily A member 7 (ABCA7) gene and the SNP location therein.

Figure 120 shows a structure of ATP-binding cassette subfamily G member 1 (ABCG1) gene and the SNP location therein.

Figure 121 shows a structure of ATP-binding cassette subfamily G member 2 (ABCG2) gene and the SNP location therein.

Figure 122 shows a structure of ATP-binding cassette subfamily G member 4 (ABCG4) gene and the SNP location therein.

Figure 123 shows a structure of ATP-binding cassette subfamily E member 1 (ABCE1) gene and the SNP location therein.

Figure 124 shows a structure of carbohydorate sulfotransferase 1 (CHST1) gene and the SNP location therein.

Figure 125 shows a structure of carbohydorate sulfotransferase 3 (CHST3) gene and the SNP location therein.

Figure 126 shows a structure of NADH: ubiquinone dehydrogenase flavoprotein 1 (NDUFV1) gene and the SNP location therein.

Figure 127 shows a structure of NADH: ubiquinone oxidoreductase flavoprotein 2 (NDUFV2) gene and the SNP location therein.

Figure 128 shows a structure of NADH: ubiquinone oxidoreductase flavoprotein 3 (NDUFV3) gene and the SNP location therein.

Figure 129 shows a structure of NADH: ubiquinone oxidoreductase A10 (NDUFV10) gene and the SNP location therein.

Figure 130 shows a structure of high-mobility group protein 17-like 1 (HMG17L1) gene and the SNP location therein.

Figure 131 shows a structure of UDP glycosyltransferase 2 family polypeptide A1 (UGT2A1) gene and the SNP location therein.

Figure 132 shows a structure of human organic anion transporter polypeptide 1 (hOATP1) gene and the SNP location therein.

Figure 133 shows a structure of human organic anion transporter polypeptide 2 (hOATP2) gene and the SNP location therein.

Figure 134 shows a structure of human organic anion transporter polypeptide 8 (hOATP8) gene and the SNP location therein.

Figure 135 shows a structure of human organic anion transporter 1 (hOAT1) gene and the SNP location therein.

Figure 136 shows a structure of human organic anion transporter 2 (hOAT2) gene and the SNP location therein.

Figure 137 shows a structure of human organic anion transporter 3 (hOAT3) gene and the SNP location therein.

Figure 138 shows a structure of aldehyde dehydrogenase 1 family member A2 (ALDH1A2) gene and the SNP location therein.

Figure 139 shows a structure of aldehyde dehydrogenase 1 family member A3 (ALDH1A3) gene and the SNP location therein.

Figure 140 shows a structure of formyl tetrahydrofolate dehydrogenase (FTHFD/ALDH1L1) gene and the SNP location therein.

Figure 141 shows a structure of cytochrome P450 subfamily IIIA (aromatic compound-inducible) polypeptide 4 (CYP3A4) gene and the SNP location therein.

Figure 142 shows a result of typing performed on two different groups of patients using the INVADER method.

[Abstract]

[Problem]

The present invention provides a method for detecting a genetic polymorphism(s).

[Means for solving the problems]

A method for detecting a genetic polymorphism(s), comprising creating oligonucleotide probes and/or oligonucleotide primers so that the probes and/or primers contain a polymorphic site(s) present in a gene encoding a drug metabolizing enzyme or so that the polymorphic site(s) is/are contained in the amplified fragment when at least one of said gene encoding the drug metabolizing enzyme is amplified; and detecting at least one genetic polymorphism in a gene of a subject encoding the drug metabolizing enzyme using the resultant oligonucleotide probes and/or oligonucleotide primers.

[Representative drawing] none

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ABCB2	1	5' flanking - 673	agctaagagtcaaagcaccc G/C ctttttccaccagcctcgcg	1
ABCB2	2	5' flanking - 646	ccaccagcctcgcgtgcctg T/G tcccttcacggacactctag	2
ABCB2	3	5' flanking - 563	ttgcaagcgctggctgctac A/C ggcgacctccctgcgctccc	3
ABCB2	4	5' flanking - 236	gctttgcgcgcggcgctaac G/T tgtgtagggcagatctgccc	4
ABCB2	5	Intron3 + 408	aaggaaactgaggccaagac C/T ctaaatgctgaaactgcaca	5
ABCB2	6	Exon4 + 153	ccctcaccatggtcaccctg A/G tcaccctgcctctgcttttc	6
ABCB2	7	Intron4 + 289	gtatttctttagcatccaag G/T ggcatagctgtgtctctttc	7
ABCB2	8	Intron4 + 291	atttctttagcatccaaggg C/G catagctgtgtctctttctc	8
ABCB2	9	Intron5 - 63	ttccttcaggttaatgactg C/T ggttctttgtgtcccctcca	9
ABCB2	10	Intron7 - 185	gtctctgcccttgtctttgc C/T gcttcttctatctctactcc	10
ABCB2	11	3' flanking + 71	agcgcacttttcagctgcgg G/A tgtctcctcttttatcatcc	11
ABCB2	12	3' flanking + 129	aactgcatcacctttttccct T/C aagctttttaattcctatga	12
ABCB2	13	3' flanking + 459	cattcagggaggcccaggtc G/A tgtgacgtcgacagttgctg	13
ABCB4	1	exon3 + 3	aacacccttattttatagat C/T caatgactgagtcaagaatt	14
ABCB4	2	intron3 + 45	cagcatctctacttatacca T/C gctctgctttaaggttctct	15
ABCB4	3	intron3 + 498	actcaaataggtggtaggag C/T agagacaattcaatacagac	16
ABCB4	4	intron3 + 515	gagcagagacaattcaatac A/G gacagaagtcttagatgaga	17
ABCB4	5	intron6 + 1030	tagttttgccatgtagaatt G/C aaaaagtgatagatggtgtt	18
ABCB4	6	intron6 + 1437	gttaagcctgcttcaatcaa G/A ttagttatattcttgttcta	19
ABCB4	7	intorn6 + 2449	ttgacttagcgacactgtta G/A catacttatctttcctgtgt	20
ABCB4	8	intron7 + 451	ccttgctgcacctgtgctgt A/C taagtttggcttattatagt	21
ABCB4	9	intron7 + 530	agtagagacaggctggcgat C/G acaccggacagagctaactg	22
ABCB4	10	intron7 - 152	aacagaatcatgaaattaag T/C tgttaatgatttgaaggcct	23
ABCB4	11	exon8 + 40	aggataaattgtttatgtcg C/T ctgggtaccatcatggccat	24
ABCB4	12	intron8 + 130	ctggttgactccagatatca T/C agaaggagttgtaaaattct	25
ABCB4	13	intron8 + 248	aatacacaggaagcttctaa A/G taaagtaaggaagtcactct	26
ABCB4	14	intron8 + 531	ctaaagagtgaatggattca A/G tacgtcccttggaactcacc	27
ABCB4	15	intron8 + 4240	ctgaggttccagcttatctc T/A tagagatgtttacttagtct	28
ABCB4	16	intron8 + 4343	tgttagaagaaaaaaaggtt C/T atattacaagagggtctgac	29
ABCB4	17	intron8 + 4677	cccaagatatcttcataact G/C tccatagtgcctagggtgcc	30
ABCB4	18	intron9 + 113	tttacccagattcacctatt A/G ttatcatttttgctcccaaa	31
ABCB4	19	intron9 + 982	tgtcctatacagtttttgtt T/A taagtttagtaaattgatta	32
ABCB4	20	intron11 + 457	tccagcttgggtgacagagt A/G agacttcatctcaaaaaaaa	33
ABCB4	21	intron11 + 1337	tactcttggggagcctatca C/G cagggtgggtcagatatagc	34
ABCB4	22	exon12 + 3	tgtttcttttctgtccagat A/T ctctcggcatttagtgacaa	35
ABCB4	23	intron12 + 1288	cagaccacactaaccctcag T/C tggacctcaggatgtcagtg	36
ABCB4	24	intron13 + 206	tgtggataagaaaatagcat G/A tggttagaccatttgtgaaa	37
ABCB4	25	intron13 + 988	cagtcggtttggaagcttgc T/C acccttttcttcacttcctca	38
ABCB4	26	intron13 + (1413-1414)	tttatcttcacttatgtttt (T) ctcagttaagttatgctaat	39
ABCB4	26	intron13 + (1413-1414)	tttatcttcacttatgtttt ctcagttaagttatgctaat	40
ABCB4	27	intron13 + 1931	cttgcaaatgttgctcttcc A/G caaaaaaaaaaggaaaggat	41
ABCB4	28	intron23 + 784	agtatctcctaaactcttgc T/C atgcaggaaaaattatttta	42
ABCB4	29	intron25 + 158	gaaatattttactgtattaa T/C gtctagaacttaaatataag	43
ABCB4	30	intron25 + 2920	ctgagtcttcctatacatct T/A ttccattcctcggatgctgt	44
ABCB4	31	intron29 + 411	cttctcttaccttgaattct A/C ggctctcgaactttgacttt	45
ABCB4	32	intron32 + 458	agaaaatgaaattgccctac T/C gagctaactctgaaagcaca	46
EPHX1	1	intron1 + 110	tgcaaaatgtgtcttactag C/T ttctagtgcataaaatattg	47
EPHX1	2	intron1 + 143	aaatattggtggagctcttc G/A ctgtgctgggccagtcacca	48
EPHX1	3	intron1 + 1097	aatccagagagggagataga T/G tggaagttcaagggtggaca	49
EPHX1	4	intron1 + 1717	ttccaagacagagcgagggg T/C gctgctggggcgtggtttgc	50
EPHX1	5	intron1 + 1772	aactcgatgctttctcctcc G/T tctgggtcctaactgcagtg	51
EPHX1	6	intron1 + 2054	gaaatgtaacaggcaacact A/G tggacacagaaagtagatta	52
EPHX1	7	intron2 + 1414	atttccaaaatctgtttggg G/T gtaactgaaacacttgggaa	53
EPHX1	8	exon3 + 174	taccctcacttcaagactaa G/A attgaaggtatgtttgcaaa	54
EPHX1	9	intron3 + 6583	ctgtcaataccatgaagggg G/C ggcgggggcactaagggtgg	55
EPHX1	10	intron4 + 34	agaggttccataactgcccc G/A tcctcgccaagggtgggccc	56
EPHX1	11	intron4 + 63	aagggtgggcccggtgttcc C/T accaggctctccttccggcg	57
EPHX1	12	intron5 + 154	gcagtgcctgaggcacgttg G/A cttggatcctcctgtctgta	58
EPHX1	13	intron5 + 276	tgctggaccaagctctggga T/C agccctgagcagaactcccc	59
EPHX1	14	exon6 + 130	gatgtggagctgctgtaccc C/T gtcaaggagaaggtattcta	60
EPHX1	15	intron8 + 206	ggtgcctggctcccgggcgg C/A cctcagtaccgctccccagt	61
EPHX1	16	intron8 + 353	tggccctcccagaaaagaga A/G ggccctcagtgaggggagag	62
EPHX1	17	3' flanking + 708	aggtgcagactcatgcactc A/G gccctgaagaggtgagagag	63
EPHX2	1	5' flanking - (523-522)	aaagtcactggatatgcccc (C) tcccccgccccccaacacgg	64
EPHX2	1	5' flanking - (523-522)	aaagtcactggatatgcccc tcccccgccccccaacacgg	65
EPHX2	2	5' flanking - 522	aaagtcactggatatgcccc T/C cccccgccccccaacacggt	66
EPHX2	3	5' flanking - 521	aagtcactggatatgcccct C/T ccccgccccccaacacggtc	67
EPHX2	4	5' flanking - 516	actggatatgcccctccccc G/C ccccccaacacggtcttatg	68
EPHX2	5	5' flanking - 515	ctggatatgcccctcccccg C/G cccccaacacggtcttatgt	69
EPHX2	6	Intron1 - 74	tggctgcttctcaatgaata T/C gaacagtgtctgtttccatg	70
EPHX2	7	Intron3 + 72	gagcattaggtcagaatcca T/C tgaagtgagctttgagatca	71
EPHX2	8	Intron4 + 473	gtgtgtctctactttaatct A/G caaaaggtgattgaatggag	72
EPHX2	9	Intron5 + 276	caagagtgggatgttcaagg C/T catcctgacctcacttttga	73
EPHX2	10	Intron8 + 8	tctgctcctcccggtgggtg T/C gctgtcttgcagctgtctta	74
EPHX2	11	Intron9 + 1573	atgtcgtgaagactgatgaa C/T gatggacggctgcactgctc	75
EPHX2	12	Intron10 + 207	gaacaggatggagatgagct T/C gtttatttgtctttttaatga	76
EPHX2	13	Intron12 + 911	tgaagagacctcgacatgtc G/T catcccacatactacaggga	77
EPHX2	14	Intron12 + 2425	atcttctcagctgagcaaac C/T gaggctcagagggcttaacc	78
EPHX2	15	Intron12 + 2460	ttaacccccaactggcccaag G/A ccaggtacatgattgggtca	79
EPHX2	16	Intron12 - 281	aagtcctttcaagagattat T/C ataagtagtaccttctcatt	80
EPHX2	17	Intron12 - 268	agattattataagtagtacc T/G tctcattataggaatattga	81
EPHX2	18	Exon13 + 50	cctgagtcggactttcaaaa G/T cctcttcagagcaagcgatg	82
EPHX2	19	Intron13 + 1739	ttgtcgtaacagggttttca G/T atgagcatatttccttttgta	83
EPHX2	20	Exon14 + 33	atgcataaagtctgtgaagc G/A ggtaagagacatgcttggga	84
EPHX2	21	Intron14 + 314	ggattgagagcttacctcta T/C gggggtcacctcgtgtatgc	85
EPHX2	22	Intron14 + 878	attcccttattccttcacac C/T gtctgtcactcattcattca	86
EPHX2	23	Intron14 + 948	gcacaggctgggtatgaagc T/C ggggctgcatgctcagctac	87

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
EPHX2	24	Intron15 + 259	agagggttttcactactttt C/T agtcatggctcctcagagaa	88
EPHX2	25	Intron16 + 459	tcctcatttgtcaagcagaa G/C atgagtttccaatctctggg	89
EPHX2	26	Intron16 + 645	gtaagtgaacacactgctac G/A tgccagacttcctgccagac	90
EPHX2	27	Intron16 +985	gtcattatcatcatatgacc G/A atgaaaatgaccaaactgca	91
EPHX2	28	3'flanking + 12	aggtggccttacacacatct T/C gcatggatggcagcattgtt	92
EPHX2	29	3'flanking + 374	tgttcacggagaatgcacgg C/T atggggatgaacccctttccc	93
EPHX2	30	3'flanking + 544	tagccacctgcctttctccc G/A gcttccctagcagagtttgc	94
GAMT	1	intron1 + 429	ctcggaaagctgagctcagg G/A agacagctgtcccc ggggtg	95
GAMT	2	3'flanking + 626	cactgacctccttgccctga G/A agaaggccggctcctgtgct	96
NNMT	1	5'flanking - 228	ataattttcctgacgagctc A/T agtgctccctctggtctaca	97
NNMT	2	intron1 + 44	ccccactaatgtgagtcata T/C agatggagtctcagggcacg	98
NNMT	3	intron1 + 149	ggataaaaacgaatattggt A/G tagcgattccacagtttaca	99
NNMT	4	intron2 + 158	agataggcccatgtgtgtgc G/A tgttagtaaatttgtgtatg	100
NNMT	5	intron2 + 433	gctgtagccatccaagccta T/C agaacttggctgtgagtgtg	101
NNMT	6	intron2 - 3064	atcatctgactggtaagttc C/T agttctgtggtaactcaagt	102
NNMT	7	intron2 - 260	atttcatggagggaagtcca T/C ggtagaagcaggctgctagg	103
NNMT	8	3'flanking + 71	ggctcagtggttggggccca A/G tggttcatctaggacggggac	104
PNMT	1	5'flanking - 390	aagaggtgaatggctgcggg G/A ggctggagaagagagatggg	105
PEMT	1	exon2 - 4	agctcagcagacctcctggc C/T gtggtgggtagctcctttcc	106
PEMT	2	intron4 + 39	actgtccagacgggagtatc C/T cactgcttggtgagccccac	107
PEMT	3	intron4 + 1317	accgtccccagctggcccca G/A cctcctgacatgggcctctg	108
PEMT	4	intron4 + 1355	ctggagccaggctgcagccg A/C agtgcctggccatcctggcg	109
PEMT	5	intron4 + 5925	gtccaggcactgtggcccta C/T gtgggagtctccagtctcca	110
PEMT	6	intron4 + 6028	ggcagtggtccaaggaccag G/C atggactccctcttctcacc	111
PEMT	7	intron4 + 6078	atctgtaccctcgcggactc C/T acctggcttcgtgccatcac	112
PEMT	8	intron4 + 6089	cgcggactctacctggcttc A/G tgccatcacccccgccagat	113
PEMT	9	intron4 + 6379	tcaggtgtcccctccctcat G/A cctcctcaccctgccctctc	114
PEMT	10	intron4 + 7339	tgtaaggaatcctgccaaga C/T ggcagatgcacacggggtca	115
PEMT	11	intron4 + 7619	ctcctgcacatgtgctccag A/G gaggaaaggcatttgacagg	116
PEMT	12	intron4 + 8858	ggcatgtgtgtgtgtgtgta T/G gtgtgtgagtgtgtgcatgt	117
PEMT	13	intron4 + 9029	tttctggaccagaaagcgtc G/A tcctctgccagggcctcttg	118
PEMT	14	intron4 + 9056	gccagggcctcttgcacttg C/T gggaaagctgagctgagctg	119
PEMT	15	intron4 + 9512	ctgagctgggcagcagcatt A/G ctctgtgtgctgctggcact	120
PEMT	16	intron4 + 9523	agcagcattactctgtgtgc T/C gctggcactggcctggtggg	121
PEMT	17	intron4 + 9622	gacaaagtgtacaacaaggt G/A tctcgaactgggtcagctca	122
PEMT	18	intron4 + 10776	ccattcctgggtcttctttg G/A aggctgaatgaaattccatg	123
PEMT	19	intron4 + 10912	tctgccccactttgctcaga G/C gtgcaacaaggccttcagga	124
PEMT	20	intron4 + 11590	ggacactggcctgatgcaga G/C gtgtggtctctctcctgcag	125
PEMT	21	intron4 + 12090	ggccagggcaccctaccag G/C ctgagtcccacctgtccagc	126
PEMT	22	intron4 + 12263	tacccgccttcccagatgga G/A cgggctgctcatgggactta	127
PEMT	23	intron4 + 12448	tctggtcccctctcctgctt G/A tagtttcctgggctaaaatc	128
PEMT	24	intron4 + 12730	tgggaccagtgccgccacca C/T ggcccaaggacctggtgttc	129
PEMT	25	intron4 + 13240	gggctccaggcacacagcgg T/C cccagtacacctgtcgcttt	130
PEMT	26	intron4 + 13494	tccgtggaactcagagatgg T/C acctccctgcgaggtggggc	131
PEMT	27	intron4 + 13817	aactctcccctgctgctgag A/G cagatcttggagcctcggcc	132
PEMT	28	intron4 + 14773	ccgccctgtgcttcatgccc C/T ctatgcctctcactgcctgg	133
PEMT	29	intron4 + 14951	gtcctgaggcccctcccacc G/A gagcctggggtgccctcaca	134
PEMT	30	intron4 + 16896	gctgtgactgtcttggagac T/C gggtcttggcgggcctggtg	135
PEMT	31	intron4 + 19439	ccaggagcctctgaggcagc G/A ggggcttctcaaccacacac	136
PEMT	32	intron4 + 19559	attttgtcagcatgtcacgt C/T cctttcataatgaagcaagg	137
PEMT	33	intron4 + 20051	acagcactgcgggagccacg A/G catctgcagacgcatttgat	138
PEMT	34	intron4 + 20816	tggactctctggcgtccatc C/T agccacttcagtgcgacgtg	139
PEMT	35	intron4 + 21196	ggctggctgggccctgggat C/G atcgtgacaggctttagtgg	140
PEMT	36	intron4 + 21528	acaggtgggagccgaggctc G/T ggaggtgggccgggctgagc	141
PEMT	37	intron4 + 21596	ccgcttccccgtgctctggc C/T gtagcagaaagtgtcccact	142
PEMT	38	intron4 + 22672	agcctcccactgccttgtgg C/T tgaggggaggggccgggtc	143
PEMT	39	intron4 + 22713	tctaacgctgtcttctttgt A/T ctgaaaaccaaacaccttct	144
PEMT	40	intron4 + 23010	tgccgggcagcggggaggga G/A ggcgagtggttcccccaagt	145
PEMT	41	intron4 + 23588	gtgcaggcgccctgcatccc C/T gcagccaagttctgggcgga	146
PEMT	42	intron4 + 23627	gacactgccctgagccagga C/T ggtgaggtgggacgccttcc	147
PEMT	43	intron4 + 23941	tgaggggttgggactctaca G/A aggagagtggactcacgggg	148
PEMT	44	intron4 + 24091	gacacctcttcactgtcagc G/T ctgagacacgcccctgccct	149
PEMT	45	intron4 + 25348	caggccagttggaatcctac G/A tagagtgaaagcatctcagc	150
PEMT	46	intron4 + 25603	taagcagttaacactgatgc G/A tgatgaaaattccaacagca	151
PEMT	47	intron4 + 31540	cctccaggtggcaggaacac T/C gtgaggagcatgcaacgtgc	152
PEMT	48	intron4 + 31637	gtgggctgggacgccaggac G/A gtgaggggcttcaaggtgtg	153
PEMT	49	intron4 + 31642	ctgggacgccaggacggtga G/A gggcttcaaggtgtgtttgt	154
PEMT	50	intron4 + 35593	ggaggagctgaaagagctgg G/A gctcgggatcaggtggttca	155
PEMT	51	intron4 + 35647	actttgaggcaccaccgcac C/A tgtccgtgcgtgagggagac	156
PEMT	52	intron4 + 35862	tcccagtggtggctctgtcc C/T cgtctcagccgagcactcag	157
PEMT	53	intron4 + 35882	ccgtctcagccgagcactca T/G cggccagggtggctggactc	158
PEMT	54	intron4 + 37141	ccacaggccggatgccttga T/C acttctcagctgcagggctg	159
PEMT	55	intron4 + 38862	tggagagaccacctcagaca C/G caaggacgggcatgccatgg	160
PEMT	56	intron4 + 38872	acctcagacagcaaggacgg G/T catgccatgggtcccggcag	161
PEMT	57	intron4 + 39140	atgtctcaaatctccctccc C/T gggaaatctaggcacaggtc	162
PEMT	58	intron4 + 39635	caggcccaggagcaggtggg G/T cctcctcacaggagcagggc	163
PEMT	59	intron4 + 39713	actctgagcatgctggctcc C/T tccttctttccagggcagca	164
PEMT	60	intron4 + 40436	cctggttgtgcttcggaccc G/A gaggcagacagaggaggcct	165
PEMT	61	intron4 + 47485	acaatgactgttggagccct C/T gagcaggctgtgtcacgtgg	166
PEMT	62	intron4 + 48131	actgggggatcctgaatccc G/A cctcctgatgccagtggagc	167
PEMT	63	intron4 + 48558	cacagtgtgaactgttaggc C/G acagccacatcttgccggag	168
PEMT	64	intron4 + 48702	gagatgggggcggttcggga G/A gcaaaagcaggaaggcagaa	169
PEMT	65	intron4 + 50302	gcatgtgcatgggcagaggc T/C gttcccatctgagtgggacc	170
PEMT	66	intron4 + 54102	ggccgcgtgctcctgcagcc A/T tgggctcctctggcagttct	171
PEMT	67	intron4 + 54220	cccagggacagatcttctcc G/A ccagacgtctctttctgcct	172
PEMT	68	intron4 + 54371	gcagataatgtgcagctggg G/A tgcatgtggttgttgctccc	173
PEMT	69	exon5 + 79	tggcctgctactctctaagc G/C tcaccatcctgctcctgaac	174

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
PEMT	70	intron5 - 6796	ggaggaagtcagcttcttac A/C gatggtggctcccagctttc	175
PEMT	71	intron5 - 6636	ttttctcctctcacctttttg T/C gttcagaggcagaggtgtgc	176
PEMT	72	intron5 - 6448	gttgggccaggctctgacag G/A accctcgggaccagctcctg	177
PEMT	73	intron5 - 5218	ggagccctggctgaagaagc C/G ttacgaccaaggcctggagg	178
PEMT	74	intron5 - 4824	ggacaggccgggggttgagc G/A gctgcatgaaggagggaggg	179
PEMT	75	intron5 - 4249	tcaccagagtgatttcctcg C/A ggcaggtgcctggggtagcc	180
PEMT	76	intron5 - 4230	gaggcaggtgcctggggtag C/T cactgggcggggtccatgag	181
PEMT	77	intron5 - 4182	ggagagtaaggggtgggggg G/A cacttaggacagggaagctg	182
PEMT	78	intron5 - 3369	ccaggtggggccgtgtgcct G/C tggcctggtgtgtggcccag	183
PEMT	79	intron5 - 2625	cagggaagctgggccctgaa C/T gagctgggcttttgggccac	184
PEMT	80	intron5 - 1200	attattgtgagcatgggaag A/T gcacatttggtcacacatgt	185
PEMT	81	intron6 + 606	gcctggctagacgcccacca A/G tgaccctgatgatggcagca	186
PEMT	82	intron6 + 1229	tttggtccaggaagggggac G/A gcagccaggagcgtctggat	187
PEMT	83	intron7 + 716	atggagatgtgctcccccgg C/G gggtcagaggacctgcggtc	188
PEMT	84	intron7 + 1537	ctctgggggacgcataagcc G/A cctccagaggacatcagcca	189
PEMT	85	intron7 + 1718	gggcttccaggtgtctgagc T/C ccccggcatgtaggacccca	190
PEMT	86	intron7 + 2695	ggctttgggggaccctggac C/T catttctagaaaaacagcctt	191
PEMT	87	intron8 + 140	ccagggctcccaggtcagag C/T ggccatggtagcttacaatg	192
PEMT	88	3'flanking + 179	tacttaggaggcgtcagggg C/T tcacctggccatggccatgg	193
PEMT	89	3'flanking + 394	gatgacactgtcattcctaa A/G tgaatggccttgtgctgacc	194
GSTM3	1	5'flanking - 144	ccaacgccggcattagtcgc G/T cctgcgcacggccctgtgga	195
ALDH5	1	5'flanking - 2808	cgttgcactgtaggactctc C/T ccacgtcccctaatcccatc	196
ALDH5	2	5'flanking - 2575	gcagttcccgcggatagaga A/G ggtccggtccttcccgctgt	197
ALDH5	3	5'flanking - 2537	tgtgggtgaactgtaaaaaa C/T tgcctgtattcaggaggata	198
ALDH5	4	5'flanking - 940	cttcaactaatctgggaaca C/T tacactctgtttaattttca	199
ALDH5	5	5'flanking - 785	tgggaaagctgaaaagggat G/T ctgagacctgtggttggggg	200
ALDH5	6	exon1 + 183	ccgacggtcaaccctaccac T/C ggggaggtcattgggcacgt	201
ALDH5	7	exon1 + 257	cgtgaaagcagccccgggaag C/T cttccgcctggggtccccat	202
ALDH5	8	exon1 + 320	gcggggccggctgctgaacc G/T cctggcagacctagtggagc	203
ALDH5	9	exon1 + 605	acttgccccggcactcgcca C/T aggcaacactgtggttatga	204
ALDH5	10	3'flanking + 1527	aaagtgcaactgtaagaccc G/A tagagaaaaactctggttcc	205
TGM1	1	Exon2 + 179	tgccgaaatgcggcagatga C/T gactggggacctgaaccctc	206
TGM1	2	Intron9 - 611	acttaccactctgtcctctc C/T tgccaggcctcttcctgtca	207
TGM1	3	Intron9 - 272	ccgcacatctgtaccctgcc C/G ccatcctccagcagagcagc	208
TGM1	4	Intron10 + 54	tcagtcatgggttctctggt C/T ccaacttcaccgctgactga	209
TGM1	5	Intron10 - 51	aggaggccgggagtcaggcc A/G ccctcagaccctctggctca	210
TGM1	6	Intron12 - 47	gggagtccctgggggaagcc T/G catgtagggaagcaggcctc	211
TGM1	7	Intron13 + 72	ggataaggacatcagaggtg G/A gcgctaagccagcagcaggc	212
TGM1	8	Intron14 + 1671	atctcttacccacaccccca C/G catggtggggaggttcctca	213
TGM1	9	Intron14 + 1691	ccatggtggggaggttcctc G/A tcctaagggatccgcagagc	214
TGM1	10	Intron14 - 1634	tccctgcctccctccttcag G/A gagctcagaaacaccttcaa	215
TGM1	11	Intron14 - 1459	ggaaaccccctcagaaccagg T/C tccaagccaaatgctttgcc	216
TGM1	12	Intron14 - 801	cagaatacaaaagtgggatg G/C gaggcaaggagtcccgttag	217
TGM1	13	Exon15 + 233	ctcgaggtggagcttagccc T/C gtgccaggagcaatgggact	218
TGM1	14	Exon15 + 369	ggagtcagtcttcacttgca C/A tgggggaacagatgctaata	219
GGT1	1	intron1 + 85	ttatccagtaaggtggctcc G/A tcacctcttttcctggtggg	220
GGT1	2	exon3 + 68	gacggccaggtccggatggt G/T gtgggagctgctgggggcac	221
NQO1	1	1 intron 1 80	aggaggttgtaggggcttgg C/A ctgaattttgttccttgact	222
PIG3	1	5'flanking region -47	gggaaggaggaaaggaaaga G/A ggggagggtggttctgctta	223
PIG3	2	intron 2 243	taacaccggacgcccagcag A/C agtcccagcttcttagaatc	224
PIG3	3	3'flanking region 282	agcaggccccagccctgccc G/A ctactcacctgggccccacc	225
NQO2	1	5'flanking region -434	tttctgttgcaccacggacc C/G tcattctgtaaccgggatac	226
NQO2	2	5'flanking region -406	gtaaccgggataccagccag A/G gatggggagcgggaggcgca	227
NQO2	3	5'untranslated region -102	tcctgcggctcctactgggg A/C gtgcgctggtcggaaggtga	228
NQO2	4	intron 1 1919	tcactcaaatagagctgagt T/C agtcactcagctcttggacc	229
NQO2	5	intron 1 2004	acaaactcacatgccaccag C/G catatgatgtaaacatgtaa	230
NQO2	6	intron 1 3391	aaagcagagggctgtgcagg C/T gcccctgcccctaggctagg	231
NQO2	7	intron 1 3456	caaaggcctcatcctcaggg C/A ggccaactcttctgttttag	232
NQO2	8	intron 1 3595	actgcccagctttaggttca T/C tcttgtaagtgttgctggtg	233
NQO2	9	intron 1 3596	ctgcccagctttaggttcat T/C cttgtaagtgttgctggtgt	234
NQO2	10	intron 1 3598	gcccagctttaggttcattc T/C tgtaagtgttgctggtgtca	235
NQO2	11	intron 1 3651	ccctgcgctttgaagggatg A/G atgtgacctctccacattc	236
NQO2	12	intron 1 6036	tggtgtggcggttcactgat C/T ccccagccttctgctcgatc	237
NQO2	13	intron 2 14	atggcaggtaatgattcact A/G ttgtggagtaagacttttttt	238
NQO2	14	intron 2 192	gccacgtggaagtgtataaa C/T tatctggaattatcttgttt	239
NQO2	15	intron 2 635	caccctgtttagcacctagc A/C ccatccctggcctctgccca	240
NQO2	16	intron 2 685	agtagcacccctcccccacc G/A gctgtgacaaaccaaaatgt	241
NQO2	17	exon 3 139	ctgatttgtatgccatgaac T/C ttgagccgagggccacagac	242
NQO2	18	intron 3 36	aatgctctatttataaaaac T/C atctttatgttttttacttt	243
NQO2	19	intron 3 728	aacgtgggcataaaccacca T/C ctagtgccaaaaagcaggtg	244
NQO2	20	intron 4 1577	tgcctctgcacacccttcc C/T gacaccagccctttctttac	245
NQO2	21	intron 4 1832	tcggccggccacgtggagcc C/T gctttcctcctcgcacccac	246
NQO2	22	intron 4 2583	tggtgttacgcacagctcct C/T gtcccctccctgcctgccca	247
NQO2	23	exon 5 330	ctgtactggttcagcgtgcc A/G gccatcctgaagggctggat	248
NQO2	24	exon 5 405	atcccaggattctacgattc C/T ggtttgctccaggtatgtgc	249
NQO2	25	intron 5 21	gtatgtgctcttggataagg A/T tcactatggatagttggagg	250
NQO2	26	intron 5 253	atggcaaacaagggagtggg T/C caggtgtcaggtgacggggg	251
NQO2	27	intron 6 2435	ccccccttaaatcatttaac T/C gaatggtatgtaacaggtgt	252
SULT1A1	1	5'flanking region -1597	gcagagtaaagggactcact C/G aagaagaggaacgtgggggt	253
SULT1A1	2	5'flanking region -1491	gaggggtatattcatgaaga G/T tccaggaaaaggtaaagatt	254
SULT1A1	3	5'flanking region -1376	cggtttcatatgttactgat C/T atacaatgagatcctaggtg	255
SULT1A1	4	5'flanking region -1375	ggtttcatatgttactgatc A/G tacaatgagatcctaggtga	256
SULT1A1	5	5'flanking region -1370	catatgttactgatcataca A/G tgagatcctaggtgaaacct	257
SULT1A1	6	exon 1B -65	aaccctgcattccccacaca G/A cacccacaatcagccactgc	258
SULT1A1	7	intron 1B 442	gagccaccctgcctaggcct G/A tgcttttgctgagtcatcag	259
SULT1A1	8	exon 1A -197	gctgggggtcccagcaggaa A/G tggtgagacaaagggcgctg	260
SULT1A1	9	exon 1A -159	ctggctggcagggagacagc A/C caggaaggtcctagagcttc	261

Designation of Gene	No.	Location	Sequence	SEQ ID NO
SULT1A1	10	exon 1A -95	gagaccttcacacaccctga T/C atctgggccttgcccgacga	262
SULT1A1	11	intron 1A 60	ctggttttcagccccagccc C/T gccactgactggctttgtga	263
SULT1A1	12	intron 1A 69	agccccagccccgccactga C/G tggctttgtgagtgcgggca	264
SULT1A1	13	intron 1A 174	tgtgatggtggtaagggaac G/A ggcctggctctggcccctga	265
SULT1A1	14	intron 6 11	catgaaggaggtgagaccac C/G tgtgaagcttccctccatgt	266
SULT1A1	15	intron 6 17	ggaggtgagaccacctgtga A/T gcttccctccatgtgacacc	267
SULT1A1	16	intron 6 35	gaagcttccctccatgtgac A/T cctgggggccggcacctcac	268
SULT1A1	17	intron 6 71	ctcacagggacccaccaggg T/C cacccagccccctcccttgg	269
SULT1A1	18	intron 6 108	ttggcagcccccacagcagg C/A ccggattccccatcctgcct	270
SULT1A1	19	intron 6 111	gcagcccccacagcaggccc G/A gattccccatcctgccttct	271
SULT1A1	20	intron 6 270	ctccctgccaaagggtgtgc C/T acccagggccacagtcatgg	272
SULT1A1	21	intron 6 488	ttttacttttcctgaatcag C/T aatccgagcctccactgagg	273
SULT1A1	22	intron 6 509	aatccgagcctccactgagg A/G gccctctgctgctcagaacc	274
SULT1A1	23	exon 7 600	ccctctgctgctcagaaccc C/G aaaagggagattcaaaagat	275
SULT1A1	24	exon 7 645	gagtttgtggggcactccct G/A ccagaggagaccgtggactt	276
SULT1A1	25	exon 8 902	gctgtgagaggggctcctgg G/A gtcactgcagagggagtgtg	277
SULT1A2	1	5'flanking region -547	tgttctttcttggttctatg G/C atccatgctctgctccaccc	278
SULT1A2	2	5'flanking region -425	tgtgggttgcactgggccag G/A acccctggcaccttcaagac	279
SULT1A2	3	5'flanking region -358	ctttccagggcctgcctatc C/T cagctttctccttcttgcct	280
SULT1A2	4	5'flanking region -355	tccagggcctgcctatccca G/T ctttctccttcttgcctggg	281
SULT1A2	5	5'untranslated region -28	actgcgggcgaggagggcac A/G aggccaggttcccaagagct	282
SULT1A2	6	intron 1A 85	ctgactggccttgtgagtgc G/A ggcaagtcactcagcctccc	283
SULT1A2	7	exon 2 24	gagctgatccaggacatctc T/C cgcccgccactggagtacgt	284
SULT1A2	8	intron 2 34	gccacccaccctctcccagg T/C ggcagtcccccaccttggcca	285
SULT1A2	9	intron 5 77	cagcaaccctgtgtcggcac T/C ccctgcccgcttctccagtg	286
SULT1A2	10	intron 6 684	actggggtcccaggggtcga G/C gagctggctctatgggtttt	287
SULT1A2	11	3'untranslated region 895	gctctgagctgtgagagggg T/C tcctggagtcactgcagagg	288
SULT1A2	12	3'flanking region 98	cctccccgctccagctcctc A/T acttgccctgtttggagagg	289
SULT1A2	13	3'flanking region 817	ccactgactcggggcttgcc A/C aggctgccagggctggcaaa	290
SULT1A2	14	3'flanking region 1006	cctctcccctggaggctgct T/C tacccgctgtgggggcgcat	291
SULT1A2	15	3'flanking region 1464	tcccgtagcccaggcaagtt C/T ggtgaccagagagcagcccc	292
SULTX3	1	intron 1 332	cctgcttctccctttacctg G/T ctggctgtgtgaccttggac	293
SULTX3	2	intron 1 1167	taggaatggctaagcgtgtc G/A ttggcttctgtggccactca	294
SULTX3	3	intron 1 2872	cattctcactgatgcagacg G/A aagcttctgggcctgggcgt	295
SULTX3	4	intron 1 6242	caccccttggcttttaccagc A/G tggaaacattttacctgaat	296
SULTX3	5	intron 1 6601	gcgtgggcttctggaggggag C/T gagaggagagtggagggccc	297
SULTX3	6	intron 1 6768	agcttgaaatgagccagact C/T tcctgggacctgttgacccc	298
SULTX3	7	intron 1 6905	agtactttgttttatcctcc C/T catcctcacaactttgccat	299
SULTX3	8	intron 1 7464	gccaggatcccttgagagac G/A acatgaacacagccaggagc	300
SULTX3	9	intron 1 7833	tgcttcgggctgggcttggc G/A ggggcagctgtgctccaggc	301
SULTX3	10	intron 1 8189	caaactggggcccttaatgc C/T gcacaccagagcctcctttc	302
SULTX3	11	intron 1 8316	ctctcacacaagggcggagc C/G tcttcccctgaggcagagc	303
SULTX3	12	intron 1 8617	agacagaggctggggccaag C/T cagggttgccggagcttcct	304
SULTX3	13	intron 1 8631	gccaagccagggttgccgga G/T cttcctggactggtcaggcc	305
SULTX3	14	intron 1 9493	ttttcctcttagagcttccc G/A tcgtgctctgtgtcgagggc	306
SULTX3	15	intron 1 10306	caggcggggagcctgaatgc C/T gcagtcgtgagggtggccag	307
SULTX3	16	intron 1 11987	tcataaaataatgatatcag T/C acacttttggaaatttgag	308
SULTX3	17	intron 1 13085	ctctgtgcccggtgttgaga C/A aggccatgccctagagtcct	309
SULTX3	18	intron 1 13108	gccatgccctagagtcctgg G/A gagttccaccccagaacagc	310
SULTX3	19	intron 2 700	gaaccatctgggagtcgttc C/T gtactgccgtgccgagggcc	311
SULTX3	20	intron 2 818	agccatagtagctagccagc G/A atcagcgctgggaggggagc	312
SULTX3	21	intron 2 1677	actccacttcccctgaaccc C/T accccttccttcctcctctg	313
SULTX3	22	intron 4 4954	gcgtgccgaaggcgggaggg C/T tgggatggctcaagacgtga	314
SULTX3	23	intron 5 3632	ccagctgactcccacaccag C/T ggtcagagaacattgtcttt	315
SULTX3	24	intron 5 3662	acattgtcttttaaggtttc C/T gaagtgctgcaataaagaaa	316
SULTX3	25	intron 6 1874	tctgatctcagagagctgac A/G atggaaagaattctaaacga	317
SULTX3	26	intron 6 2133	agaccggtgcctgcagttta T/G cccacagctcagccctccct	318
SULTX3	27	intron 6 2524	ggaagggccagggctgcctg T/C gatgcccagagcagtgcact	319
SULTX3	28	intron 6 2573	agatcatactcgctcctggg A/G tgtttattaaacacctgcca	320
SULTX3	29	3'flanking region 12	gttcccggcgttgcgtcgag C/G gtttctgcttgtgggggtag	321
SULTX3	30	3'flanking region 445	tccaaagcctgtcttcctga T/G ttcctgtggaaggagagtcc	322
TPST1	1	5'flanking region -298	acccgccaccatgcccagct A/C atttttttgtatttttttt	323
TPST1	2	intron 1 3520	agaaaagcagattaatgtaa C/G agtgacgcttagacaacaag	324
TPST1	3	intron 1 3610	ggcagaaagagaatatagca A/G ctattaaacacaaataaatt	325
TPST1	4	intron 1 20828	tattgctgtccacctggtca A/G tgtgtcctgctgataagtgc	326
TPST1	5	intron 1 -6761	aatacaatacttattctgta T/C aattctagagggcccagaga	327
TPST1	6	intron 1 -544	tagaacaagtgaatatttta C/T gttcttagtggtttatggtt	328
TPST1	7	intron 1 -526	tacgttcttagtggtttatg G/T ttggcagttttcccccaaca	329
TPST1	8	intron 1 -234	tcaagacatttaataatgca C/T atgtttcagctaacccttttt	330
TPST1	9	intron 1 -48	ttatagtgggtttaagcatg A/G tttctaaaaaatttaaataa	331
TPST1	10	intron 2 -18944	aaaacattagaactgggaag G/A ttaaaaaatctttagtcttt	332
TPST1	11	intron 2 -18687	tatgtgcaccctaataacat A/G tttccttaaaactagtacta	333
TPST1	12	intron 2 -18501	ttggaaggtaacttaatgta A/G gtgcctgaaaaacagggata	334
TPST1	13	intron 2 -159	gaatggggatttccctcagt C/G ctgcccactggctgctcttg	335
TPST1	14	intron 2 -19	acctgttgccttaaactcac G/A cctgctttgtttttccaggt	336
TPST1	15	intron 3 158	tgctggggaagaaagatcag C/G gtctgggacttgttgatttt	337
TPST1	16	intron 3 3779	agcagggcacgtcaccctcc C/T ggcacacccatgtgttcacc	338
TPST1	17	intron 4 292	ttgttattttcattatgaac C/T atgaaatatttcagctgaaa	339
TPST1	18	3'untranslated region 1518	gttgtctgtacatgttctaa T/G gttttgtagaacacgtgtgc	340
TPST1	19	3'flanking region 264	acggtgcttggcctgcatta C/T cattttgtagtgaagtttct	341
TPST2	1	intron 2 578	tcacctatcatcctcactgc G/A aggatgccaggatacctccc	342
TPST2	2	intron 2 789	cttaagccatcgtgcaggtc A/G ttgctgtcttctgctcactt	343
TPST2	3	intron 3 2009	cccaggctggagtgtagtgg T/C gtgatctcggctcactgcaa	344
TPST2	4	intron 3 2017	ggagtgtagtggtgtgatct C/T ggctcactgcaacctccgcc	345
TPST2	5	intron 3 2035	ctcggctcactgcaacctcc G/A cctcccgggttcaagcagtt	346
TPST2	6	intron 4 104	aatgttcagtctctcaattc C/T tggtcatctgatttgttcct	347
TPST2	7	intron 4 379	taaataaataaactattggt C/T cctttcttgtcttataaggt	348

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
TPST2	8	intron 4 588	tactgcagcctgatacttct C/T ggcttaagccatcctctcac	349
TPST2	9	intron 4 626	caccccaggctcctgagtag C/T taggactgcaggtgcacgcc	350
TPST2	10	intron 4 718	cccaggctggtctagaactc C/G tggccgtaagggatgcccct	351
TPST2	11	intron 4 873	gttgatggccttatttatac G/A tttccattacagcttctagt	352
TPST2	12	intron 4 949	caaatatttgaaaatgggac C/G caggcctgaggaagagcttt	353
TPST2	13	intron 4 1033	taagctcagcatttctgagc G/A tgtgctgattttaggaaata	354
TPST2	14	intron 4 1051	gcgtgtgctgattttaggaa A/G taaacagttatcgtattgaa	355
TPST2	15	intron 4 1356	gattcaacgtacataccagc C/T gacattgacaggtgaatggc	356
TPST2	16	intron 4 1707	gtctccttaaaaggtggctc G/T ctgcccctggcttgccccag	357
TPST2	17	intron 5 215	aagaccagcctgaccaaaac G/A gtgaaaccccgtctctacta	358
TPST2	18	intron 5 341	tgggaggcagaggtcgcagt G/A agctgagatcacgccgttgc	359
TPST2	19	intron 6 31	ggacttcactgggggttccc G/A ctgcttctgggtggccccgg	360
TPST2	20	intron 6 273	gtttgtctgacactggggac A/G gggcaggaagcaccactatg	361
TPST2	21	intron 6 693	aaagggatttttttgaacttt G/C gtaattcaaagatttaagat	362
TPST2	22	intron 6 1635	tcctgggtacagagttggcc T/G tgaacaaacatgagtccttc	363
TPST2	23	3'untranslated region 1147	cttccccactttcagatctc C/T gcaaatgacttcattgccaa	364
SULT1A3	1	exon 8 843	cgcttcgatgcggactatgc G/A gagaagatggcaggctgcag	365
CST	1	intron 1b 6302	agagctccccagagaggact A/G tgaggctgcatgatgcatga	366
CST	2	intron 2a 1004	gagtgagacccccatctcta C/T aaaatttttttttaaaaagta	367
CST	3	intron 2a 1395	atgcctaagtttacagtagc T/C aggcaggaaaggcacaacca	368
CST	4	intron 1d 473	ccagagcctgaggttggtgc T/A ggggcccctccatggctgcc	369
CST	5	intron 2b 726	ctatctctccagtgcctctc T/C gtccctgtctggaccctgct	370
CST	6	intron 2b 745	ctgtccctgtctggaccctg C/A tgggggccacagagcaggc	371
CST	7	exon 3 85	tcactagtttcctgctgctg G/A tgtactcctatgccgtgccc	372
CST	8	intron 3 308	tcgtctgaggtcaggagttc G/A agaccagcctggccaacatg	373
CST	9	intron 3 853	ttttgtcctataaaatggca G/A tttcatgtggcccaagctga	374
CST	10	exon 4 198	gaggcagtgatccgggccaa C/T ggctcggcgggggagtgcca	375
SULT1C1	1	intron 3 2280	gcaaatttttggtatttttа G/T tacagtcagggttttaccat	376
SULT1C1	2	intron 3 3742	gcagatctcactttctggca G/A attccctgaatttgctcccc	377
SULT1C1	3	intron 3 4453	ttcatagggcttttccctca C/T ttgttttgtaattttgtata	378
SULT1C1	4	intron 3 5234	gaaaagagactagaggcagg A/G gagctttgcagttcttctaa	379
SULT1C1	5	intron 3 6175	tggctggcaggaaggtgagg G/C agtcctctcttctctggtcc	380
SULT1C1	6	intron 4 205	acatgaaggcaggatccaga T/C tgaatgtttggagggaacta	381
SULT1C1	7	intron 4 408	ggctcacgcctgtaatccca G/C cactttgggaggccgaggcg	382
SULT1C1	8	intron 4 429	cactttgggaggccgaggcg G/C gtggatcacaaagtcaggag	383
SULT1C2	1	5'flanking region -110	tcctgttaactcacagagaa C/T ggaagggctggaacgggacc	384
SULT1C2	2	exon 1 15	acactaatggccttacacga C/G atggaggattttacatttga	385
SULT1C2	3	intron 1 297	gtagacttgtttatttattc A/C ttcccaatctaggcccttat	386
SULT1C2	4	intron 1 363	gagtgtgtgagctagaaagg T/G gatcctgagtctgatttggg	387
SULT1C2	5	intron 1 2300	gggctactatcagcagccac C/T acctcaggaaggatgacttc	388
SULT1C2	6	intron 2 455	aagacttggaagcaaataga T/G aaaaaaaaaatcgtagaaat	389
SULT1C2	7	intron 4 55	caaaatctccaaacacccta G/A aaggaaagaatcttttcttt	390
SULT1C2	8	intron 4 111	ctgccttctttaatggaaca T/C tctcacttctcttcaggaat	391
SULT1C2	9	intron 5 1657	ctttgtgtttactttgtttt T/C acttggtacaaaagtgttgt	392
SULT1C2	10	intron 5 2082	tctgctcctagagatggagg C/A gtcccacagccacagtgatg	393
SULT1C2	11	intron 6 933	agctactgaacctctcccac A/G taactgtatttcaggggcag	394
ST1B2	1	intron1 80	acttgtccataaaatcatta C/T cattctaaataaagttaata	395
ST1B2	2	intron 2 -352	aacatttaaatagtcattta T/C agcaatgcacaggtataata	396
ST1B2	3	intron 2 -85	attacataatgctcaaaaat G/A tcttgaaaaactggttggca	397
ST1B2	4	intron 4 460	gtacttgacattaaaaaata T/C ctgatgtttatatatccata	398
ST1B2	5	intron 4 470	ttaaaaaatatctgatgttt A/G tatatccataaatagctaat	399
ST1B2	6	intron 4 518	tttaagattgtcctcatatt C/G ttacttcctttggttactaa	400
ST1B2	7	intron 4 616	aatgtttatgaaaatagact T/C ttatctggttttagtggcct	401
ST1B2	8	intron 5 58	ctgcatcatgctgtaaaagg G/A ttgatatttgctttccaact	402
ST1B2	9	exon 6 612	taatagaatccaaaggagga A/C atcaagaagatcattagatt	403
ST1B2	10	intron 6 582	aatacattacttccatttaa G/A tagtctgtttattgtggctt	404
ST1B2	11	intron 6 3130	agatgtaaaaaattattcaa A/T ttttaaaagcctgaaaaatt	405
ST1B2	12	3'untranslated region 907	tttaaagtgtctaaatcaca C/A atctgaagaaataagagatt	406
ST1B2	13	3'flanking region 50	tcagatcccagttttgttcc T/G ttgattctgagtttccaaat	407
ST1B2	14	3'flanking region 328	tttgacccaggacactgtgt T/G ccactgctgtctaccgagtt	408
ST1B2	15	3'flanking region 446	gtagttcagattttggaaat C/A ttttttctatatcataccta	409
CHST2	1	5'flanking region -260	agccggacagtccgccgggc G/A gtgatccgggggccgctccc	410
CHST2	2	5'flanking region -56	gcgctggggaccagccgccg C/T gcccgcctcggagtcgcggc	411
CHST2	3	3'flanking region 218	aggagtgaaacacatctttg T/A attctaaaggcagaaaccaa	412
CHST2	4	3'flanking region 383	gcagagaccaatgttttggt G/C ctgaggctggttcagaaaaa	413
CHST2	5	3'flanking region 952	tactgaaacattctgcagaa T/C gttatactatgagaagaaat	414
SULT2A1	1	intron 2 478	ggactgggctctgtacacac T/C tcgtcttactgtgtgtaaat	415
SULT2A1	2	intron 3 382	caaaaccctcttaatattct G/A tttctatctgtctcagaact	416
SULT2A1	3	intron 3 409	tctgtctcagaactgattgc A/G tgactctaggatcgctatat	417
SULT2A1	4	intron 5 249	agctggaaattacaggcaca C/T gccaccacacccagctaatt	418
SULT2A1	5	intron 5 395	aggcatgagccacggcgccc G/A gccaatttatcagctttaat	419
SULT2A1	6	3'flanking region 33	ttccttgttaaaagttacca G/C ggttggccaggcacggtggt	420
SULT2A1	7	3'flanking region 46	gttaccagggttggccaggc A/G cggtggttcatgcctgtaat	421
SULT2A1	8	3'flanking region 199	ttagccaggcgcattggctc A/G tgtctgtaatcccagcactt	422
SULT2B1	1	intron 2 4162	ttctcccctctcctcaccat C/T cgcacacaggtgatctacat	423
SULT2B1	2	intron 3 879	gagggcatccagctctgggg G/A ctggacctgggggtttgtgg	424
SULT2B1	3	intron 4 3882	ttccacgctccttccttggc C/T gagtgccctccctccgctga	425
SULT2B1	4	intron 5 1780	cctgcagaaggggtccctt C/T catgtccaagcagtaatggc	426
SULT2B1	5	intron 5 1814	taatggctgcagcatggagc G/A ttgtgggggcattgagacag	427
SULT2B1	6	exon 6 789	ccctcttctccaggggtctg C/T ggcgactggaagaaccactt	428
CHST4	1	5'flanking region -1092	atgaagccttgtgccatctc G/A ctgtgtcgtgccagcacctg	429
CHST4	2	5'flanking region -941	ctgccagagagaaacaggaa G/A ggaggaagagccacacaatt	430
CHST4	3	intron 1 -150	caggaaatgatttggagaag G/T actggtgccattgttggcac	431
CHST5	1	intron 1 -144	ggcctcttaggtttcagcca A/C gacaggtgactcttagcacc	432
CHST5	2	intron 2 17	caacgtaagagcggcttctca T/A tgtccagctcctttgtttct	433
CHST5	3	intron 2 139	aatcccagcactttgggagg C/A ggagatgtgcggatggatca	434
CHST5	4	intron 3 1829	gactgtatgtctgctattca T/C ataggaacaaataattcatg	435

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
CHST5	5	intron 3 2037	aaatgaaaccaacaccaaca C/G tgcagagaagcaaacaaaag	436
CHST5	6	intron 3 2134	aagcagctaaattgtgttcc G/A tacaggtgcaattaggcagg	437
CHST5	7	intron 3 2528	atggtaaagttcgcctgggt G/A cagtatgtcagcatcctgct	438
CHST5	8	intron 3 2674	gcacttatcctagaaaggcc A/G tttctgaagactcagcagga	439
CHST5	9	intron 3 7039	ctggctcccgccggccaccc T/C gggaccgcagccacgtctga	440
CHST5	10	intron 3 7211	gtagccccaggacaccccca T/G cctcaacatcccattctggg	441
CHST5	11	intron 3 7294	ggagcttccagtggcttggt T/C acccccgactcttcgtccat	442
CHST5	12	intron 4 108	gcagggtcctgcactctgca G/A ggggcaatcacaggtgggag	443
CHST5	13	intron 4 402	agcactggaaaaagtacagt T/C gcacttgtagcggaggtggg	444
CHST5	14	intron 4 547	ctcctgtccccgcattgagg C/G gaaggagcagaggtgagatc	445
CHST5	15	intron 4 1142	gccccaggtctcatagctcc C/G cattggcagtgctgggattt	446
CHST5	16	intron 5 1187	cactgggcagtaattggggc A/G tgggatgggcatgagggccc	447
HNK-1st	1	intron 1 139	gtgttttggcgacttgaaga C/T ctccctagttcgcgggagta	448
HNK-1st	2	intron 1 1020	acctgagcagaaaattctct T/C cttcgctgaaatgaaaattg	449
HNK-1st	3	intron 1 1091	aagaatttgtaaacatcaca G/A gcaacttgcagttatattcg	450
HNK-1st	4	intron 1 1971	ctataactatttcaaacata C/T gaaacaggcataattggatt	451
HNK-1st	5	intron 1 2096	atttagaatattcatttacc A/C agaaatccaaaatataacctg	452
HNK-1st	6	5'untranslated region -91	ctatccagtgacaagaggaa C/A caagaacctcagttcagggg	453
HNK-1st	7	intron 2 -530	agtgggcggaggcgagaagc G/A tcagtgttcattcctttgct	454
HNK-1st	8	intron 2 -466	gctacatcttgtcagccagt C/T agaattttaaacacagccag	455
HNK-1st	9	intron 2 -92	acggaaatatttgtgctgat A/T cttactgactgaaatcacct	456
HNK-1st	10	intron 3 152	catggcctccgttccttcat G/A ttacagaggtgtgaggggag	457
HNK-1st	11	intron 3 312	cacagtggccttatgccttg C/T agcagggcgcctctcaggct	458
HNK-1st	12	intron 3 1948	tcctttgatgtatcaagttt T/C gtgctgaatgttttcagtgt	459
HNK-1st	13	intron 3 2140	ttacacctggagaggagcac C/T gcagcggtccttaatactgc	460
HNK-1st	14	exon 4 187	agaagcacattcctgaggaa C/T tgaaggtgggcacagccagg	461
HNK-1st	15	intron 4 581	cctgatcattccctagctgg G/A atgaggggtgcactctggaa	462
HNK-1st	16	intron 4 615	tctggaaggcctctcacttc G/C taacccccattctggatcta	463
HNK-1st	17	intron 5 7	gattgttctaaatggtgtgt G/A tgggtctactgaatgtccac	464
HNK-1st	18	intron 5 123	acctgaagggactggtggcc G/T tccagacaggcctgtttttg	465
HNK-1st	19	intron 5 721	ataattatgggctctgctta T/C gaaatttagcttcagacagg	466
HNK-1st	20	intron 5 867	tgctgcccacagagtcggtg G/A tcactcctggccactgtttg	467
HNK-1st	21	exon 6 444	ccaggagcattttcttccat T/C gaggagatccccgaaaacgt	468
HNK-1st	22	intron 6 94	ctgagttctgtacttggcag A/G ttgatcggaggaccacagag	469
HNK-1st	23	intron 6 247	catgaaggtgacatcatttt G/A ttaatagaaattagcaggca	470
HNK-1st	24	exon 7 696	aggaggaaccggacagagac C/G cgggggatccagtttgaaga	471
HNK-1st	25	exon 7 870	gagaccctggaggacgatgc C/T ccatacatcttaaaagaggc	472
HNK-1st	26	3'untranslated region 1110	tcaaatatctttattagacc T/C ggggctaaccaggtgaagat	473
HNK-1st	27	3'untranslated region 1178	ccacacccctcctttgagga C/T gcccggggtctcccacaggc	474
HNK-1st	28	3'untranslated region 1393	ggaagcatcacacagcgtta G/A gagccgtttccttcaggtgt	475
HNK-1st	29	3'untranslated region 1452	tgaggttctcctggctagtc A/G gggtggcttcacccatcact	476
HNK-1st	30	3'untranslated region 1540	gcaaggggggctgctgaaatc G/C cagagacttttgcagcatca	477
HNK-1st	31	3'untranslated region 1696	gggtggtgtggtgtccaggg G/A tccatctttccagaatccat	478
HNK-1st	32	3'untranslated region 1829	aggggaggctttttctacct G/A agaaggggagtgtctttgag	479
HNK-1st	33	3'untranslated region 2211	tccagcagtgcggcttcctg G/T caacaaggtaggccctggtg	480
HNK-1st	34	3'untranslated region 2212	ccagcagtgcggcttcctgg C/T aacaaggtaggccctggtgc	481
HNK-1st	35	3'flanking region 1016	cacacgaaggtgtgcactca C/T ggcctgcagggcacccaggt	482
HNK-1st	36	3'flanking region 1152	gcatgctttgctcatctgga A/C tctccagaagcagggaacag	483
HNK-1st	37	3'flanking region 1291	gccgagaccctcagcaggat A/G gtgcagttacagggctgagc	484
STE	1	5'flanking region -605	caggtttctaaaataataat C/T gaaaggtgagtgatgtttac	485
STE	2	5'flanking region -536	taaaattttcaggtctgctt A/G agagttaaaggcaaagagtt	486
STE	3	5'flanking region -231	ccttcttccccaacccctga C/T ggcagacttgggaatttgaa	487
STE	4	5'untranslated region -64	tgcagcttaagatctgcctt G/A gtatttgaagagatataaac	488
STE	5	intron 1 69	aaatatagaatgaaaattat G/A tattacaaagctcttaaaaa	489
STE	6	intron 1 311	caatgagaaaataaagcaag C/G agggtagaaggaggtagaat	490
STE	7	intron 1 655	tctaagaaagtagggactat G/A agaacccctatgtatctata	491
STE	8	intron 1 671	ctatgagaaccctatgtat C/T tatatccaccatagtattct	492
STE	9	intron 1 772	aaaaggcaggttggaagatg C/A aggaggggagtatgcagaaa	493
STE	10	intron 1 1715	taaccatcttgcttaacctt A/G tcatttttagccaagtcatt	494
STE	11	intron 1 1928	aaatgatacatattcaggaa A/G tcaaaaatctctgacttaga	495
STE	12	intron 1 1953	aaatctctgacttagatacc C/T ggcaataataatcaaatgta	496
STE	13	intron 1 2087	aattttgaaagaaattgaag T/G tctgtggtttttatttatca	497
STE	14	intron 1 2323	taggtatgtaggagggtccc G/C ttatatacatagttgttaat	498
STE	15	intron 2 165	tctattccatgaccacaatt T/G ttacctgtaacttgaatagt	499
STE	16	intron 2 1707	cctaggacccaacatgagac A/G taatataccatcagtaaaat	500
STE	17	intron 3 850	ggtgtccattccctcaagaa T/G ttatactttgtgttacacac	501
STE	18	intron 4 1653	agtaacaggctagtagataa T/C ataaataactgaggccaacg	502
STE	19	intron 4 1899	tacatgaacttagagaatca A/G gtagatcacacacaccaaca	503
STE	20	intron 4 1930	cacaccaacaataaaattac A/G cagaatgataaaagaatttg	504
STE	21	intron 5 666	ttctgatcatgtagtaacaa T/C tataaagaaaataataatgt	505
STE	22	intron 5 982	aggcaaagcagaacctttg A/C ctcacacaacattatattat	506
STE	23	intron 7 369	agattttattcctctctctt T/C ttgagttgaagaaataagtt	507
STE	24	intron 7 447	caccttcaagggtaagtgg C/A aaaaaatagaaattcaaata	508
STE	25	intron 7 672	aatcttgctctttgaaccat A/T ctgtcagtgagagtcaggga	509
STE	26	intron 7 856	tgttacagaggacttaaaac A/G gttgtcttgcttgcaaacgg	510
STE	27	3'flanking region 218	cagcctcccaagtagctagg A/G ctacagacatgtgcaaccat	511
ADH1	1	5'flanking region -55	atcatgtgtggaactggaat C/T gggtgttattcaagcaaaaa	512
ADH1	2	intron 1 268	acatttgcggtaaagcgata A/G tttattccaagctaatcatg	513
ADH1	3	intron 3 442	aaatggaggctacatggcta C/A ggctgaatgagcatgacctt	514
ADH1	4	intron 6 56	tacaacttggaggatgcatt T/G aggctgcagaatatatgttt	515
ADH1	5	intron 8 74	gtctagcagaaaatgaaaag G/A tggaaggatgagaaaaatta	516
ADH2	1	intron 2 340	ctatttttaaagcgtgcat T/C cttacataagacttaaatat	517
ADH2	2	intron 3 91	aaggcaatgagagacgaaag T/G gcttgcacaaggtcaccgcg	518
ADH2	3	intron 3 205	atgtattgtacccttcaacc A/G ttatgtaccgagtatctact	519
ADH2	4	intron 7 108	acaattgacaaggcaagatt T/C tgaaaacaaatcaaaaataa	520
ADH3	1	5'flanking region -254	tgagagaagagaagcaggaa C/G ttgagagaggaggaagagag	521
ADH3	2	intron 2 355	tatgcattcttctatattat A/G caagacaaaaattttaggat	522

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ADH3	3	intron 3 32	acactcagggaacatgcctt G/A gttcaccatcacaagattag	523
ADH3	4	intron 4 6	ctgcttgaaaaatgagtaag C/T ttctgatgctttctttgcac	524
ADH3	5	exon 5 453	agcaccttctcccagtacac A/G gtggtggatgagaatgcagt	525
ADH3	6	exon 6 815	ttcgtttgaagtcatcggtc A/G gcttgacaccatggtatgat	526
ADH6	1	intron 3 249	tgaaactggacttgaaagta C/A aaatgagacaaaaatttatg	527
ADH6	2	intron 6 1072	taacccctatactgtattgc A/G tcactttctaacaggcagct	528
ADH6	3	exon 7 885	gtctgtgtggttgttggggt G/A ttgcctgccagtgttcaact	529
ADH6	4	intron 7 1292	gttgagaaacactgcctagt C/A ccgtctgtggtcctagaatt	530
ADH6	5	intron 7 1616	ctatcacagaataatccgca T/C agaacactaagcagattacg	531
ADH7	1	5'flanking region -528	tgtgcagacacagaaagttt T/C acttaactttctcacacctaa	532
ADH7	2	intorn 1 361	tcagtagcatgtgctgcact C/T gctgcagtagttcaatggga	533
ADH7	3	intron 3 183	aacctcaacctttagaaggc A/G aaccttacggtgtttataaa	534
ADH7	4	intron 4 76	tgaattgaattaattaatac G/A tgtatttgatgtatcaaaca	535
ADH7	5	intron 6 615	tggcatagcgtaaagagact T/A ggaaaaatggaataaagcca	536
ADH7	6	intron 8 532	aagtctaaccatatcaccaa T/C ttagtatgccattgtactat	537
ADH7	7	intron 8 651	gctgctatttatttcaagta G/A gccacaaaatttccttattt	538
ADH7	8	intron 8 760	catttttagatgaagaccaa T/G gttgtgaaagcaaataaata	539
ADH7	9	intron 8 1207	tctccacatttggtctagcc T/C acaggatcatcatattatga	540
ADH7	10	intron 8 1691	tccctcatctcattgcccac G/A ctcattgctttaattcagtc	541
ADH7	11	3'untranslated region 1364	atttacattttgtaaggcta T/C aattgtatcttttaagaaaa	542
ADH7	12	3'untranslated region 1498	gatatagtaaatgcatctcc T/C agagtaatattcacttaaca	543
ADH7	13	3'untranslated region 1584	aaacacttgttatgagttaa C/G ttggattacattttgaaatc	544
ADH7	14	3'untranslated region 1818	aatataaacatagagctaga A/G tcatattatcatacttatca	545
ADH7	15	3'flanking region 865	tacatcaaaagaaataaatc C/T aagaaggaataaacacattt	546
HEP27	1	5'flanking region -191	tcagcactctgtgtctagct A/T aaggtttgtaaatgcaccaa	547
HEP27	2	5'untranslated region -163	gaacccatcaattccgtaca C/A attttggtgactttgaagag	548
HEP27	3	intron 1 1941	aaatttaccctaaccagcct G/C actctctgccactttctgtt	549
HEP27	4	exon 3 289	ttgtgtgccacgtggggaag G/A ctgaggaccgggagcagctg	550
HEP27	5	intron 4 1070	tgtctcagttcacaggatca T/C gactctttttctcgaaactg	551
HEP27	6	3'flanking region 362	ggctttgtgtgtgctccatt A/G tctgaactgggcctgctggg	552
L1CAM	1	intron 1 + 767	tttgacttccttacatgggt G/A actgtgtgagtcactctgtt	553
L1CAM	2	intron 1 + 862	gcattgggtcatgtgtatgt G/C tgagtggggctgaatgtaag	554
L1CAM	3	intron 1 + 1332	cagggatgaaggagcagagc C/T gctgagaggccacacaggtg	555
L1CAM	4	intron 4 + 502	tttccctggggttttccctt T/C gcattccatcctccctgagc	556
L1CAM	5	intron 18 + 147	agcgacgttatgaaattccc C/A acacttcacatttctataat	557
L1CAM	6	intron 24 + 221	ctccttagccccccagaggg C/T cccaactttaagagcatact	558
AANAT	1	5'flanking-542	aggggtgcaggatggggtgt G/T agctggagggcaggggtag	559
AANAT	2	5'flanking-263	ccccccacataagaggtggg C/G ttgtccaagactccgaggga	560
AANAT	3	intron3 39	cgcccagctccagggaggcc T/A ctgaagacagaggtcagcca	561
AANAT	4	exon4 150	cagccggccgtgcgccgggc C/T gcgctcatgtgcgaggacgc	562
ARD1	1	intron1 + 317	ccgtcggtctgctcggcccc C/G ctccctcggggctgggcagg	563
ARD1	2	intron6 + 322	gctcctcagcatctgctcac G/A ccagggacccacacctctct	564
ARD1	3	intron6 + 1095	aaggctccatcctgagacaa A/C aagtccagtgtgacctgccc	565
ARD1	4	intron6 + 1179	aggaggaagacctgtatccc A/G gggacaccctcctccactcc	566
ARD1	5	intron7 + 159	cctccaggctgctaggcaga C/T ggcctcctctaaagcccagc	567
ARD1	6	intron7 + 295	tgaccagccctgccacccga G/T gagccttgggcagaaccctg	568
ARD1	7	intron7 + 416	actaccatggaggcccccac G/A acagagcgctgccccttgac	569
NAT1	1	3'UTR 215	aataataataataataataa A/T aaatgtattttaaagatggc	570
NAT2	1	exon2 867	cgtgcccaaacctggtgatg G/A atcccttactatttagaata	571
NAT2	2	3'flank 521	ccatccatactttgccacaa G/A agaaggaacatgagctttat	572
NAT2	3	3'flank 573	gatttgaaatcctgtggaca C/T ggggtgaattacttttaaaa	573
NAT2	4	3'flank 918	attttctgtttgtaaattcc A/G gtatcagggctatagtttaa	574
NAT2	5	3'flank 979	actattctccctcttcgact C/T gtgatgactataataatctt	575
NAT2	6	3'flank 1958	tacctattgaagtaagccta C/T gtcatatccacctatttgtt	576
NAT2	7	3'flank 2034	ccactgattcccagagctag T/G tcattaagaagacagtgcct	577
NAT2	8	3'flank 2201	cagattactggagggctact G/A tttgctcaccaatgcaaatg	578
NAT2	9	3'flank 2818	gggatatttgtctcctttct C/G cccagtgcatgttggaaacc	579
NAT2	10	3'flank 3237	atatatattccaattaaaaa A/Δ caaaataaatttccgaaact	580
NAT2	11	3'flank 3386	caacaaagagatttttttaaa G/A ctttttaaaacaccagacag	581
NAT2	12	3'flank 3660	cagcactattcgcaatagca A/G agatgtggaatcaatctaaa	582
NAT2	13	3'flank 3973	agcagaaaaaaataaataatg C/T gtactaggcttactacctgc	583
NAT2	14	3'flank 4029	caaaacaaaacccccatgaca T/C gagtttatctatataacaaa	584
NAT2	15	3'flank 4118	ataagattaatatctgcata C/A aaatctttgtttacagcttg	585
NAT2	16	3'flank 4146	tgtttacagcttgttatata C/T tgaattatgtctgctccccc	586
NAT2	17	3'flank 4279	ttaatctgataggattggtg G/C ctttataagaaaaagaaaag	587
NAT2	18	3'flank 4323	ttgctctctccccagtgcag T/G taccaaggaaaggccatgtg	588
NAT2	19	3'flank 4446	tcaattggctttatctgcga T/C tctggaatcaggcaatactc	589
NAT2	20	3'flank 4462	gcgattctggaatcaggcaa T/C actccatttcataaaaacaga	590
GZMA	1	5'-flanking -462	cctcagcttgcacttggcct A/G ctaattcttatataatccaa	591
GZMA	2	5'-flanking -172	agcctgcctgctggcagtga G/C ccatcatccaccattctcac	592
GZMA	3	intron1 1949	gacataaggttctctctatc A/T gcatgtatggtttgccttgt	593
GZMA	4	intron2 + 683	gactgcgtgaccaggtggaa C/T tagcctcagcatggaagggt	594
GZMA	5	intron2 + 1250	gttggtgtagtttatactag G/A ttatgaatgatagccttaat	595
GZMA	6	exon4 + 105	tgccaagttgcagggtgggg C/G aggactcacaatagtgcatc	596
GZMA	7	intron4 + 696	atagagccttacctgaagaa A/G ggtgtgcagtatgcatggtt	597
GZMA	8	intron4 + 1141	ctgttcagggaggatcccgg G/A ttccaacatggttctttatt	598
GZMB	1	5'flanking + 529	gcctccgtctcacaccaaca A/G gcagatttccccaccacggc	599
GZMB	2	intron3 + 141	gaggggaagattgtgcagccc C/T atcactgtgtcggggcccag	600
GZMB	3	3'flanking + 448	ttttcagggcctgtccctcc G/A atgggggcaggcttctccca	601
ESD	1	5'-flanking -333	gtcttgggacagaggagttg G/A gggagttgaaattaggccct	602
ESD	2	intron 1 603	gtcatttctgatggggtcat C/T agggaaatgggattgagcgc	603
ESD	3	intron 1 717	tgtgtggtagaagcagcatt C/T taagcactacgtgaattaac	604
ESD	4	intron 1 1864	gctttcatgcaggattgatc G/C tagtgggatgtattaggaag	605
ESD	5	intron 1 2389	ttttgggaacacctgtctag G/A tgttaagagccagtggaata	606
ESD	6	intron 2 21	taaacttgttttattgttta T/C atgttactctgaacattgaa	607
ESD	7	intron 2 588	taaaattagtatctctctct G/A taagttcattatttaagata	608
ESD	8	intron 2 1498	tagaaaaatgtgtatcacac C/T gtaagtgttcagtaatgtta	609

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ESD	9	intron 3 92	ctttatctagatattatagt C/A cctcattttacttttaaact	610
ESD	10	intron 3 422	gtaaagagattaaacacaca C/T gcacacatacatatacctat	611
ESD	11	intron 3 581	agaaaacctgagaaatgaca C/T aatttatttaaagccatagt	612
ESD	12	intron 3 2270	gccagtaattacatgtagcc G/A tttacatcaaattagctaat	613
ESD	13	intron 3 2951	taatgaaagtaaatgtttca A/G cttccctaacaaaagttgaa	614
ESD	14	intron 3 3001	aaatgtcagaaatttttttgt G/A ccgtcagtcatcaacaagaa	615
ESD	15	intron 3 3096	aaggagcatacagaaaacttt G/C ccatgatggggccttttgtgg	616
ESD	16	intron 4 2611	tctaatagtccccagtatta A/G tggtgcacatcttcatgtcc	617
ESD	17	intron 5 390	tctttttttcatctctgttaa C/T atcaaccatacagttaaaca	618
ESD	18	intron 7 107	ttagtattggaactaaaactt T/C tctagtgttgagaactttgg	619
ESD	19	intron 8 1090	aaattctaactaattaaagg G/T ttcatcctttagtaactaga	620
ESD	20	intron 8 1651	tataaagttgtggttaatga A/G tatatatgaataagaatatt	621
ESD	21	intron 8 2047	agaaggaaaaaggccatttt G/C ttaagaatccctgagatatg	622
ESD	22	intron 9 -3490	atagaaggagaggctatact A/G cctccttaagtctcaggacc	623
ESD	23	intron 9 -2596	actaaggataaaaatatggc A/G tactcagtcacattggaact	624
ESD	24	intron 9 -666	aggccttaatgacatatttc T/C cctcacataaagatacaaca	625
ESD	25	intron 9 -660	taatgacatatttcccctca A/C ataaagatacaacatgcttt	626
ESD	26	intron 10 799	tatggtaactgaagaaaatg A/G cattaagttcctaaagttat	627
DDOST	1	intron2 629	attctgttaagaagttctta T/C attaagaaatattgtctcct	628
DDOST	2	intron2 3125	gagaatataggagcttctgc G/A tatgcctgaaagtcagtcag	629
DDOST	3	intron2 3920	attactcatttaatgaataa A/G tggattactgagcactgtct	630
DDOST	4	intron3 189	actgctgtccaggggtccat C/T tggggctgagcccagctgga	631
DDOST	5	intron6 185	ctgtcctcttgttcgggagg C/T gtggcagcttttcccttact	632
DDOST	6	exon8 37	aactatgaactagctgtggc C/T ctctcccgctgggtgttcaa	633
DDOST	7	intron9 37	tcctgcccaagaatgctgcc A/Δ aaaaacggccccaggcctca	634
MGST1	1	5'flanking - 5	tctggaccctgaacaggagg G/C gacatcgtgacaaagcaaat	635
MGST1	2	intron1A+330	atcagcaggcgatggttact C/G tgggcgggtaaatcaggtga	636
MGST1	3	intron1C+1428	gtaaagggaaagggcgttcc T/A caactgagaagtgaagattc	637
MGST1	4	repeat	attatttgctctacctcagg G/A tttttcgggtcaagcgagat	638
MGST1	5	intron1C+2914	ctcatcaggtgtgtgtcaga G/T ggcttggtgctggccagtct	639
MGST1	6	intron1C + 4274	attgtaatagattaacaaag G/T tgatgaaagtagtgtacata	640
MGST1	7	intron1C+4276	tgtaatagattaacaaagtt T/G atgaaagtagtgtacataat	641
MGST1	8	intron1C+4306	gtgtacataatgtacatagt A/G tagttgaacacatagcaagc	642
MGST1	9	intron1C+4406	gatggctatatgaccaataa T/A gatacatataaatgtataga	643
MGST1	10	intron1C+4464	agaaagattgcagctgatag A/G tgtcaggctaataaggacac	644
MGST1	11	intron1C+4683	aatggcagaggactggaaat G/T tacattttaagctttaccct	645
MGST1	12	intron1C+4767	gccttcctcttcagcacatt C/T ccaattatacttccaattcc	646
MGST1	13	repeat	atttcaattttttttttgg G/A gggggagacagagtctcact	647
MGST1	14	repeat	aattacctcccaaaggcctc A/T tatcccagatactatcacat	648
MGST1	15	intron2+2379	ttctcaaatttcattataca C/G tattcttcaacccaaagttt	649
MGST1	16	intron2+2767	tttaactatagatgccttct T/G ctcctcttgtgtttgattta	650
MGST1	17	repeat	tcactgcagcctcaacctct C/T gggctcaggtgatcctccaa	651
MGST1	18	repeat	aaaaaaatttgtagatatgg T/G tactccctatgttgcccagg	652
MGST1	19	repeat	ctccctatgttgcccaggct A/G atcttgaattcttgggctca	653
MGST1	20	intron3+1495	gtcagacaatggccttcagc G/A tcctctctttgcagaatatg	654
MGST1	21	intron3+2528	ttttggagacacttttcaga G/C agagcgtttccagcatcttc	655
MGST1	22	intron3+2567	tcccttccatttttaagtt A/Δ gacttttttttttcacctct	656
MGST1	23	intron3+2731	atacacatatggaacaatta A/C ctaaaaacttaaggtaatat	657
MGST1	24	intron3+3288	gggtttatagtgttcccccc C/Δ tccccgccccaaaagaccc	658
MGST1	25	intron3+4288	ccattctatttgtcaactgc G/A taacacaggcgtagaagtgg	659
MGST1	26	intron3+4378	aaatgtctgtccttttggca T/C gttgtgaaggagaacactaa	660
MGST1	27	intron3+4429	attggaggtgacgatatctc T/C gtgatgctgggggagaaatc	661
MGST1	28	intron3+4817	attgctatagaagagagtaa C/T gtaaagcagaaatagttttc	662
MGST1	29	intron3+6077	tttgaaattagtgtctttaa T/C agttatctttttccacagag	663
MGST1	30	exon4+304(3'UTR)	aagaattctgtacttccaat T/G tataatgaatactttcttag	664
MGST1	31	3'flanking+1581	tctgtgtgcatgaacatgca C/T gcgtgcacgcgcacacacac	665
MGST1	32	3'flanking+1729	tatgtggagcaatttgaaaa A/T agtatattctaagccattaa	666
MGST1	33	3'flanking+3407	ggatcactgctaaagatccc G/A gagtcactccatgtcccagt	667
MGST1	34	intron1B+36	ggagaaggggaccgcatgca G/A agggtggcaggcagggaggg	668
MGST1	35	3'flanking+25	gggtaaacccatttttgaata T/C tagcattgccaatatcctgt	669
MGST1	36	exon4+266(3'UTR)	aaagaaaatcatacaactca G/A catccagttggctttttaag	670
SULT1A2	1	intron 4 1728	tcagcttcctcctttgccaa A/Δ ccaagagatgagctggcctg	671
SULTX3	1	intron 1 6415	tgacctctccctgttagtgt G/Δ ggggcagctctttccagtgt	672
SULTX3	2	intron 5 2457	gcccttaaagggaagttcat C/Δ cttctctgccttccaggctc	673
PIG3	1	5'untranslated region-93	tccgcgaggatacagcggcc (CCTGY)n cagacaatatgttagccgtg	674
ADH2	4	intron 7 + 108	acaattgacaaggcaagatt T/C tgaaaacaaatcaaaaataa	675
ADH2	5	intron 3 + (1721-1723)	actgcatagaaatttaagaa GAA/ Δ cttgttttattcctctccag	676
ADH2	6	3' untranslated + (2305-2306)	gttaatgctttcccactctc AG/Δ gggaaggatttgcattttga	677
ADH5	1	5' flanking - 115	taactgctgtaaagttacac G/A gggaagcccttccgacaa	678
ADH5	2	5' flanking - 114	aactgctgtaaagttacacg G/A ggaagccctttcccgacaaa	679
ADH7	16	intron 8 + 727	ttcagatccctgtaagccag G/A tattatttttaccatttttta	680
GSTM1	1	5' flanking - 694	tacgaagtggctaatttaca C/T agtacttagccagatgaccg	681
GSTM1	2	5' flanking - 661	gatgaccgaaggactcagta C/T ccgagggcccctaacagaaa	682
GSTM1	3	5' flanking - 658	gaccgaaggactcagtaccc G/A agggcccctaacagaaaaca	683
GSTM1	4	5' flanking - 656	ccgaaggactcagtacccga G/A ggcccctaacagaaaacaca	684
GSTM1	5	5' flanking - 537	tagaggggagactaagccct G/C ggagtagctttcggatcaga	685
GSTM1	6	5' flanking - 525	taagccctgggagtagcttt C/G ggatcagaggaagtcctgct	686
GSTM1	7	5' flanking - 465	aattaaattcccaggttggg G/A ccaccacttttagtctgac	687
GSTM1	8	5' flanking - 383	gcggagagaaggctgaggga C/T accgcgggcagggaggagaa	688
GSTM1	9	5' flanking - 382	cggagagaaggctgagggac A/T ccgcgggcagggaggagaag	689
GSTM1	10	5' flanking - 378	gagaaggctgagggacaccg C/T gggcagggaggagaagggag	690
GSTM1	11	5' flanking - 343	agggagaagagctttgctcc G/A ttaggatctggctggtgtct	691
GSTM1	12	intron 2 + 118	tgctggagctgcaggctgtc T/C cttccctgagccccggtgag	692
GSTM1	13	intron 3 + 233	agtgagtgcccggtctcctc T/C ctgctcttgcttatgggaag	693
GSTM1	14	intron 4 + 26	tgtgggtggctgcaatgtgt G/A gggggaaggtggcctcctcc	694
GSTM1	15	intron 5 + 140	actatcagcagttattctca C/T gactccaatgtcatgtcaac	695
GSTM1	16	intron 5 + 577	ctgccaccccattagaagga A/G ctttctactttccctgagct	696

Designation of Gene	No.	Location	Sequence	SEQ ID NO
GSTM1	17	intron 5 + 645	gctggtctggatccagaggc T/A gccaggtgcttgggcgctcc	697
GSTM1	18	exon 7 + 519	caccgtatatttgagcccaa G/C tgcttggacgccttcccaaa	698
GSTM1	19	exon 7 + 528	tttgagcccaagtgcttgga C/T gccttcccaaatctgaagga	699
GSTM1	20	intron 7 + 2421	cagcaccgtgtagaatcttc A/G taagtgttagctgttactgt	700
GSTM1	21	3' flanking + 42	atttgctcctggccatctac C/T cagactgtctgtctgtctgt	701
GSTM2	1	intron 1 + 7	ggaacatccgcggggtgagc C/G agggtccgctgggcggtggg	702
GSTM2	2	intron 1 + 45	gggacgggggtgcgtgggggg C/T ggggaagtgtggagcagctg	703
GSTM2	3	intron 3 + 70	gactgcatctcctctcccca G/C cttagaggtgttaagatcag	704
GSTM2	4	intron 3 + 224	agcaggccctggtctcctct T/C tgccttgcatatgggaagg	705
GSTM2	5	intron 5 + 100	ttgattccttctggtgagtt C/A ttggtcttgctgactctaag	706
GSTM2	6	intron 5 + 341	tcctcttggtgggttcatgg T/C ctggctggcttcaggagtga	707
GSTM2	7	intron 5 + 696	accttagctagacacagag C/T gctgatttgtgcatttacaa	708
GSTM2	8	intron 5 + 723	ttgtgcatttacaatccttt A/G gctaggcagaaaagttctcc	709
GSTM2	9	3' untranslated + 1006	ctcagccccgagctgtcccc G/A tgttgcatgaaggagcagca	710
GSTM2	10	3' flanking + 139	ttctgctgggcatagtaagg C/T gcttgagaattcttgctccc	711
GSTM3	2	5' flanking - 144	ccaacgccggcattagtcgc G/T cctgcgcacggccctgtgga	712
GSTM3	3	intron 7 + 165	agcctaacttctatacctg A/G aggcactgtctacaaaaaaa	713
GSTM3	4	intron 7 + 257	ctgttggactgggtggggtc T/G ttataagattggtgtatttt	714
GSTM3	5	exon 8 + 91	cccagtggggcaacaagcct A/G tatgctgagcaggaggcaga	715
GSTM4	1	intron 4 + 67	ttggctggattggggtgcta T/C gctcagagtgagtctgtgtt	716
GSTM4	2	intron 7 + 77	gatgctttcccagtcctgga T/G ctgcataaagaataacttgc	717
GSTM4	3	intron 7 + 80	gctttcccagtcctggatct G/A cataaagaataacttgcatt	718
GSTZ1	1	5' flanking - 546	agcagggcccaccagccgac C/A gcctcgaagcgccgtgagcc	719
GSTZ1	2	5' flanking - 321	tgtctgaccagccgccccgc T/C aaggagtcacaagagggcag	720
GSTZ1	3	intron 1 + 2890	aaaatactgcatcaaaacca G/A gccacgctctgttgggggga	721
GSTZ1	4	intron 1 + 2896	ctgcatcaaaaccaggccac G/A ctctgttgggggacaccaa	722
GSTZ1	5	intron 2 + 255	tctcccaacactgctctcca A/G agcccctggcaaccatgtt	723
GSTZ1	6	intron 2 + 1560	caccactgtttaaggccctg G/C gggggcagagttaaacacaa	724
GSTZ1	7	exon 3 + 94	ccttgaaaggcatcgactac G/A agacggtgcccatcaatctc	725
GSTZ1	8	intron 4 + 297	agaaggaggagtttgctggc C/T ctgtcccctctggtccaggg	726
GSTZ1	9	intron 6 + 94	tatctgaaccagcctcccag G/A ctgctttgggcctgacagtt	727
GSTPi	1	intron 1 + 269	ctccccccgggctccagcaaa C/G ttttctttgttcgctgcagt	728
GSTPi	2	intron 2 + 134	ccccgggcctccttcctgtt C/T cccgcctctcccgccatgcc	729
GSTPi	3	intron 5 + 438	gtgtgtgcgcgtgcgtgtgc G/A tgtgtgtgcgtgtgtgtgtg	730
GSTPi	4	intron 6 + 162	cccgctggctgagtccctag C/T ccccctgccctgcagatctc	731
GSTT1	1	5' flanking - 103	taaagagtgtcccaggcgtc C/T gtgccgcccaatggggcaca	732
MGST1L1	1	5' flanking - 105	tgctgccgctgccgtggggc G/A gggcgtgggcggtgctggct	733
MGST1L1	2	intron 1 + 277	agtgtctgtgagagaagcag G/A ttctggagggtggagtgtgg	734
MGST1L1	3	intron 2 + 8030	ggggttatacagagcccctc C/G gcccccaccacacatatgca	735
MGST1L1	4	intron 2 + 8499	gtatggcaggagtggggtcc C/T ggcaagccatagaggtatgg	736
MGST1L1	5	3' untranslated + 468	cgccacctgtgaccagcagc T/G gatgcctccttggccaccag	737
MGST2	1	5' flanking - 46	ggtcagcattcaaagtcaag A/T agcgccatttatcttcccgt	738
MGST2	2	intron 1 + 176	ggtcacccatgccgcctgct A/C ccctccttcccaggggcaag	739
MGST2	3	intron 1 + 204	tcccaggggcaagcagagac T/C gagaacattccagagattag	740
MGST2	4	intron 1 + 373	ttacaagtgttccaaaggaa A/T cgtgcctgcttctaaacctg	741
MGST2	5	intron 2 - 3245	cctcgtgatttgcccacctc G/A gcctcccaaagtgctgggat	742
MGST2	6	intron 2 - 1998	aggccgaggtgggcggatca T/C gaggtcaggagatcgagacc	743
MGST2	7	intron 2 - 1640	tgtttattccttgcatagcc A/G taatataaagtatgaatttt	744
MGST2	8	intron 3 + 41	actgtgttctaatgatgact A/G tgatgcttaaacgattaagg	745
MGST2	9	intron 3 + 453	atcagagtgctatgttgcag A/G tatatgaactttggcttcat	746
MGST3	1	5' flanking - 520	acaaaaaggccctaacagcg A/C taaatccattcacttcggga	747
MGST3	2	5' flanking - 355	cgcctaaaaccgctacggtg G/A ctctgctggggacaaattat	748
MGST3	3	5' flanking - 234	ctgggggagtagatatatgt T/A tttgagaatgagaggagtaa	749
MGST3	4	intron 1 + 74	agcctttgcgcaggcactcc C/T atatttcagcctatgcgagc	750
MGST3	5	intron 1 + 682	agaaaatgccccttctttat G/C tggggtggcagcacggagcc	751
MGST3	6	intron 1 + 832	cgagtttacaagctacataa T/C agcgtcgggggcaagtaagt	752
MGST3	7	intron 1 + 1919	aataaaattcctgagtttct G/C tcactcgctcttacagtacc	753
MGST3	8	intron 1 + 1991	tgtaattaggcaacaggaaa A/G ttgtactatctttcaaatgc	754
MGST3	9	intron 1 + 4458	tcttccatcctcctaacata T/C agttagcttccactctccaa	755
MGST3	10	intron 1 + 4676	tgaatatgcaatgcaattgt C/G gggggatagttacttttcat	756
MGST3	11	intron 3 + 278	cagcatgacccatctaaacc G/C atgttgactctcccaggcct	757
MGST3	12	intron 4 + 423	cttgccttttgttgtgggg T/G gtggggtggtcacagagaag	758
MGST3	13	intron 4 + 506	gtgcagagaagaaaacaaag T/C ggggaaggtggaaaggggat	759
MGST3	14	intron 4 - 162	tcacagatattttattttcc C/T gactgaaactaacttaattc	760
MGST3	15	intron 4 - 130	acttaattctacctaatttg C/G gtggggagtagttggccaaa	761
MGST3	16	intron 4 - 105	ggagtagttggccaaatcat C/G aaattgttaacttttgcta	762
MGST3	17	intron 4 - 65	aacatattgtgtaatcaacc C/T taggtgttaaaaaaggtttg	763
MGST3	18	intron 5 + 105	atcccagcactttgggaggc G/C aaggcaggcagattgcttga	764
MGST3	19	intron 5 + 197	aaaaaatacaaaaattagcc G/A gatgtggtggtgcacacctg	765
MGST3	20	intron 5 + 222	tggtggtgcacacctgtagt C/T ccagctacttgggaggctga	766
MGST3	21	intron 5 + 374	tcttatgctactatatttttt T/C ttcttgggaatttgagaaaa	767
MGST3	22	3' untranslated + 517	atgacttacctttatttcca G/T ttacatttttttttctaaata	768
MGST3	23	3' flanking + 166	agtctgattgtggtgatgta G/T gtatagtcatgccacagtga	769
GSTA1	1	5' flanking - 266	ttgcaaaaagagcaaaatct C/A ggtgaaatgtattgtgtaaa	770
GSTA1	2	intron 2 + 1220	gagacacaggctttcctaag A/C tatgacaacaccataactag	771
GSTA1	3	intron 4 + 1813	aaaggcacccactggaggtg A/C attattttgccatcacctga	772
GSTA1	4	intron 5 + 732	gaagagtgttgtcatgaagg T/C ggagtcactgcccaagggag	773
GSTA1	5	intron 6 + 333	ttatcccatatgtgcccaca A/G tgagccggtctgagcagagc	774
GSTA1	6	3' flanking + 412	ctttcttatgcatttgcaaa A/C caatgattctgtctgctgtg	775
GSTA4	1	intron 1 + 280	gcattggtggaaggtgggct C/T ggatcgtccccgggcctggc	776
GSTA4	2	intron 3 + 176	ggaaatcacttcttattcaa T/C agttccataaaagctggccg	777
GSTA4	3	intron 4 + 94	acaccacatttactttatgt C/G ttacatagttagtgagatca	778
GSTA4	4	intron 5 + 1062	cacacttgtgcacatgcaga C/T acccatgggcatccaagagt	779
GSTA4	5	exon 6 + 487	cagatgtgattttactccaa A/G ccattttagctctagaagag	780
GSTA4	6	intron 6 + 595	tgagctctgagagcaaatga G/A agatgttagcaccctaaaca	781
GSTA4	7	intron 6 + 630	taaacatcaccccaaaggat T/A cctaccattctccttctgag	782
GSTA4	8	intron 6 + 3943	tcttcgtagtatctaatacc T/C tttttgttagccttaaagtt	783

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
GSTA4	9	3' untranslated + 1099	taataacaaccgaatgtcta G/A taaatgactctcctctgagc	784
GSTA4	10	intron 5 + (370-371)	gttgtcgaacagctgtctca (TA) gctgacatcctccctgataa	785
GSTA4	10	intron 5 + (370-371)	gttgtcgaacagctgtctca gctgacatcctccctgataa	786
NDUFA1	1	5' flanking - 1437	agggctaaaaatcctgatta T/A acctaccttgaagcttttaa	787
NDUFA1	2	intron 2 + 3071	aataaaagtacatggcatat C/A tttgatgggaacagacttgt	788
NDUFA1	3	3' flanking + 1218	aactccatgtgtataaagca A/G caccacagatgacacttcca	789
NDUFA1	4	3' flanking + 1411	ggattgtgccatcccttgat C/T/G ggcaatgacctttttacttttt	790
NDUFA1	5	3' flanking + 1411	ggattgtgccatcccttgat C/T/G ggcaatgacctttttacttttt	791
NDUFA2	1	intron 2 + 1087	aacatacaaaaattagccgg A/G tatggtggcgggcacctgta	792
NDUFA2	2	intron 2 + 1089	catacaaaaattagccggat A/G tggtggcgggcacctgtaat	793
NDUFA2	3	intron 2 + 1356	ttccctgaaacaacccattg T/C ggccatccagaatcagccaa	794
NDUFA2	4	3' flanking + 467	cacagcctcatgggtcagcc C/T actccagagggtgcattccc	795
NDUFA2	5	3' flanking + 744	ggaagcaggggccctggcca C/T agccgctggcagtaagcagg	796
NDUFA2	6	3' flanking + (844-845)	tatagtctacaaagaatgaa (ACAC) aaagatcataacaatagcta	797
NDUFA2	6	3' flanking +(844-845)	tatagtctacaaagaatgaa aaagatcataacaatagcta	798
NDUFA3	1	intron 2 + 2656	tccctgctgccctccctgc G/A cactttatcttccctttgcc	799
NDUFA3	2	exon 4 + 241	agggccccagcctggagtgg C/G tgaagaaactgtgagcacct	800
NDUFA3	3	3' flanking + 1019	tccttacctgcactggcacc A/G gctctggagccccagtccct	801
NDUFA5	1	intron 3 + 2155	agactctagcatggtacctg G/C aacataaggttccttagaaa	802
NDUFA5	2	intron 3 + 2493	ggcatattgctagttttctc G/T gtctcaatttcatcatctat	803
NDUFA5	3	intron 3 + 2712	acaaattttgaactgttcac C/T taacacaggctttttctgaa	804
NDUFA5	4	3' flanking + 1296	aggtatctaaaaggtattgc A/C atttggtcattggttctttc	805
NDUFA5	5	intron 3 + (30-31)	aagtcagttttgttgtcttg (GATTTGTGGTATCCAG) tgtaa catttaaccaaaaaa	806
NDUFA5	5	intron 3 + (30-31)	aagtcagttttgttgtcttg tgtaa catttaaccaaaaaa	807
NDUFA5	6	intron 3 + (427-428)	attaagtagcagttaataaa AG/△ tctagactgctgattcatac	808
NDUFA5	7	intron 3 + (4733-4734)	tataggaattttaaaatata TA/△ ggatattgaaacattcagtt	809
NDUFA6	1	5' flanking - 1148	tttataatttatatatgtta C/T gtgctttcttttgtatagct	810
NDUFA6	2	5' flanking - 363	actaccaaggagcgcggcgg G/A cagccggatagcaggacgct	811
NDUFA6	3	exon 1 + 26	ggggagcggcgtccgccaag C/T tacttctaccgccagcacct	812
NDUFA6	4	intron 1 + 1318	attcagcagtttgaaaacat A/G atgtttgcctggcagaatac	813
NDUFA6	5	intron 2 + 562	agttaaagaatctgaaaagt G/C tcagaaatgatttaccctga	814
NDUFA6	6	5' flanking - (861-862)	ctgtaaaatggggatgctga (T) ggtacctacctgacctatga	815
NDUFA6	6	5' flanking - (861-862)	ctgtaaaatggggatgctga ggtacctacctgacctatga	816
NDUFA7	1	5' flanking - 731	accaaccaaaggtctatcaa A/G ggggtgtcctctttgcaccc	817
NDUFA7	2	5' flanking - 434	aaagggaaccatcagaaccc C/T gtgatgaaatgagaatcggc	818
NDUFA7	3	5' flanking - 395	gctcccggattccggctggc A/G ggggttagggcagggtagag	819
NDUFA7	4	5' flanking - 100	agaggagtcacgtgcttcgg G/A gagagcctttataggacgtt	820
NDUFA7	5	intron 1 + 92	tcacctccctcctaagccgg G/A acccttcgctctccccgaat	821
NDUFA7	6	intron 1 + 133	ctccctgggaaccccccagct A/C gtcaccccttcagcccgggg	822
NDUFA7	7	intron 1 + 136	cctgggaaccccccagctagt C/G acccccttcagcccgggaccc	823
NDUFA7	8	intron 2 + 89	tcctttagacccctgaaacg G/C agggctgacatcctgccacc	824
NDUFA7	9	exon 3 + 196	gccgccgggaatctgtgccc C/GL cttccatcatcatgtcgtcg	825
NDUFA7	10	intron 3 + 4203	gcctccaccccctggggcgcc T/G cctccatcaccccaccctcc	826
NDUFA7	11	intron 3 + 4604	gggccttgtgtacgctggag A/G ccaaaagtgggaagggagga	827
NDUFA7	12	5' flanking - (1360-1353)	agggtccagggtcccctgct (CAGAGGCT) aacactggccg aagagaaag	828
NDUFA7	12	5' flanking - (1360-1353)	agggtccagggtcccctgct aacactggccgaagagaaag	829
NDUFA7	13	5' flanking - (1240-1239)	tgatagagccctgatccacc CA/△ ctctctgaaacttctttgct	830
NDUFA7	14	intron 2 + (4142-4143)	cattttgtgactgaggtgac AG/△ gggcccacagcggggccatg	831
NDUFA8	1	intron 1 - 75	tttgtgttctctattctgac C/T cgcatgaggtaaagctgaga	832
NDUFA8	2	intron 2 + 790	caaacctagacaaagtgtgc C/T ctttatccagaagtgagcag	833
NDUFA8	3	intron 2 + 900	ttcaggagataaaaagctct G/A attgctcaggcctgagatgg	834
NDUFA8	4	intron 2 + 3837	gaagttgtcttgtaagtgag A/G taagaatatgtactcacata	835
NDUFA8	5	intron 2 + 3942	tcattgttttgcaaagagat G/T cccctaacccagctttcttt	836
NDUFA8	6	intron 3 - 66	gaggagacaccaggaggcgc A/G ttgatggttacagattcctc	837
NDUFA8	7	3' untranslated + 520	tttatttctggaccaagtaa A/G gatgggtccgtggcccacac	838
NDUFA8	8	3' flanking + 367	gtcatacaaggggagcctcc A/G ggatagaagtgcagaaactt	839
NDUFA8	9	3' flanking + 777	attcttttttcactactagg C/T tgtttcctccacatctgact	840
NDUFA8	10	3' flanking + 1053	aaagaaaaagcactgtgtga T/A ctgccatggccgcttctgca	841
NDUFA8	11	3' flanking + 1190	gattctctaatgaaaaataa G/T actttttttgcatttttttt	842
NDUFA8	12	intron 2 + (449-453)	ggtcattgtgcatgatacttaa (GTAAA) aaaaaactaagctgtgtaat	843
NDUFA8	12	intron 2 + (449-453)	ggtcattgtgcatgatacttaa aaaaaactaagctgtgtaat	844
NDUFA8	13	intron 2 + (707-708)	ctcattttggaaagactctc (A) accttgctgtaccaaaaatg	845
NDUFA8	13	intron 2 + (707-708)	ctcattttggaaagactctc accttgctgtaccaaaaatg	846
NDUFAB1	1	intron 1 + 8451	cagcaccctgtagaggcctc G/A ggatgctgaagatgccatga	847
NDUFAB1	2	intron 1 + 8495	gacacaggcattctgcagac G/A ctagacaattttagtggcag	848
NDUFA9	1	5' flanking - 807	gatggctctttgtagaacaa T/G gcagattctcaaaggtgacc	849
NDUFA9	2	5' flanking - 769	accacagttaaagaaaaaat T/C acaagccattgcgctagaga	850
NDUFA9	3	5' flanking - 353	cacaccctattttggtttct C/G ttctccactttttcccctcgt	851
NDUFA9	4	5' flanking - 322	ttcccctcgttcttgtcccc C/T cttttctctctcctgggccc	852
NDUFA9	5	intron 1 + 447	attcatatgagcacaatgga A/G atgataatattacaatacca	853
NDUFA9	6	intron 1 + 1039	ggcttgatgttcagcctgag G/A caagaattaggagtgtttag	854
NDUFA9	7	intron 1 + 4010	aatgtatccaaaagagattc T/G cattcctgccatatgaagaa	855
NDUFA9	8	intron 3 + 49	gacaaatataaattactaag G/A tcatttttaggagtgatagg	856
NDUFA9	9	intron 3 + 107	aatttcttcccagaatggac C/T aaaggcatcctctgttccca	857
NDUFA9	10	intron 3 + 1183	atctctggtaatattcatac A/G gattatttgtaatcccttta	858
NDUFA9	11	intron 3 + 1395	attcctagttctttgtccct C/T aagtttgttggtcaccttgt	859
NDUFA9	12	intron 3 + 2363	agaaaatagtcatgaatggc C/T ccaactaacactagtctttta	860
NDUFA9	13	intron 3 + 2608	gtcatttgattacctgagta A/C agtgtactgttacctgtttg	861
NDUFA9	14	intron 4 + 561	attttataaattctttgatg A/C cttgggggtcttattcaact	862
NDUFA9	15	intron 4 + 860	attgtgtagagtaatgacag C/T agagctgtcaacttttttaa	863
NDUFA9	16	intron 4 + 879	gcagagctgtcaacttttttt A/T aaaaaataattttagcttaa	864
NDUFA9	17	intron 4 + 893	ttttttaaaaaaataatttt A/G gcttaaaaaaaattaaaaatt	865
NDUFA9	18	intron 4 + 1090	atcattgctgtttaaaagtt T/C aagtagtgtgaatttcagta	866
NDUFA9	19	intron 4 + 1188	aaccaatccttttattttttt A/T tcttccagaaactttgattt	867

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
NDUFA9	20	intron 5 + 161	gggtgtgtgtgatgttttga C/T gttttgattgattgccttct	868
NDUFA9	21	intron 5 + 373	ctttctcacccttgcactg C/T agtggttttgtgccactctt	869
NDUFA9	22	intron 5 + 457	gccagggaagatgcctattc A/C cacagtgcttatgctccttt	870
NDUFA9	23	intron 5 + 3113	gatttttctccttcttcaat G/A taagcttcccttaaaataaa	871
NDUFA9	24	intron 5 + 3339	tctaaactcaaaacaggttt G/A tttggttattgtttaggctg	872
NDUFA9	25	intron 6 + 414	tatagttttgccttttccag G/C atattacatatatggttaga	873
NDUFA9	26	intron 6 + 518	ctttcatttcttttcatagc T/C tgatagctcatttctttata	874
NDUFA9	27	intron 7 + 974	ggattatgcgtacttggaaa A/G tacttggatagcggtgatta	875
NDUFA9	28	intron 8 + 368	acattaattttgatggagta T/G cacaatgcctccagaggctg	876
NDUFA9	29	intron 8 + 954	gcatgcaatcagttatatag T/C ctagataagaattacaattc	877
NDUFA9	30	intron 8 + 1253	tcctcttgaaattgtagata G/T gtatctacacatttctcatc	878
NDUFA9	31	intron 8 + 11608	gaaaagatagatgtataaat G/A accaaaaattcgtgaagaaa	879
NDUFA9	32	intron 8 + 11930	ctacaaatatattctaaatg C/T gtaatcatggataagtacaa	880
NDUFA9	33	intron 9 + 1998	tgtttttcaagcctttaaac G/A gctgtggaaccctgtgctca	881
NDUFA9	34	intron 9 + 2238	ccagctacttgggaggctga A/G gtgggaggatcacttgagcc	882
NDUFA9	35	intron 9 + 2885	acagcggtctgtcttcctgc A/G gttctcataggctagcttac	883
NDUFA9	36	intron 10 + 801	tacactaaagtgtctcttac G/A tttatacttgagaaagtgtt	884
NDUFA9	37	intron 10 + 910	tgcagactttcaggtgggta G/C gatgagggattgctgctgct	885
NDUFA9	38	intron 10 + 1180	aaaactgagtcagaacgccc G/A tgctcagaaaacaggggcgt	886
NDUFA9	39	3' flanking + 554	gtgccagcacttaggaatta T/G gaccttctaatgaagttctt	887
NDUFA9	40	5' flanking - (1129-1128)	taaacagtaggggcaagata (TC) gagtggaaacagccaagatt	888
NDUFA9	40	5' flanking - (1129-1128)	taaacagtaggggcaagata gagtggaaacagccaagatt	889
NDUFA9	41	5' flanking - 341	tggtttctcttctccacttt T/△ cccctcgttcttgtcccccc	890
NDUFS1	1	5' flanking - 3	tcctaggggtcgtcgtggt C/G cagacagtttagcagaacag	891
NDUFS1	2	intron 1 + 445	gtgttagcaatggctcacgc T/C tctgtttgttgtccttgttt	892
NDUFS1	3	intron 1 + 470	tttgttgtccttgtttgttt G/T gtccattgaccacgttggac	893
NDUFS1	4	intron 1 + 502	acgttggacagcatttttttt A/G ttcctttaactaacgggaaa	894
NDUFS1	5	intron 1 + 557	ttttgaaaagttagcccagg A/G ttgcattgcaaaataacaaaa	895
NDUFS1	6	intron 1 + 5218	tatctcagaatatctcagga A/G catttagtagacagctatgc	896
NDUFS1	7	intron 3 + 1371	aagccctaaaatagatagtg T/G caatgggaatgaaaacaaga	897
NDUFS1	8	intron 5 + 414	ttttgaaacgaggtctcact A/G tgttgtccaggctgggcttg	898
NDUFS1	9	intron 10 + 812	gagtgcggtggcgcgatctc G/A atctcgggtcactgcagcct	899
NDUFS1	10	intron 11 + 233	ggaggccaaggcaggcagat C/T gcctaagtgcaggagtttga	900
NDUFS1	11	intron 11 + 283	ggccaacatggcgaaacccc G/A tctctactaaaaatacaaaa	901
NDUFS1	12	intron 11 + 585	ctgtatgtcttaattttaaa G/T taaatttgcattttatatat	902
NDUFS1	13	exon 12 + 1251	gcaccactgtttaatgctag A/G attcgaaagaggttggtaat	903
NDUFS1	14	intron 13 + 5159	attacttttagaaaacgtgt T/C ttagctgatactcaggcata	904
NDUFS1	15	intron 14 + 250	aaaaattgttatattagtta C/T accttggttcaaaaattgca	905
NDUFS1	16	intron 14 + 550	gataaagtctcactatgttg C/T ccaggttgatctcaaactcc	906
NDUFS1	17	intron 14 + 2429	ctgaaaatacaaaaattagc C/T gggtgtggtggcatgtgcct	907
NDUFS1	18	intron 14 + 2530	ttacagtgagccgagatcac G/T ccactgcgctccagcctggg	908
NDUFS1	19	intron 14 + 2659	acacatttaatttttttacat T/C gaaaatactgcagttatggt	909
NDUFS1	20	intron 16 + 150	agaaaacatgtattcagaaa C/T aggaattcaaggttacagtg	910
NDUFS1	21	intron 18 + 279	cactgtgtagcaatttatgg T/C gaattttccaaagtggcaaa	911
NDUFS1	22	3' flanking + 182	tctaggataattataattaa T/A aataatcatagtaacaatgg	912
NDUFS1	23	intron 11 + 3226	aaatgtattgtctgtgcttt T/△ aacattttgtaatagtaaat	913
NDUFS3	1	5' flanking - 194	tctgccacaaggagctagga C/T cacgctcacctcacgatttc	914
NDUFS3	2	intron 1 + 46	cggggtcaggcgcagcggcg T/C gcccagtgcagagagctcct	915
NDUFS3	3	intron 6 - 439	aaagctgtgtcaaatgtact G/A ctttagatctggactgtgaa	916
NDUFS3	4	intron 6 - 280	ggtgggtgagcagtcagttc G/A gagctcctgatgtgggagtg	917
NDUFS4	1	5' flanking - 439	aactgaatacagccctgtcc T/A gagggcttgcaaagtgaatc	918
NDUFS4	2	intron 1 + 1829	gaaaaaaaatcttaatgcca G/T ggaagacgtttttttaaatac	919
NDUFS4	3	intron 1 + 2057	attaatgggaaaatctacat C/G taaaattcattttattgtaa	920
NDUFS4	4	intron 1 - 521	ttcattttaactaattttat T/G tctcccattttgtgaatggg	921
NDUFS4	5	intron 3 - 1259	ataaaattatgatattatta G/A tactaatatagccagccata	922
NDUFS4	6	intron 3 - 1174	aatatatataattataggaa T/C ctcagagtagcaaccatggt	923
NDUFS4	7	intron 4 + 10682	cacaatataggcacaaactt A/C ctaccaaagcactaacaagt	924
NDUFS4	8	intron 4 + 12299	tttactatatagatatatgg A/T atagactatagagtatctct	925
NDUFS4	9	intron 4 + 12560	accaaataaggtattatgca G/A gctcatctttttatataaga	926
NDUFS4	10	intron 4 + 18801	ggaaagacttgctttgccag T/C gtatccgaaacctctgttat	927
NDUFS4	11	intron 4 + 19888	tcgcacagctgagaagagca A/G ggggctggttttcagtaccc	928
NDUFS4	12	intron 4 + 20178	agaaaagatgagtataattc G/A tctaacttaccattcttaa	929
NDUFS4	13	intron 4 + 23016	ctactctgtgaaagtaaggt T/A atgttgaacaagtaaattaa	930
NDUFS4	14	intron 4 + 23124	actttctttggagatggagt T/A ccagcagttgggaatgtaat	931
NDUFS4	15	intron 1 + 766	tgtgatgatttttttttttt T/△ ggctgtattaaccttccatt	932
NDUFS4	16	intron 1 + 1261	tttctttctctttttttttt T/△ gagatacattctcactctga	933
NDUFS5	1	intron 1 + 388	ccaaacatagccagcacttc C/T ggctgtaactccgggctgtt	934
NDUFS5	2	intron 1 - 13082	agtgagccgagattgcacca G/A tgcattccagcctgggcaac	935
NDUFS5	3	intron 1 - 12905	gttttcaacaaaggactcca G/T agtagtagagaagtttctgt	936
NDUFS5	4	intron 1 - 12564	attttcatcacacctcaact T/G aaggtataacagccttaaga	937
NDUFS5	5	intron 1 - 12561	ttcatcacacctcaacttaa G/A gtataacagccttaagaatg	938
NDUFS5	6	intron 1 - 10561	aacaatgtggtatagtgggg C/G gggtggtgagcaggtgtcat	939
NDUFS5	7	intron 1 - 9065	cctgatgctcctggctccag G/A gtagacctttttccctttaga	940
NDUFS5	8	intron 1 - 8871	tcaccacgtgtctgtagata T/C aggaccgcagaccttcgctt	941
NDUFS5	9	intron 1 - 7312	aaatccttggcttctagaat G/T ggtcactgatggtatataat	942
NDUFS5	10	intron 1 - 6827	aacctctgcctccccgattc A/G cgccattctcctgcctcagc	943
NDUFS5	11	intron 1 - 6725	agtagagacggggtttcacc G/A tgttagccagcatggtctcg	944
NDUFS5	12	intron 1 - 6631	aggcgtgagccactgcgccc G/A gcctagaccttcttcttata	945
NDUFS5	13	intron 1 - 6531	cccaacagctcccaatgtaa A/G acagatctattaatattctg	946
NDUFS5	14	intron 1 - 6346	gcaacagatcttgacctata T/C cccatagggtacagctgagg	947
NDUFS5	15	intron 1 - 6327	atcccatagggtacagctga G/C gactttaatcagaaaaggag	948
NDUFS5	16	intron 1 - 6122	tagccttgcttttactctac T/C gttcctcccaaatcacaccc	949
NDUFS5	17	intron 1 - 2512	acaaactcttaatgcgaatt T/C tgcagatcaaagtgggctta	950
NDUFS5	18	intron 1 - 1945	tttaatctccttaaatttc G/A caatttcacaacctagggta	951
NDUFS5	19	intron 2 + 75	ttttttttttttttgagac G/A aagtctcactcttgtcccct	952
NDUFS5	20	intron 2 + 148	ctgtagcctctgcctcccag G/A ttcaggcgattcgcgtacct	953
NDUFS5	21	3' flanking + 150	cagattcaagtggttctcct G/C cctcagcctcccaagtagct	954

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
NDUFS5	22	intron 1 - (10682-10681)	attataaacactaaacaaac AT/△ gtgtggtctctttagagggg	955
NDUFS5	23	intron 1 - 10272	aggaacaagtgactaccctg A/△ aaaaagaagagatgaaacaa	956
NDUFS5	24	intron 1 - 2069	accagacagagttcccttta C/△ ttgttttcctgtggcaaaga	957
NDUFS6	1	intron 1 + 26	ggccgctgggtacaggatgc A/C ccttcctccagccgcacctc	958
NDUFS6	2	intron 2 + 1076	ggatcatggtggtggagagg G/A gcttgtgtctggtgggtttg	959
NDUFS6	3	intron 2 + 1260	cagttgtcgagtaagtggtg T/C atagggtaagtgctctttct	960
NDUFS6	4	intron 2 + 1413	caaaggagctcatggcattg C/T gaatgggacatttcttccgt	961
NDUFS6	5	intron 2 + 1568	tggagaaggggaggtttctc T/C tagtgtggatgcggtatggt	962
NDUFS6	6	intron 2 + 1692	gaccgtggtgacggaggttt C/T ctgggcatcgatgggtggtt	963
NDUFS6	7	intron 2 + 6488	tagcttaaataattattggc A/G ttcatgttcagaatgcctga	964
NDUFS6	8	intron 2 + 6563	tttaaacttttattttaaat G/A tccatgaatggggtcggtat	965
NDUFS6	9	intron 2 + 6740	aaagatttaaacctacatat C/T tttatgcccaatcatttgat	966
NDUFS6	10	intron 2 + 6832	gcgagggactcattttacag A/T ggttggacacttcactgtgt	967
NDUFS6	11	intron 2 + 7054	ttcactgccggagcttggcc G/A tgtgaacccggagccgggct	968
NDUFS6	12	intron 2 + 7186	ggtcagggtcaccctgagc T/C gcgcacactaaatgacggga	969
NDUFS6	13	intron 2 + 7225	gagggcatcccgcgtcagtc G/A ccagtgtcgaggcgtcagca	970
NDUFS6	14	intron 2 + 7810	cttccactctggggcgggga C/T gctgtagaaggagcacaaag	971
NDUFS6	15	intron 2 + 11080	gtaactgttcagtgctttct C/T ctttggatttcatgtaaatc	972
NDUFS6	16	intron 2 + 11657	gggacagaacgatgtggtgg G/A gagaagagggcgtggcagag	973
NDUFS6	17	intron 3 + 208	cgaaaaccccctttcaactg T/C gaagtggtgggcggcatgtt	974
NDUFS6	18	intron 3 + 1031	ctagagtgggactgggcacc C/T ggcatgtccctcctgggct	975
NDUFS6	19	3' flanking + 270	gcttcagagagccaaggtgg G/C tcttgaggtgcatagtgaag	976
NDUFS8	1	5' untranslated - 45	agtgtagcctccgcctcccg A/C ttgactggcctgcttggcaa	977
NDUFS8	2	intron 1 + 163	aggtgcagcggggagccggc T/C ctcagggcgcatgcgccgcc	978
NDUFS8	3	intron 3 + 123	tctctgagcctgtttccact T/C ttaaaatgattatggtgatg	979
NDUFS8	4	intron 6 - 505	aggcaaggcaggccgggcac G/A gtggctcacgcttgtaatcc	980
NDUFS8	5	3' flanking + 491	ggccctgagctggcctgcgt C/A cagccacatcctctttcctg	981
NDUFS8	6	3' flanking + 693	ttcacttcatttgcagtgag G/A aaaccagctccgagaggtga	982
NDUFS8	7	3' flanking + 1267	ttttcccagacgtaaccgcc G/A tcagagcgtggcatggagcc	983
NDUFS8	8	3' flanking + 1362	cgctgggttctttcccttac C/T gtggtctcccaggcacttac	984
NDUFS8	9	3' flanking + 1449	tgtcagaacaggcctatggc G/A cccaaccacaagtcccccaa	985
NDUFS8	10	3' flanking + 1572	cagccccacaggcctgtgct C/A gctgtgtggggcttagggat	986
NDUFS8	11	3' flanking + (783-784)	cagagaccttgacccccccc (C) atctaccatcatttccaaaa	987
NDUFS8	11	3' flanking + (783-784)	cagagaccttgacccccccc atctaccatcatttccaaaa	988
NDUFB3	1	5' flanking - 1439	ttaaaagttgacttttttct G/A ccgggcacggtggctcacgc	989
NDUFB3	2	5' flanking - 1436	aaagttgacttttttctgcc G/A ggcacggtggctcacgcctg	990
NDUFB5	1	5' flanking - 213	ggcggatgaaactctcctac A/C aagaagggccaaaccggccg	991
NDUFB5	2	intron 1 + 6288	ggggatgttgattacctagg T/C cagtaaagtaaagaaggcat	992
NDUFB5	3	intron 1 - 1581	cttctgggccactgtatcct A/G tttctttcccttgttaccct	993
NDUFB5	4	intron 1 - 1487	ccctcttagaccgtatatag T/G tctagcataggatctgcaca	994
NDUFB5	5	intron 2 + 556	ttgtctggaccatctgccac G/A gtagataaagctctgaatca	995
NDUFB5	6	intron 3 + 467	ggcgccatcgcactccagcc C/T gggcaacagagtgagactct	996
NDUFB5	7	intron 3 + 497	agtgagactctgtccccccc C/G caaaaaaaaactataatcct	997
NDUFB5	8	exon 5 + 397	atgatagtcctgaaaagata T/C atgaaagaacaatggccgtc	998
NDUFB5	9	intrion 1 + (231-215)	attagcatttctaaaacgtt GTT/△ attcaccatcccaattaatg	999
NDUFB7	1	intron 1 + 68	cctgaacacctggcacccca G/A ggctggcaccccagggctgg	1000
NDUFB7	2	intron 2 + 266	gggctctctaggggcctgtt T/C gatggggacagggcaggtgg	1001
ABCA1	1	5' flanking - 278	gggcccgggcgggggaaggg G/C acgcagaccgcggaccctaa	1002
ABCA1	2	5' flanking - 99	acataaacagaggccgggaa G/C ggggcggggaggagggagag	1003
ABCA1	3	intron 1 + 159	gcggtgttaaatggggagac G/T atgtcctagtacgagctctg	1004
ABCA1	4	intron 1 + 506	gaattggctatatgctcccc G/C ggactggagcggcacagtcc	1005
ABCA1	5	intron 1 + 5897	gtacaaaaccctttagctttt T/G gcaaacctcctttaagaccc	1006
ABCA1	6	intron 1 + 5929	ttaagacccgatttaaatgc C/T tccctcctcatgaagctctt	1007
ABCA1	7	intron 1 + 5962	aagctcttctggatccactc T/C ttcccatcactaagttgaaa	1008
ABCA1	8	intron 1 + 5985	cccatcactaagttgaaagt A/C agatcccctttctctttactt	1009
ABCA1	9	intron 1 + 11416	ttacagtgccctttatagga G/A agaaagaagaaattgtgtct	1010
ABCA1	10	intron 1 + 11935	tctctgtggagcaaatagag G/A gctgtctgacacttggttcc	1011
ABCA1	11	intron 1 + 12281	gaatgtttgatttgtgaaaa T/A cttaataacagtagtttttt	1012
ABCA1	12	intron 1 + 12924	gtgctgacaatcttatactc T/C aggttgaacctccggggaag	1013
ABCA1	13	intron 1 + 13002	gagcctcaatcacagattct C/G tctagctcacatgaagttaa	1014
ABCA1	14	intron 1 + 17715	ggagcatgactttgtggaag C/T ctctcctcttccacccagag	1015
ABCA1	15	intron 1 + 17848	gagggctgactgtcaccctt T/C gataggagcccagcactaaa	1016
ABCA1	16	intron 1 + 21384	gtgggtgggaggaattggag G/C aggaagcttgcctaagtgtg	1017
ABCA1	17	intron 1 + 22145	gtagcttctaaatcaacgaa C/G tgattcctggagagcagctt	1018
ABCA1	18	intron 1 + 23063	ggaggcacctgtgacaccca G/A cggagtaggggggcggtgtg	1019
ABCA1	19	intron 1 + 23131	agtgtgcatatgtgctgacc G/A tgggagcttgtttgtcggtt	1020
ABCA1	20	intron 2 + 156	ggacacaggactgtgtggtc T/C ggatatggcatgtggcttat	1021
ABCA1	21	intron 2 + 384	gctgtgggtgaagtgagtta A/G tggccccactcttagagatc	1022
ABCA1	22	intron 2 + 1081	agtgcagccaaaattgcaaa G/A tcataccattcaaattaata	1023
ABCA1	23	intron 2 + 2801	aagaaaagtgatttatttca A/G gttgctgatgcttagattgt	1024
ABCA1	24	intron 2 + 2830	tgcttagattgttagagttg C/G aaagatctggcttgcatctt	1025
ABCA1	25	intron 2 + 2856	tctggcttgcatcttgtaca A/G ctgacagaactggggctcag	1026
ABCA1	26	intron 2 + 3187	tgatagctgttgcctgcagc A/G tacggacgttcattgcgcag	1027
ABCA1	27	intron 2 + 3190	tagctgttgcctgcagcata C/T ggacgttcattgcgcagttc	1028
ABCA1	28	intron 2 + 3194	tgttgcctgcagcatacgga C/T gttcattgcgcagttcctgt	1029
ABCA1	29	intron 2 + 3204	agcatacggacgttcattgc G/A cagttcctgtctcctgagat	1030
ABCA1	30	intron 2 + 3401	acataaagcctgtgtgctgc T/C gccaggaagactagaaacgc	1031
ABCA1	31	intron 2 + 13927	gtcaccacatacctggcact A/G tgctaaggctgggaatgcag	1032
ABCA1	32	intron 3 + 4163	ccagcccacttcatcttacc G/A tagttacctccttagagtat	1033
ABCA1	33	intron 3 + 4262	tgtcaaagaggaactaagga T/C gccagggactttctgcttag	1034
ABCA1	34	intron 3 + 4306	ccctctcatcacttctccaa C/T gctggtatcatgaaccccat	1035
ABCA1	35	intron 5 + 240	gacagaagaaaagtccccag G/A gaagaatactacagacttgg	1036
ABCA1	36	intron 5 + 490	gatgggcatttgaacttgtt G/A tctttaaaaagtgaaatctt	1037
ABCA1	37	intron 5 + 583	tatctggggagtgggcattt T/G ctgactgaggcattggctgc	1038
ABCA1	38	intron 5 + 1051	ggctacaaaactgtgctttc C/T ttgggcagtaaaagaggcaa	1039
ABCA1	39	intron 5 + 3051	tagagaacaagtctaattct G/A ttttccttgaaatagtcgaa	1040
ABCA1	40	intron 5 + 3127	aagtccatgatttttttaggc A/G aaatggcctcctttcctctt	1041

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ABCA1	41	intron 5 + 5924	ctttctttcacaaaattgcc C/T cccagagctttctggaaggg	1042
ABCA1	42	intron 5 + 6831	ccagtccctcagccttgcca T/C tgcttatgctggtctggaaa	1043
ABCA1	43	intron 5 + 12678	gctcaccgctctgctcaccc G/C accctctggccatctcctct	1044
ABCA1	44	intron 5 + 14214	cagcttggtcccagaggcct G/A gacctgggtcccagaggtcc	1045
ABCA1	45	intron 5 + 14257	gctggttccccggcttggtc C/T cagaggcctggatgtgtggc	1046
ABCA1	46	intron 5 + 18078	cctaccacaccatgcacgtg C/T acagccaagggttgttgact	1047
ABCA1	47	intron 5 + 18795	ctgggctcttcctggacctg G/A ccagctaaaaggaaatctcc	1048
ABCA1	48	intron 5 + 18948	gcattggtggtactaagaac G/A catattccctatcctatagg	1049
ABCA1	49	intron 5 + 19053	ctcccccaacattaaaagtg T/C aagggatgcttattcaaatg	1050
ABCA1	50	intron 5 + 19148	ggcccaagaaactgcatttt C/A gcatgctccctaaatgaagc	1051
ABCA1	51	intron 5 + 19229	atgctaacagtgtagagtca C/T atgtgatgggaagcatcagg	1052
ABCA1	52	intron 5 + 19405	cttgctcaatttattctgtc T/C atataactcaatattactga	1053
ABCA1	53	intron 5 + 19534	catgtgaccctcttagctcc G/A cggattaactcctgtcctca	1054
ABCA1	54	exon 6 + 474	gaaaccttctctgggttcct G/A tatcacaacctctctctccc	1055
ABCA1	55	intron 6 + 210	gcaacctggcgtcatgggcc A/C gctggttaaaataaaattga	1056
ABCA1	56	intron 6 + 334	acagttctgaggcaataacc G/A tggttaagggttattgatct	1057
ABCA1	57	intron 6 + 2288	cttctttcaaagcttgtggt C/T cactggaccacgtatgaagt	1058
ABCA1	58	intron 6 + 2322	atgaagtagaatagtttagg T/C ccagaaaggcaattaagtaa	1059
ABCA1	59	intron 6 + 2820	gtgctttgatacattctgag T/G ttcagtaaagagacctgatg	1060
ABCA1	60	exon 7 + 656	tgagctttgtggcctaccaa G/A ggagaaactggctgcagcag	1061
ABCA1	61	intron 7 + 416	catcataaagatgacattgt G/A ggctgtcacagttggaaggc	1062
ABCA1	62	intron 7 + 471	agaccacactatttagctta C/T ttagtaataacattgcaaag	1063
ABCA1	63	intron 7 + 504	ttgcaaagaaaaattccgac G/A aagtttttcagcctaggaa	1064
ABCA1	64	intron 7 + 679	gctctggtgaaattcctctc G/C ctaccccaaacatcatcatt	1065
ABCA1	65	intron 7 + 1740	acaaatgctcacccttcag C/T tggaatgattgaaatttttgg	1066
ABCA1	66	intron 7 + 2122	tgattaaggtggctactacc A/G ggtgctttctgcatatctcg	1067
ABCA1	67	intron 7 + 7753	taggaattccaagctgtgaa T/C ttttactgaagctctttgg	1068
ABCA1	68	intron 7 + 8973	atggaaatttgtttatattg A/T ctacagattgccaatattat	1069
ABCA1	69	intron 7 + 8976	gaaatttgtttatattgact A/G cagattgccaatattattag	1070
ABCA1	70	intron 7 + 11327	ctaacaatcttatttccatt G/C agtccttataaaagaagtgg	1071
ABCA1	71	intron 7 + 11738	ctgacgtttaagggagaccg C/T gtaggtcccttgaggactg	1072
ABCA1	72	intron 7 + 12295	agtctgtaaattattgttct T/A ttttttctttagcttatgct	1073
ABCA1	73	intron 8 + 387	tagcaaggccaatcatttta C/G caacacacatgcttgctaac	1074
ABCA1	74	intron 8 + 697	ggaactgtctggtgtccccc A/T gcataggaagctgagccagg	1075
ABCA1	75	intron 8 + 1312	attgctctgcagatccccctc G/A cagccctctgtccttgttc	1076
ABCA1	76	intron 8 + 3036	ctttatgtgggaagaaattt T/G ttttttttgattggggagtgg	1077
ABCA1	77	intron 8 + 3176	aaatggcctggttctctgtc C/A cctttctgtctgtatgcctc	1078
ABCA1	78	intron 8 + 3364	ggcagaaggcaaagcttagg A/T cctagagagtgctggaccac	1079
ABCA1	79	intron 8 + 3373	caaagcttaggacctagaga G/A tgctggaccacgccactcac	1080
ABCA1	80	intron 8 + 3561	cagggatttattaatgattt C/A ttgtgaaatgtttggaaata	1081
ABCA1	81	intron 8 + 3654	agtgccggaatacatttgca T/C gtaagacagaacgctgcctg	1082
ABCA1	82	intron 8 + 4715	ggcagaggggtctcagaatc C/T gcatttccaacaatgtctcc	1083
ABCA1	83	exon 9 + 936	cgtattgtctgcgggcatcc C/T gagggaggggggctgaagat	1084
ABCA1	84	intron 9 + 2309	cccctcaagagtcagtttaa A/G tgttggtcatgttagttgtc	1085
ABCA1	85	intron 9 + 2392	atgggagggcttgtgcttca T/C gaaaacatttttccagatca	1086
ABCA1	86	intron 10 + 228	tggggatggggaggactggc A/G cagggctgctgtgatggggt	1087
ABCA1	87	intron 10 + 319	ttctgcggtccctggctccc C/T acctgactccaggtgaacaa	1088
ABCA1	88	intron 11 + 377	gaaagaagtgtgggagcaaa A/C gcatgatgttacatgtagac	1089
ABCA1	89	intron 11 + 521	agtgctctagagacaattgg G/A ttcaaatgtggagcaggctg	1090
ABCA1	90	intron 11 + 2850	ctctatacaatcattatgct G/C ccattgaaataataaataca	1091
ABCA1	91	intron 11 + 2976	ctccaattcggtagaaccag A/G gcttcatcttctctgtcgaa	1092
ABCA1	92	intron 11 + 3056	gtttgcagctgctgtttttc C/T ggcagcacatctgtgcaggc	1093
ABCA1	93	intron 12 + 340	ggcattatttgtgaaactta T/C ctaaaatcgaattcgggtcc	1094
ABCA1	94	intron 12 + 381	aattaaatttttgaaatttt A/G tattaaaaattatattagta	1095
ABCA1	95	intron 14 + 1728	caggctcagaggccttggcc C/T atcaccctggctcacgtgtg	1096
ABCA1	96	exon 15 + 2040	atgggcctggacaacagcat C/A ctctggtttagctggttcat	1097
ABCA1	97	intron 15 + 1382	cttttagacagaaaagttac G/A tgggatattatctcccacag	1098
ABCA1	98	intron 15 + 1453	tatataaggagaaaccagtt G/A aaattacctattgaagaaac	1099
ABCA1	99	intron 15 + 1567	ttctgcgtagttttgggtaa G/A tcacttatcttctttaggat	1100
ABCA1	100	intron 15 + 1617	cagttgcctcatcagaaaga T/A gaacagcattacgcctctgc	1101
ABCA1	101	intron 16 + 95	agttgagaacagaagatgat T/A gtcttttccaatgggacatg	1102
ABCA1	102	intron 16 + 452	tggtgttttgcttgagtaat G/A ttttctgaactaagcacaac	1103
ABCA1	103	intron 16 + 657	ctgttgcctcagtctgggct T/C cataggcatcagcagcccca	1104
ABCA1	104	exon 17 + 2473	gcttcaatctcaccacttcg G/A tctccatgatgctgtttgac	1105
ABCA1	105	exon 18 + 2649	ggttccaaccagaagagaat A/G tcagaaagtaagtgctgttg	1106
ABCA1	106	intron 18 + 1730	tgaaagttcaagcgcagtgc C/G ctgtgtccttacactccact	1107
ABCA1	107	intron 19 + 426	aggaccttacagtgggtagt A/G tcaggaggggtcaggggctg	1108
ABCA1	108	intron 19 + 468	aaagcaccagcgttagcctc A/G gtggcttccagcacgattcc	1109
ABCA1	109	intron 20 + 876	ccctcctcatctaaagtgaa C/T acatggggctcatgtgcagg	1110
ABCA1	110	intron 22 + 118	catgggatactcttctgtta T/G cacagaagagataaagggca	1111
ABCA1	111	intron 22 + 560	aaagctttgccattctaggg G/A tcatagccatacagggtgaa	1112
ABCA1	112	intron 23 + 102	acccctttgccatgttgaa A/G ccaccatctccctgctctgt	1113
ABCA1	113	intron 23 + 287	gtcaaagaaaagagacttgt C/T aagaggtaagagccttggct	1114
ABCA1	114	intron 23 + 1063	acctttcaccctcaggaagc G/A aggctgttcacacggcacac	1115
ABCA1	115	intron 25 + 321	ctctttacttaagtacagtg T/G gaggaacagcggcatcagga	1116
ABCA1	116	intron 25 + 376	gttagaaattcagcaacttg G/C gcccagctcagacctactga	1117
ABCA1	117	intron 25 + 478	catacataggaaatgacaaa C/T gtttatggatggatagtcta	1118
ABCA1	118	intron 25 + 579	tcatttaattctcaaaaaaa G/T atgaaaaaatgaacactcag	1119
ABCA1	119	intron 27 + 153	aatggtaaaagccacttgtt C/T tttgcagcatcgtgcatgtg	1120
ABCA1	120	intron 28 + 1058	actatcatgggagataatga C/T tatggttgtccatgattgga	1121
ABCA1	121	intron 28 + 1317	caggacccagtgttctgagt C/T accctgaatgtgagcactat	1122
ABCA1	122	intron 30 + 372	tatatgatttttaggttttg T/C ttatcagcttcttcgctttt	1123
ABCA1	123	intron 30 + 506	ccttttaaaaagtaagcagt A/G gataaataaattcagtgaag	1124
ABCA1	124	intron 30 + 1033	ctggatttcatggtgccttt G/C attttccacatgaaggttgt	1125
ABCA1	125	exon 31 + 4281	tcttccctttgcagagacac G/A ccctgccaggcaggggagga	1126
ABCA1	126	intron 33 + 626	ggctccttgttactgatttc C/T gtcttttctctctgcctttt	1127
ABCA1	127	intron 33 + 719	taatagccctcatgctagaa G/A ggagccggagcctgtgtata	1128

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ABCA1	128	intron 33 + 726	cctcatgctagaagggagcc G/A gagcctgtgtataaggccag	1129
ABCA1	129	intron 33 + 889	ctttcctcaatgtctcagct A/G tctaactgtgtgtgtaatca	1130
ABCA1	130	intron 33 + 1097	ctgtgcaccccactgtctgg G/C ttttaatgtcaggctgttct	1131
ABCA1	131	exon 35 + 4760	tatgacaggactggacacca G/A aaataatgtcaaggtaaacc	1132
ABCA1	132	intron 35 + 234	aacctatctaaacctcagtt T/C cctcatctgtgaaatggaga	1133
ABCA1	133	intron 37 + 411	aactctgtacattttatcag C/T agcttatccatccattgcaa	1134
ABCA1	134	intron 37 + 1224	caggcataggtgattcagag A/G tgaaaggtcaagtccctgaa	1135
ABCA1	135	intron 37 + 1720	aaattaaaattactctgact G/T ggaatccatcgttcagtaag	1136
ABCA1	136	intron 40 + 251	tgaaggtaaggaaaatagtg T/G tatttgcttggatccactgg	1137
ABCA1	137	intron 40 + 252	gaaggtaaggaaaatagtgt T/C atttgcttggatccactggc	1138
ABCA1	138	intron40 + 319	agcactggaaaagtcaaacc A/G taactttgagaattaggtga	1139
ABCA1	139	intron 40 + 957	cttgttactctttttccttt G/C tcatgggtgatagccatttg	1140
ABCA1	140	intron 41 + 146	tgatgtgggcatcccgcagc C/T ccctccctgcccatcctgga	1141
ABCA1	141	intron 42 + 239	cattggttttatatgcttac A/C tttatgtgttagttattaaa	1142
ABCA1	142	intron 42 + 321	aataaatggttgattttgag T/A ttgagtttcatagtccaaaa	1143
ABCA1	143	intron 42 + 322	ataaatggttgattttgagt T/C tgagtttcatagtccaaaaa	1144
ABCA1	144	intron 42 + 533	agatgaaaaattatgtagat G/A ataatgaatgatacggttct	1145
ABCA1	145	intron 42 + 546	tgtagatgataatgaatgat A/G cggttctaaaaagacaggtt	1146
ABCA1	146	intron 43 + 739	tacagccacacttaaaatgg T/A cccattatgaaatacatatt	1147
ABCA1	147	intron 44 + 18	taggtgagaaaagaagtggc T/C tgtattttgctgcaaagact	1148
ABCA1	148	intron 44 + 264	acaatataatttgcttgttt T/C ttaagagtataatttagtga	1149
ABCA1	149	intron 44 + 279	tgtttttttaagagtataatt T/C agtgatttttggtaaattga	1150
ABCA1	150	intron 44 + 508	tttacattgctacataaaat C/T cccctatgtacatgtaccta	1151
ABCA1	151	intron 44 + 1477	gatctcctctcctgtctctt A/T cattttgcagtagcaatgt	1152
ABCA1	152	intron 44 + 1665	tggttgtaagaactgatttg G/A ttggtatagctgtgagggcc	1153
ABCA1	153	intron 44 + 1956	gtgttgctcacactcaaaat T/G tctgggccttctcatttggt	1154
ABCA1	154	intron 45 + 68	aatatatacctatggcttt T/C ccacacgcattgacttcagg	1155
ABCA1	155	intron 46 + 608	ttatactgacttcaatagag G/C tttcagacaaaaagttgttt	1156
ABCA1	156	intron 47 + 336	ttcacaattgtaaacaccac T/C acactgaacagcatcatccc	1157
ABCA1	157	intron 49 + 55	agggtgtggattcctgcccc G/C acactcccgcccataggtcc	1158
ABCA1	158	3' UTR(exon 50)+7949	aacaaaaatgtgggtgtctc C/T aggcacgggaaacttggttc	1159
ABCA1	159	3' UTR(exon 50)+8226	aggagcccactgtaacaata C/T tgggcagccttttttttttt	1160
ABCA1	160	3' UTR(exon 50)+8682	aacttcttccacttttttcca G/A aatttgaatattaacgctaa	1161
ABCA1	161	3' UTR(exon 50)+8697	ttccagaatttgaatattaa C/T gctaaaggtgtaagacttca	1162
ABCA1	162	3' UTR(exon 50)+9097	aactattttgaagaaaacac A/G acattttaatacagattgaa	1163
ABCA1	163	5' flanking - (1033-1032)	tgacttaaatatttagacat (AT) ggtgtgtaggcctgcattcc	1164
ABCA1	163	5' flanking - (1033-1032)	tgacttaaatatttagacat ggtgtgtaggcctgcattcc	1165
ABCA1	164	intron 5 + 6368	ttctgatggggttgttgctg C/△ tgagaatcatgactgggtgg	1166
ABCA1	165	intron 5 + 9709	cattttctgtctgaaccccc T/△ cacccattcaggcagctgct	1167
ABCA1	166	intron 5 + 13816	tccctacttctcctttttt T/△ catttgcctcctccacccac	1168
ABCA1	167	intron 10 + (270-271)	cttttcagggaggagccaaa (G) cgctcattgtctgtgcttct	1169
ABCA1	167	intron 10 + (270-271)	cttttcagggaggagccaaa cgctcattgtctgtgcttct	1170
ABCA1	168	intron 20 + (611-612)	tttagcccatcctctccccc (C) gccaccctccttattgaggc	1171
ABCA1	168	intron 20 + (611-612)	tttagcccatcctctccccc gccaccctccttattgaggc	1172
ABCA1	169	intron 32 + (391-392)	gagtgccttgggtactctct (T) gatgggggactccatgataa	1173
ABCA1	169	intron 32 + (391-392)	gagtgccttgggtactctct gatgggggactccatgataa	1174
ABCA1	170	intron 37 + 847	gctgtatattgtgaatgtcc C/△ gttttcaaaagcaaagccaa	1175
COMT	1	5'flanking - 1287	cgtatgatattccccattct G/A agtccagaatacctagaaat	1176
COMT	2	5'flanking - 1217	tgtgagtatgggaaggggaa G/A cttttctgtctgttgtcccc	1177
COMT	3	5'flanking - 503	caggggctccaggaggacga G/A tgtgtatcctcccattgctc	1178
COMT	4	5'flanking - 425	gagaagttgggaagtctggc C/T agtggggccggtgcctggtg	1179
COMT	5	5'flanking - 277	cccagccccagtttccccac C/T tgggaaggggggctacttgtg	1180
COMT	6	intron1 + 12058	ctggcccatggaagggaggg G/A agggggccccgacggggcca	1181
COMT	7	intron1 + 12070	aggggaggggaggggccccg A/G cggggccacagtaaaggagt	1182
COMT	8	intron1 + 18831	tgtgtatgttcttggtaaac C/T agcccttggtcttacacatc	1183
COMT	9	intron2 + 832	cctctcctttggccacccgt G/C actacccccaactccgggcc	1184
COMT	10	intron3 + 90	ggagaagctgttatcacccc A/G tttccaggggggctgggaacc	1185
COMT	11	intron3 + 425	ccccaaggtgggcggttcgg T/G gattcagagagggcagctct	1186
COMT	12	intron3 + 671	ggctcctgctctttgggaga G/A gtgggggggccgtgcctgggg	1187
COMT	13	intron3 + 676	ctgctctttgggagaggtgg G/T gggccgtgcctggggatcca	1188
COMT	14	intron5 + 75	tcagcctcagcctctccaaa G/C agccaggcattccagtagag	1189
COMT	15	intron5 + 310	accagacaccagggcagaaa C/T ggcacaggaccaaggagatg	1190
COMT	16	intron5 + 346	agatggggtggggaagggcc G/A ctctgggcccagcctgctct	1191
COMT	17	intron5 + 3023	aaggcagccgccctgctcaa G/A gcctaggccattgtcctcct	1192
HNMT	1	5'flanking - 211	cagaggcagatgacagtctt C/T cgttaaagatttcactgctg	1193
HNMT	2	intron1 + 5409	aatataactgatataattgg A/G acatttcatgttggcctagt	1194
HNMT	3	intron2 + 2561	cacttgtgcttggacaagaa A/G agaaggcctacaagaaaaag	1195
HNMT	4	intron2 + 2895	caatcagaaatgtaagaaaa A/C ctccaagaaaaatttaagtt	1196
HNMT	5	intron2 + 3977	accaaacttggaagtgtaaa G/A ttatgcatgtatgttcatgt	1197
HNMT	6	intron2 + 5296	ttaacatagtgagtttggag T/C cccaggattttattttcctt	1198
HNMT	7	intron2 + 13317	caaccctcatgaattcttag C/T tgggatgggtccctataaca	1199
HNMT	8	intron2 + 14682	gtagatgagcaaatgagttc A/△ ggagagatttaaatacccta	1200
HNMT	9	intron2 + 15406	gtctatgcattcatgcatcc G/A tctaaccagctgtctaccta	1201
HNMT	10	intron2 + 28943	atgtgacttaaacttcaggt A/G tatcaatatcccttgaatgt	1202
HNMT	11	intron4 + 49	cagaaagaagacttttcaga A/G tatatatataatgaatatct	1203
HNMT	12	intron4 + (1942-1943)	tttgagaaaaatttaaggta (A) tcttctatggcccacttcca	1204
HNMT	12	intron4 + (1942-1943)	tttgagaaaaatttaaggta tcttctatggcccacttcca	1205
HNMT	13	intron4 + 2405	ccctgtgaccaagcagataa C/A ctcatgctttatttagtcca	1206
HNMT	14	intron5 + (80-81)	cctgtgtttgaaagaagctt (TT) atatattttgtcttcattat	1207
HNMT	14	intron5 + (80-81)	cctgtgtttgaaagaagctt atatattttgtcttcattat	1208
HNMT	15	intron5 + 235	ctttcttttgggaaaatatg T/C ctttgtcttctatatatgaa	1209
HNMT	16	intron5 + (702-703)	tacttacaggttgattttag (AT) acacagcagactctgtcttc	1210
HNMT	16	intron5 + (702-703)	tacttacaggttgattttag acacagcagactctgtcttc	1211
HNMT	17	intron5 + 749	ttacaccagaccccatactt T/G aacaccatatgtcacaaaat	1212
HNMT	18	intron5 + 1101	gtaggcagcctattcttgat T/G atattcatcaatcatacaga	1213
HNMT	19	intron5 + 1137	acagaaaaagtattgtagac G/A gaaataacaattcattgaga	1214
HNMT	20	intron5 + 1348	aagggagcatgaatagtcca C/G aagtaactgagaactgatta	1215

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
HNMT	21	intron5 + 1673	caaaagaaagggagtaaaga C/G tcaacaatcagttagctttt	1216
HNMT	22	intron5 + 2022	attttatttggggctttcta C/T gtctctctctcctaagccta	1217
HNMT	23	intron5 + 2285	tgtcatacttaactcttaaa G/C atccagagtaaatgatggag	1218
HNMT	24	intron5+4159	taccagttgacccagcaacc C/T tcttatagagtagtttaaat	1219
HNMT	25	intron5 + 4501	aatgatccacaaaattacta C/G tcattgttttctttcaatga	1220
HNMT	26	intron5 + 5251	cacacacacacacacacaca C/G caaatggaagcagccagaca	1221
HNMT	27	intron5 + 5802	gaaaaagaaaatctggctta C/T atcatgttgaaaacaaaagt	1222
HNMT	28	intron5 + 6189	tccaattccaccttctcctа G/C agcatatcctgcagttacct	1223
HNMT	29	intron5 + 6297	gtcttggttcatctcttgag T/A taaattagatctgggaactt	1224
HNMT	30	3' flanking + 458	tatgtcactctcaagaactc C/T tataagaccaagagtcatct	1225
HNMT	31	3' flanking + 993	ctgaaaatgaacactgaacc G/A ttaatcatactgatatgtac	1226
HNMT	32	3' flanking + 1793	gtggagcacagcattttagg G/A cttgatatttgcttattata	1227
GAMT	3	intron5 + 1411	ggtgacctggtgccatcccc G/A accaggagacgcaggtgccc	1228
PNMT	2	intron1 + 35	ctgaggcacgagggacaaga G/T gtcgtcggggagtgaaagca	1229
CYP1A1	1	intron 1+1590	ccactcttcaaaaggaggta C/T atgtgacagcagctggaaat	1230
CYP1A1	2	exon2+160	gaatccaccagggccatggg G/A ctggcctctgattgggcaca	1231
CYP1A2	1	5' flanking-731	gcctgggctaggtgtagggg T/G cctgagttccgggctttgct	1232
CYP1A2	2	intron1+371	cttccctgtgttcacactaa C/T cttttccttctttgaaattg	1233
CYP1A2	3	intron3+44	atagccaggagaagccttga G/A acccaggttgtttgttcagt	1234
CYP1A2	4	intron5+81	tccctgctaggaactgttta T/C ataatgaaaggaggggacct	1235
CYP1A2	5	exon6+181	ctggccatcctgctacagca A/T ctggagttcagcgtgccgcc	1236
CYP1A2	6	exon6+295	cggctgcgcttctccatcaa C/T tgaagaagcaccaccattc	1237
CYP1B1	1	5' flanking-3669	tgtatcctgtgaagcatcac G/A gttatccttctctgcacatg	1238
CYP1B1	2	5' flanking-3149	tgacagcacttaccaaccta G/C ttcctctgatttttgagtca	1239
CYP1B1	3	5' flanking-1222	gggggaagccacccccgccc G/A agcgcctccggcttccctta	1240
CYP1B1	4	5' flanking-376	ttccgggaagcaagctcaag T/C cgcggagagggaagggaggt	1241
CYP1B1	5	5' flanking-265	ctggggacaccgtgcggcct C/T gattggaggtggctgtgatg	1242
CYP1B1	6	intron1+129	tgcccgcagcgttgtcccca G/A attgcaggaaccgttacgcg	1243
CYP1B1	7	intron1+379	tgagtgtcacgccttctcct C/T tctgtccccagcatgggcac	1244
CYP1B1	8	exon3+(799-800)	agcttctgggagatttttt (T) gagtcaaagacttaaagggc	1245
CYP1B1	8	exon3+(799-800)	agcttctgggagatttttt gagtcaaagacttaaagggc	1246
CYP1B1	9	exon3+1284	agtatagtggggttccatga G/T ttatcatgaattttaaagta	1247
CYP1B1	10	3' flanking+2226	tttcttttttcttttttttt T/Δ aaaatttattcctatttcct	1248
CYP1B1	11	3' flanking+(2226-2227)	ttcttttttcttttttttt (T) aaaatttattcctatttcct	1249
CYP1B1	11	3' flanking+(2226-2227)	ttcttttttcttttttttt aaaatttattcctatttcct	1250
CYP1B1	12	3' flanking+2230	tttttctttttttttaaa A/Δ tttattcctatttccttaca	1251
PEMT	90	intron1 + (297-299)	attgtgtgagactcagaggt TGT/Δ ccgtgttagtctttgggatt	1252
PEMT	91	intron1 + 817	tcatgaagcctgtaaggcac A/G tctctgccccaagcagcttc	1253
PEMT	92	intron1 + 830	aaggcacatctctgccccaa G/A cagcttctaatccagttctt	1254
PEMT	93	intron1 + 1035	gagttctctgaaggagctaa T/C accagttagtgttttgaaga	1255
PEMT	94	intron1 + 1573	agtgggcagggagacctaac C/T gggtgtgtgaggggtgggct	1256
PEMT	95	intron1 + 1759	gatttttcttaaagaaagaa A/G gaaagaaacatacaacatac	1257
PEMT	96	intron1 + 2768	gcatcttgctgtccacaggc C/A ggggcacctccaggattcag	1258
PEMT	97	intron1 + 2785	ggccggggcacctccaggat T/C cagaagatgactccagtagg	1259
PEMT	98	intron2 + 4598	ccgtgggttttttttttttt T/Δ cttcatttctttggttgctg	1260
NAT2	21	exon2 + 288	atgttaggagggtatttttа C/T atccctccagttaacaaata	1261
NAT 2	22	5' flank - 2053	ctggattgcaacattttaat T/C ccaggtgtcaggtttccaac	1262
NAT 2	23	5' flank - 1299	gaatcaccagtgcgggaggt A/G taacagtgaacccaagacac	1263
NAT 2	24	5' flank - 1145	ctgtagaacacaaggatatt C/T ggaggcagtttgtacatgcc	1264
NAT 2	25	5' flank - 1036	ccttcccacagagtcccgag T/A tcatgtggcagcatgccaga	1265
NAT 2	26	5' flank - 94	aaagatttgctaagagattc G/A cagaggcaacctgaggccct	1266
NAT2	27	5' flank - 643	atgtttatattttatattaa T/C attaatgtaaataaaaattt	1267
AADA	1	5' UTR + 29	attaaagtacactattcagg C/T atatcatgtaggtttacttt	1268
AADA	2	intron1+138	gctgtggcctttgacaatgt G/A ttacttagaaatgttgtttg	1269
AADA	3	intron1+142	tggcctttgacaatgtgtta C/T ttagaaatgttgtttgtttt	1270
AADA	4	intron1+1033	ttccagcagagacaccaaca A/G gtaaaaacaccccagctaca	1271
AADA	5	intron1 + 1253	ttttttttccctcatatttgc T/C gtctgtgctacaatatgtga	1272
AADA	6	intron1+1366	ctctggtagccttttaatta A/G ttaattcattcatttactta	1273
AADA	7	intron1+1369	tggtagccttttaattaatt A/C attcattcatttacttacat	1274
AADA	8	intron1+2501	ggttacagaaagaatggtgg C/A ttggccaaaaaaatgatatgg	1275
AADA	9	intron2+1971	aaatgagagttaagtaggag A/C attttcttttattttttgtgc	1276
AADA	10	intron2+1988	gagaatttttcttttattttt A/G tgcaggagaaatataaacaa	1277
AADA	11	intron2+2341	aggtgccttttctattgtcc C/T atgcagacttaggtgatcct	1278
AADA	12	intron2+2546	gtctgacacagaaggatcaa T/A ggcaaaatgtgcaagacaaa	1279
AADA	13	intron2+2609	taggaggttcactgggaaac T/C tgaattccactgagtcatga	1280
AADA	14	intron2+2663	tataaatacagtgttaaatt T/C gtctctcgtattttaaggta	1281
AADA	15	intron4 + 605	tgtgtcagtaaaatattata T/C taagtaggtgaatgagatca	1282
AADA	16	intron4 + 621	tatattaagtaggtgaatga G/T atcatgtaattgtgagacta	1283
AADA	17	intron4 + 679	ttagagattcagacgaattc A/G tataatcttcgatggtgtat	1284
AADA	18	intron4+1680	gttaaaatgtggataaatac C/T acaatttgcaaaatatttgg	1285
AADA	19	intron4+1748	atttagaagttctatacatc T/C tttatagtatattacacact	1286
AADA	20	intron4+1771	tatagtatattacacacttc G/A aaaacacaaaattatttttt	1287
AADA	21	exon5 + 238	caagtcatctcttcaaattt A/G ttaattggagttccctgctc	1288
AADA	22	3' UTR + 121	ttagaaattggtctttctta A/G aatggtctagttaagttcca	1289
NTE	1	5' flanking - 535	cacgatctgtcctccgattc C/T tgttaactctagactttctg	1290
NTE	2	5' flanking - 15	gtaaatccccggcaaaaacc A/G gcagcgccttgcaagcccac	1291
NTE	3	5' flanking - 748	agcatggcgcggggaggagg G/T gtgggagggtcgggagggac	1292
NTE	4	5' flanking - 690	tgaataatttaaaggggccg T/C gcctgcggagccgggcggaa	1293
NTE	5	intron6 + 605	tcttgccatatacttagtgg A/G ggggtctacatcaggggttt	1294
NTE	6	intron6 + 748	agcctccagcctctcttctc C/T gggggttatctcaggcatct	1295
NTE	7	intron6 + 987	ggtgctggctctgggatccc C/T gtgcgtcatgtagtctacct	1296
NTE	8	intron6 + 1882	tggcctcaagcaatcctccc G/A cctcggcctcccaaagtgct	1297
NTE	9	intron6 + 2222	gaatgtttatgtagaacaga G/A agactgtatctgcggtcttc	1298
NTE	10	intron12 + 166	tatctggtaccgaggaagct C/G tggcctcgtccccaagggcc	1299
NTE	11	intron13 + 69	atccaggtccaccgcctgcc C/T gtcttgattgttttaatctg	1300
NTE	12	intron14 + 8	agcccccgctcgggtaaggc C/T tgggaccctgcccggtggtg	1301
NTE	13	intron16 - 113	gccaccgcgccctgcgcctt T/C atatttttcttaacccttcc	1302

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
NTE	14	intron21 + 34	agagccggccggcccagagc A/G tgctgggagatgtagtccgg	1303
NTE	15	intron21 + 128	gaagaaatcgtgcccctgag G/A gtttcaaaccctaagtagga	1304
NTE	16	intron21 + 151	ttcaaaccctaagtaggacc C/G aggtgcagagcattctgggg	1305
NTE	17	intron21 + 651	ccactgtactccagccggga C/T gacagagctagaacctgttt	1306
NTE	18	intron21 + 737	tggaaaatagtctgtggatt G/T ttgtttaggactctgggcac	1307
NTE	19	intron21 + 1752	acagctggtctaggctgtta G/C tggagaaactgggaagcaac	1308
NTE	20	intron21 + 1788	gaagcaacagctgggtcaaa A/△ gtagcttttcttttcttggc	1309
NTE	21	intron21 + 1907	cactgcaacctctgcctccc A/G ggttcaagtgattctcctgc	1310
NTE	22	intron21 + 2065	ctgcctcgttttatgttcag G/T tcccccattagacagaggaa	1311
NTE	23	intron21 + 2336	agtctgggagcacaggagca G/A gaatttcagataaggaggaa	1312
NTE	24	intron23 + 41	tggggagggtggtgggtggg G/C ctggagcctcaaattctttc	1313
NTE	25	intron23 + 71	caaattctttcagacctgag T/C tcaagttctcggcttccaac	1314
NTE	26	intron23 + 81	cagacctgagttcaagttct C/T ggcttccaaccacggagcct	1315
NTE	27	intron24 + 150	gtggggcggctggtgacctc A/C gccgtccgtattccgcagct	1316
NTE	28	intron29 + 37	gcctgcagcaaccgctgacg T/C cacgtggggttgggggatg	1317
NTE	29	intron29 + 370	cgtcccaggtcagcgagccc G/A tcgggccggctgggcctccg	1318
NTE	30	intron30 + 56	acctcccgcaccacacacac G/A cacacgcgtgggcacacaca	1319
NTE	31	intron30 + 358	aaaaatacaaaaaattaacc A/G ggctggtggggtgtgcctgt	1320
NTE	32	intron30 + 372	ttaaccaggctggtggggtg T/C gcctgtaatcccagctactc	1321
NTE	33	intron30 + 430	aaatcacttgaacctgggag G/T tggaggttgcagtgagctga	1322
NTE	34	intron30 + 655	gtgtgcacaccagctatata T/C gcaaatgctttctctcaggg	1323
NTE	35	intron30 + 659	gcacaccagctatatatgca A/C atgctttctctcaggggcag	1324
NTE	36	intron30 + 760	tgaaatagggcatttgccaa C/T gcatgccagtctgtcccgtt	1325
NTE	37	intron30 + 835	gcacacacgtagataggatg T/C ggcacctctgaccgagttaa	1326
NTE	38	intron31 + 40	tggtgcctgcataggtggtc T/C ggctaagctttgctacttaa	1327
NTE	39	intron31 + 41	ggtgcctgcataggtggtct G/A gctaagctttgctacttaaa	1328
NTE	40	intron31 + 1329	gtctgtcaagggcaggacag G/A ggatgtgtaggcgagtgtgc	1329
NTE	41	intron35 + 31	aatggcttcctgtcgttttc G/A gactggggacccaccttctg	1330
DDOST	8	intron2 + 1299	atcttctgatgactgggctt C/T ggtgcagtaactggtgtttg	1331
DDOST	9	intron2 + 1581	gatactgttggtgggagaaa T/C gacagagagtgtaaaacagt	1332
DDOST	10	intron2 + 2822	gtttctcaacaggtgcattc T/G tgacgtttcagactggataa	1333
DDOST	11	intron2 + 3392	cagaaggcgtggaggcctgc C/T gcgcctccctctgttgctgc	1334
DDOST	12	intron5 + 495	attgcttgaacccaggaggc G/A gaggttgcagtgagccaagg	1335
DDOST	13	intron6 + 226	ggaactgcttgggtcacagc C/T tcgttttgttcccagtatcc	1336
DDOST	14	intron8 + 303	aagagaaataggtcattagg A/T tgaatttgttaggcaagaga	1337
DDOST	15	3'flanking + 40	cacagcgtggagacggggca G/A ggaggggggttattaggatt	1338
MRP2	1	exon 1 + 77	catattaatagaagagtctt C/T gttccagacgcagtccagga	1339
MRP2	2	intron2+192	atcaaagtggctttgatttt T/G gcataagaatggtgactctt	1340
MRP2	3	intron 1 + 413	gataagttctagaactggca A/C ctaatgatatggactagaag	1341
MRP2	4	intron2+3639	gtcatatcccaccccaaat C/A gacccaataggtacaatgaa	1342
MRP2	5	intron2+3989	agttatgaaaccgatttttc C/T gggactggttgttctagtct	1343
MRP2	6	intron2+4078	aggtttccagatgtgttccc T/C aggcattcctggtggtagga	1344
MRP2	7	intron2+4171	cttattctttggtcagttgg C/T tttctaccacctcttagctt	1345
MRP2	8	intron 2 + 5373	gttaaggatatgtgaactca A/G aatttttatacacagtgcaa	1346
MRP2	9	intron2+4436	ggactagtggaagaattaga C/G ctttcctgaataaatagatc	1347
MRP2	10	intron 2 + 3930	aaaactggcaggagaatttc A/G ctggagctgcatgcaggact	1348
MRP2	11	intron 2 + 4257	gggtattggaaagttcttgc G/A gctgctggaggctgcggtgt	1349
MRP2	12	intron 3 + 772	ggtataaggcaagatttttt A/T aaaaaattaattgcttaatc	1350
MRP2	13	intron 7 + 1658	ggactcttaccagcttagtt G/T cctggttttctaatctaaaa	1351
MRP2	14	exon 10 + 40	tggccaggaaggagtacacc G/A ttggagaaacagtgaacctg	1352
MRP2	15	intron 11 + 1672	aacttttaagtcttaagac T/A ggaaggcctgtgtcctaggc	1353
MRP2	16	intron 12 + 148	ccctctcaccgccccatgcc A/G cttttcctcctttgtaccat	1354
MRP2	17	intron 2 + 1020	agtgctgcgattacaagcct G/C agccacctgcacagcctctg	1355
MRP2	18	intron 2 + 5227	taccataatttatgtgtcct A/G tatgacatgaatttcattgg	1356
MRP2	19	intron 2 + 5373	gttaaggatatgtgaactca A/G aatttttatacacagtgcaa	1357
MRP2	20	intron 2 + 5538	ttaatgaggttaagcacatg G/T tcatatgtttaaaagccttt	1358
MRP2	21	intron 13 + 180	catgagttttctgagcccca G/C tttatctaactataaaatga	1359
MRP2	22	intron 13 + 1497	gtgcagggtccccctgatgc T/C atagccagttcctctttaga	1360
MRP2	23	intron 15 + 169	atgagctgaaagcaaaggtt T/C tcagccccttccctgataa	1361
MRP2	24	intron 15 + 949	ttccaggtgacacatttagt A/G cctaatttgggaaatgttaa	1362
MRP2	25	intron 15 + 984	tgttaatctagtccaatccc A/C ttagtaagaaaggaggggtc	1363
MRP2	26	intron 16 + 4059	catcctgatgcacagttatt C/T aaatttaagctccatttgtt	1364
MRP2	27	intron 19 + 10899	atgtatggagtatttatgga G/A taaagtattccatgctgtat	1365
MRP2	28	exon 22 + 51	caagcaataggattgttttc G/A atattcttcatcatccttgc	1366
MRP2	29	intron23+56	tatactgaggatctttctga C/T agggaggaattattatgtcc	1367
MRP2	30	intron 23 + 734	tgagccaactactgtactag G/A cactggggcactcaatgaat	1368
MRP2	31	intron 23 + 801	atgggccagacccaactcac T/G gatttttttagtgtatctgag	1369
MRP2	32	intron 27 + 124	gggtccctaaagtttccttt C/G ctctaactcaaaggacctaa	1370
MRP2	33	exon 28 + 52	cagattggcccagcaaaggc A/C agatccagtttaacaactac	1371
MRP2	34	exon 28 + 84	aacaactaccaagtgcggta C/T cgacctgagctggatctggt	1372
MRP2	35	exon 28 + 129	agagggatcacttgtgacat C/T ggtagcatggagaaggtagg	1373
MRP2	36	intron 29 + 154	ttccctaggatggacacgtc A/G tttccagaactttgaaatgt	1374
MRP2	37	intron 30 + 91	gtgttaggtgatgcctggca T/C agaattttcatccaggtctg	1375
MRP2	38	intron 31 + 170	gccaaaattttacatcacgc A/G aatgaaaacgaacaaggtta	1376
MRP2	39	intron 26 + 154	ctggctccatcttttaccca T/C ggacgtattccttactcttc	1377
MRP2	40	3'-flanking + 739	gtgaatttttattataagct C/T gttctccttaaaactttatc	1378
MRP2	41	intron 3 + 1145	acatccttctcccctcagtc C/T tcggttagtggcagtattct	1379
MRP2	42	intron23+432	tggcagtagagcagggtgag G/A aggattattctgcagaggaa	1380
ABCB1	1	5'flanking-196	gctttggagccatagtcatg T/C actcaaaatttattttatct	1381
ABCB1	2	5'flanking-16	tactctttacctgtgaagag T/C agaacatgaagaaatctact	1382
ABCB1	3	intron1+71660	cttgctggaggaagggtgct A/C gaaaatataccaaatccaag	1383
ABCB1	4	intron1+80091	gaaataatattcaagttctg A/C aataatatcatgacctatag	1384
ABCB1	5	intron1+103126	gatatgaatcagaattcatc T/C gtgtctcaagaaaaggtcat	1385
ABCB1	6	intron1+103148	tgtctcaagaaaaggtcatg C/T gataaattaagttctgctag	1386
ABCB1	7	intron1+108428	aattaatttatcatcatctg A/G tcaccatttcacacaactca	1387
ABCB1	8	intron1+112042	cataagttgaaatgtcccca A/G tgattcagctgatgcgcgtt	1388
ABCB1	9	intron2+491	gctctctggcttcgacgggg G/△ actagaggttagtctcacct	1389

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ABCB1	10	intron4+36	attaactattcaaaatactt C/T ggaaatttgacatctcctta	1390
ABCB1	11	intron5+1596	ttagctctcttactgcttca T/C agtggaagaatcaaatactt	1391
ABCB1	12	intron8+1789	aaacactctgaatattaaac C/T gctcctggaaccacagctca	1392
ABCB1	13	intron14+24	agttgtccttgccctttgcc T/C ttctagaggtgcaaaaaata	1393
ABCB1	14	intron14+81	tgcaggaagttaggaaacta C/T tataaatcggaagaagggaa	1394
ABCB1	15	intron15+38	caaaccaacctgatttataa A/G cataagaacattctactact	1395
ABCB1	16	intron17+73	gtttggtgggctagggctac A/G gtaggagtgggaacaagaga	1396
ABCB1	17	intron18+564	caacagtaaagttacaatct G/A aaaggaatgctctctgttta	1397
ABCB1	18	intron18+2062	tttccctgaggaatggttat C/T ctctgtgttccttgagtcca	1398
ABCB1	19	intron18+2293	ccacatcaggttttccccag A/G caccttgggacagtttgaaa	1399
ABCB1	20	intron20+557	aaaaccctaaccattgacac G/A tgtgaatgttttcctgggga	1400
ABCB1	21	intron21+24	cgtgcctcctttctactggt G/A tttgtcttaattggccattt	1401
ABCB1	22	intron21+2725	ctgacctgtttttggctgac A/G ggttttagttcctcccctca	1402
ABCB1	23	intron21+4725	tcttggtattaaaagatcca A/G agagataggaatatgtaatt	1403
ABCB1	24	intron22+8507	tgcacttaggaaaaaaacaa T/C atggaaatgtgtaaaatata	1404
ABCB1	25	intron22+8537	tgtaaaatatactttttttt T/A aaaaaaaaggacacatttat	1405
ABCB1	26	intron22+8565	aggacacatttattcagcat T/C atgatcagactattacattt	1406
ABCB1	27	intron22+8952	caccttggtttcatggtttg G/A caaagtactggcctgtacca	1407
ABCB1	28	intron22+9520	caccaacaaatatctttttc A/G cagttgggtgggcatctggt	1408
ABCB1	29	intron22+9836	agactctgacttagacatga C/T ggcaggggaaagagagactt	1409
ABCB1	30	intron24+377	taaaatacagatgtgttgta C/A taagttctgcaagcctttgg	1410
ABCB1	31	intron24+1493	ggggaggtgtccaggcacga A/Δ catggagagctggacttgat	1411
ABCB1	32	intron24+1495	ggaggtgtccaggcacgaac A/T tggagagctggacttgatac	1412
ABCB1	33	intron25+342	tgcagccttgatcttctggg C/T tcaagcgatcctcctgcctc	1413
ABCB1	34	intron26+134	cttggataaagtctgagagc C/G taaatatggtctccaagtgg	1414
ABCB1	35	intron26+1272	gtccttcaattttgtggtga A/G cttaaaaacaggactctaaa	1415
ABCB1	36	intron26+1394	tattaagtggtgtgttaaag A/G ttgtgctataatgaattgta	1416
ABCB1	37	intron26+(1987-1988)	aagggctggaagagtgaaag (AAAG) gaggctatttgctcccagac	1417
ABCB1	37	intron26+(1987-1988)	aagggctggaagagtgaaag gaggctatttgctcccagac	1418
ABCB1	38	intron27+59	gcagcctctctggcctatag G/T ttgatttataaggggctggt	1419
ABCB1	39	intron27+80	ttgatttataaggggctggt T/C tcccagaagtgaagagaaat	1420
ABCB3	1	intron3+8	tctcctttggcaggtaggtg G/A tgggcagctgggtccatttg	1421
ABCB3	2	intron4+104	cttcacccgtatgccaggac C/T tggggatgcttttctcttgt	1422
ABCB3	3	intron10+219	gcagcagtggtgctccctcc A/G tgggcagccccgtcaggtcc	1423
ABCB3	4	intron11+(317-319)	atggtgcccaggtggatgtg GTG/Δ tccatctcattcctgtcttt	1424
ABCB3	5	exon12+19	agctgcaggactggaattcc T/C gtggggatcgcacagtgctg	1425
ABCB3	6	exon12+(356-357)	aggtggggtggggtggggtg GG/TGGTGGGGTGGA ggctg tctgtgtccaggaaa	1426
ABCB7	1	intron1+220	acggggcaggaggttctggg C/A agaggacacctggagcgctg	1427
ABCB7	2	intron1+480	agttaactcccttgctgaca G/A gcgtgcttcttgataggcca	1428
ABCB7	3	intron1+(512-513)	gataggccaaaaccgtaact AT/Δ ctttccaaaacatagaccgc	1429
ABCB7	4	intron1+1690	agttctccaataaggcagat G/A aagttaagataaaatttgta	1430
ABCB7	5	intron1+5309	aattaatatcatttattgct G/A tattgttgtcagtgttatct	1431
ABCB7	6	intron1-11274	tgcttctttttcaagccagcc A/G gctttaaaaaaaaagttagct	1432
ABCB7	7	intron1-11085	caggttttcagggctcatgt A/G gacctgaagaaaaatgagag	1433
ABCB7	8	intron1-10037	attctactttctcaacttct T/C ttattacattatctcatcat	1434
ABCB7	9	intron1-21	ccactctgaaacttcccct G/A ctttttttccttgtcagcag	1435
ABCB7	10	intron3+(135-136)	ttctctaatgaaaaaaaaaa (A) catattaattgaccatagtt	1436
ABCB7	10	intron3+(135-136)	ttctctaatgaaaaaaaaaa catattaattgaccatagtt	1437
ABCB7	11	intron3+333	aaaacaatttgtgtgtgtgc G/A tgtgcttcaaggttaatgtt	1438
ABCB7	12	intron12+524	taaccactctgccctcagta C/T gaaacacagtgccgaaccca	1439
ABCB7	13	intron13+1543	atcctgtgaggtggggaagc G/A tatggctagcataaatataa	1440
ABCB7	14	intron13+2400	tgttaccttactgcctcatt C/G tcattcttcccacctgctat	1441
ABCB7	15	intron15+2201	ctccttcctaaccttagcaa G/C agtctggagatttacttatc	1442
ABCB8	1	5'flanking-2272	ggcttaggcctaagggctga T/C gttggggccagtacccctga	1443
ABCB8	2	5'flanking-2070	agctatgaaaacaagaccct G/A tccttctagaggtagcaaaa	1444
ABCB8	3	intron1+25	aaacggaaaaacctactcag A/C gcgggccattgaccgcccgg	1445
ABCB8	4	exon2+308	tgctggtcctgggggtagcc G/A tcgtggtgaggctttcccca	1446
ABCB8	5	intron2+334	cccccacttaaaacatttgt C/G ccctctgtctccccattcca	1447
ABCB8	6	intron4+12	cctgctccggtactgccagc C/T gcagggtgcagagttggggt	1448
ABCB8	7	intron5+547	agttcatagcattctcgctc G/A gccccctcaggcctgctgct	1449
ABCB8	8	exon7+57	ggcaatgtgcggactgtgcg A/T gccttcgccatggagcaacg	1450
ABCB8	9	intron9+1231	tttccgcagctgcatggaca C/T cctcgcgtgccccgtttctg	1451
ABCB8	10	intron9+2164	cctcttggaggtccttctag C/T gctgcctatgtggagattct	1452
ABCB8	11	intron9+2645	ttcctgcctggtgcctcccc C/Δ ggctgcctttagcaagtgct	1453
ABCB8	12	intron9+2646	tcctgcctggtgcctccccc G/A gctgcctttagcaagtgctg	1454
ABCB8	13	intron9+3229	cagggccgagcagggagtcc G/A tgggtcagctgggctccctt	1455
ABCB8	14	intron12+(113-114)	tcctccactgccacaagggg (GG) ccttctttcctgggacaatc	1456
ABCB8	14	intron12+(113-114)	tcctccactgccacaagggg ccttctttcctgggacaatc	1457
ABCB8	15	intron13+128	tgctctcgggagaccctggc C/T gtcttcacatgtcctcagct	1458
ABCB8	16	intron13+305	atccaggtctagagaagcct A/G tagtggaggtgctgagctgc	1459
ABCB8	17	intron14+135	acagttgtgtcagggaagac C/G agaaccacagccaaagggga	1460
ABCB8	18	intron14+159	accacagccaaaggggacag A/T gtcgttgtgtggggacaggg	1461
ABCB8	19	intron15+747	gttggagccttgggctctgt A/G agggggacagagggaatcat	1462
ABCB8	20	3'flanking+333	cctatcccctggctcacccc G/A ggacccacagtccccatctt	1463
ABCB8	21	3'flanking+1168	ccctctttcaggggtgtgat G/A cagtgcattgatggagcagc	1464
ABCB8	22	3'flanking+(1719-1721)	tagaccgcaggagccgcgcc GTC/Δ ttcctaacctcgcctcggcc	1465
ABCB9	1	intron1+ 69	agggtgccaggccaggcacg G/C gttgggggcgtctgggcac	1466
ABCB9	2	intron1+8873	tgggcccagcacgtggggcc T/C ggaactacctcaaaggcttc	1467
ABCB9	3	intron1+8940	accagctcagcctgcccagc G/A tgcacacggcaccaagctgg	1468
ABCB9	4	intron1+11410	agatccaagggatccagagg T/C tggaatgtgaccctccgtgc	1469
ABCB9	5	intron1+12863	gggaagccagatgcccacaa G/A gctctgtgacttcacttcca	1470
ABCB9	6	intron1+19731	gccaagtgtcaagatcgagc G/A aggggagggcctgacgaggg	1471
ABCB9	7	intron1+29649	cagaatccagatgcccgtaa T/C gttgttaagaagcctgcaca	1472
ABCB9	8	intron1+31793	ggccaggcggggaggggtac C/T ggccagaccggtgggcaaaa	1473
ABCB9	9	intron1+37537	agagtcacagggttggggtg C/A ccccgggaaggtggcatcta	1474
ABCB9	10	intron1+38293	taccagccctgtgctttcag G/A gaccatgtgacctgtcaact	1475

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ABCB9	11	intron1+44661	cccgaggtgcctggcttcac A/G gcaggattgccgtcctgcag	1476
ABCB9	12	intron1+49576	aaagtggccccgtggcttgt C/T ccctgaagccctaaagcacc	1477
ABCB9	13	intron1+64669	ccacagacaagccgggtagc C/A cacctcgcagctcaacacac	1478
ABCB9	14	exon2+448	cctggttttgggccctgttc G/A tgtggacgtacatttcactc	1479
ABCB9	15	intron7+3364	ggtaccaggagtcgggtatc A/G gtgggacaggaacgcgtgtc	1480
ABCB9	16	intron11+113	gggccccaggagctctccca G/T actatcagcctcctgggctg	1481
ABCB9	17	exon12+370	cccaggcctgcagcactgaa A/G gacgacctgccatgtcccat	1482
ABCB10	1	5' flanking-424	tcgcgtctgcgcgctccgcc C/T ggtctgccggcgtgagaaag	1483
ABCB10	2	exon1+491	acaaggggcggttgcgcccc G/T cagcggccggactcccggag	1484
ABCB10	3	intron1+37	ccacttccctccgccgggcc T/G ctccttctccacacgcgggg	1485
ABCB10	4	intron1+217	actcgtttgcagattttaca C/T ttgttttcttgttgacacac	1486
ABCB10	5	intron1+405	gcgtttatactttttttttt T/Δ aaccaaaaacacattatttg	1487
ABCB10	6	exon3+185	agggccgggggcccaggcttc C/T gtaggcatcagtatgatggt	1488
ABCB10	7	intron6+1269	caaattcacaactgtgcctt C/G cacagaatgggttggaaaac	1489
ABCB10	8	intron9+632	ccccactccacttgggtgag G/A gcaggtggatggtgatgggt	1490
ABCB10	9	intron10+2373	tacctcagggcactcagaca G/C cctcaccaatcagaggctca	1491
ABCB10	10	intron11+108	tccttttcctgttttttgtt T/G ttttttttttcttggagtgg	1492
ABCB10	11	intron11+2379	cattggtttttagtgtattc T/A gtgttgtgcatccatcatca	1493
ABCB11	1	5' flanking-(2596-2595)	tgtggtttagagctttctct (TT) gagacatttttgctaaggtt	1494
ABCB11	1	5' flanking-(2596-2595)	tgtggtttagagctttctct gagacatttttgctaaggtt	1495
ABCB11	2	5' flanking-1746	agctgaagtgaattaagcac G/A atcaactcagtactcacact	1496
ABCB11	3	5' flanking-(326-314)	agggggaaagtttaaaggta (T)9-12 gtcttgttatgtttttaagt	1497
ABCB11	4	5' flanking-135	agagggtttcccaagcacac T/C ctgtgtttggggttattgct	1498
ABCB11	5	intron1+511	aaatatagatgcaaaaaaaa A/Δ tgagctgtggatgcatgttt	1499
ABCB11	6	intron1+581	aatttcagttttaggtcac C/T caagccagtgggagtcacat	1500
ABCB11	7	intron1+(1938-1951)	aaagacgttttaagggcttt (A)10-13 gaaagaaaagaaaactgtag	1501
ABCB11	8	intron1+4517	ggtttcccaacatctcatct G/A ataaaaaaaaataatttgcca	1502
ABCB11	9	intron1+5651	aaagagaataggttagtgga T/C tagtattcctgtgcttaatg	1503
ABCB11	10	intron1+(12200-12201)	aagagatggtctctagcccc CT/Δ gtttgatttggggcacttac	1504
ABCB11	11	intron1+13023	gtttggctactttgattaaa G/A aagaaagaagagataataat	1505
ABCB11	12	intron2+739	cctgcatctattctgaccta C/T actggggaaaacagtatgtg	1506
ABCB11	13	intron2+(921-922)	tattttgtagttcaaaaagt (CAGATCTTCTTCAGCT AATTTAGAAATGT) tgctgtccatttgatattca	1507
ABCB11	13	intron2+(921-922)	tattttgtagttcaaaaagt tgctg tccatttgatattca	1508
ABCB11	14	intron3+644	agccacacgtttcttattgc G/A tgggaagtttaaaaaatggg	1509
ABCB11	15	intron3+2231	agtgaacctgagattgagct A/G tactgaaatctctagaagag	1510
ABCB11	16	intron3+2406	aaagggtggtctttaaatcc T/C tatgtttttctcatcaggtt	1511
ABCB11	17	exon4+10	tttctcatcaggttacaaga T/C gagaagaaaggtgatggcgt	1512
ABCB11	18	intron4+434	acaatttatagtatttctca A/G tgccccacacagtttatcta	1513
ABCB11	19	intron4+518	gtagatgagtagctaaaaac G/T aaagtcagctcctgaaataa	1514
ABCB11	20	exon5+120	ggcacaatgacagatgtttt T/C attgactacgacgttgagtt	1515
ABCB11	21	intron5+320	gggaggtgacccatgaattt T/C acttgagtatcatctccaag	1516
ABCB11	22	intron5+16076	agaagaggtaacagtaagcc T/G cctgatttacagcacacatc	1517
ABCB11	23	intron6+303	atttgcaggtgtgtttgtag G/C gggcagttgagtagcttgaa	1518
ABCB11	24	intron7+1141	aaaggattcagcaggcatga A/G gaaagaaaagctttgcaaga	1519
ABCB11	25	intron8+2463	ccattggctaatagcaatga A/C ctatgacatggtctaactta	1520
ABCB11	26	intron8+2677	tcaatgatgttacagtgaga A/C tctaatattgtattaaaccc	1521
ABCB11	27	intron8+2699	ctaatattgtattaaaccca T/A gccacatgttaaatgaatct	1522
ABCB11	28	exon9+24	gtgtccaagtttacggacta T/C gagctgaaggcctatgccaa	1523
ABCB11	29	intron9+108	caccttggtctgtggcctcc A/G gaggaagtacttgttcaaga	1524
ABCB11	30	intron10+2475	taatcattccaaaccacgga C/A tttatttcattaagaacatg	1525
ABCB11	31	intron10+2478	tcattccaaaccacggactt T/A atttcattaagaacatgata	1526
ABCB11	32	intron10+2711	tttacagattggaaaagcca C/T tgaagtattgcaggtccaga	1527
ABCB11	33	intron10+3539	agtgactgtaattagtatca C/G ttgtgcacagagaaaaaatg	1528
ABCB11	34	intron10+3623	tgcagaaggttgttctttca T/C gaccttcctgagtttcagaa	1529
ABCB11	35	intron10+3661	gaattcattaataaaaataa A/T cacataatggagcgtgacat	1530
ABCB11	36	intron10+5100	gggccactctttggcttggc A/G atagactgtggccaatgaaa	1531
ABCB11	37	intron10+5292	gctatttggtaggaacatct G/A ggcatgatcaggtagccttc	1532
ABCB11	38	intron10+5912	gagtaatattcagtaaaaaa A/Δ taaagtggtattttaaatca	1533
ABCB11	39	intron12+116	tgtttccagtaatagggaat G/A gaggtgtctttctctgaaag	1534
ABCB11	40	intron12+326	gataaatgacaaggcaatta G/C aacaatcaggaagcacaggt	1535
ABCB11	41	intron12+335	caaggcaattacaacaatca A/G gaagcacaggttcttcccaa	1536
ABCB11	42	intron12+2572	cctcatccttgccaatgttt C/T cttttactggtttttgatgg	1537
ABCB11	43	exon13+23	tctaaatgacctcaacatgg T/C cattaaaccaggggaaatga	1538
ABCB11	44	intron13+70	atggcagtatattgatcaaa C/T agaaaggtgtagcatacatt	1539
ABCB11	45	intron13+(1578-1579)	ttattggcctctatttttttc (C) tgcccattggtcaagtatga	1540
ABCB11	45	intron13+(1578-1579)	ttattggcctctatttttttc tgcccattggtcaagtatga	1541
ABCB11	46	intron14+32	catacattcctgggagaaac C/T aagaggtcatagaaggaaaa	1542
ABCB11	47	intron14+80	cacaattatacacatttctt C/T tcgtatgattcccaagtcat	1543
ABCB11	48	intron14+439	tattgtgtcaaaaacaattc A/G ttgtatatctccattctaag	1544
ABCB11	49	intron14+(1262-1263)	cagcctttgcattatatttt (T) gctgtgttgtctaacaggag	1545
ABCB11	49	intron14+(1262-1263)	cagcctttgcattatatttt gctgtgttgtctaacaggag	1546
ABCB11	50	intron14+1283	gctgtgttgtctaacaggag A/C aaagagacacggatttgctc	1547
ABCB11	51	intron14+1339	tgagatagatatttaggacc G/A tgaccaattttatttttggt	1548
ABCB11	52	intron14+1359	gtgaccaatttttatttttgg T/C tgaaaaatcttatttgaagt	1549
ABCB11	53	intron14+1480	tattgattagacaataaccc G/A tctggggaagggatatttct	1550
ABCB11	54	intron15+370	ccttttctaatgtctgcaca G/A cctatttaagaatattccca	1551
ABCB11	55	intron16+(550-559)	aaagtttagtgtttctatca (T)9-12 gctacttctgatggacttct	1552
ABCB11	56	intron17+188	tttctctccccaattcatgg T/G tttttggttagcttctcatc	1553
ABCB11	57	intron17+194	tccccaattcatgggttttt T/G gttagcttctcatcttcttg	1554
ABCB11	58	intron17+(197-198)	caattcatgggtttttggtt (T) agcttctcatcttcttgggg	1555
ABCB11	58	intron17+(197-198)	caattcatgggtttttggtt agcttctcatcttcttgggg	1556
ABCB11	59	intron17+(289-296)	ttagaaaggggacttctttt (A)7G(A)4 tctgtgtttagtgttcctct	1557
ABCB11	59	intron17+(289-296)	ttagaaaggggacttctttt (A)12 tctgtgtttagtgttcctct	1558
ABCB11	59	intron17+(289-296)	ttagaaaggggacttctttt (A)10 tctgtgtttagtgttcctct	1559
ABCB11	60	intron17+1070	tcagacttgggttttcctat C/T tttcttcttgagaacaagtt	1560

Designation of Gene	No.	Location	Sequence	SEQ ID NO
ABCB11	61	intron17+1651	tgttaaaatatctcattgta T/C atgctgacggatttttcttg	1561
ABCB11	62	intron17+2226	ccttaagtctcctcctatca T/A gcaccttgttctcaccagct	1562
ABCB11	63	intron17+2979	ctctctcttcctttctcagc T/Δ ctactatttcactgttggct	1563
ABCB11	64	intron17+3288	aatccccatatcctaccttа T/G ccatctcatccatgaatctt	1564
ABCB11	65	intron17+3289	atccccatatcctaccttag C/T catctcatccatgaatcttg	1565
ABCB11	66	intron18+97	aatatgagttttctaggtat A/G tatctagcagtgtttcaagt	1566
ABCB11	67	intron18+98	atatgagttttctaggtata T/C atctagcagtgtttcaagtc	1567
ABCB11	68	intron18+892	ctctgaaagttagtgataca C/T cttatttgtgtttgaatcaa	1568
ABCB11	69	intron18+2681	atgtatgagatcaagtcagg A/G tcaaatattagacacccata	1569
ABCB11	70	intron18+3780	ggaccatcctgtggggcaat C/G gttccagaaaatgctggtat	1570
ABCB11	71	intron18+5741	ctcaccggtataaatacaac C/T gtagcaaaggttttcttttt	1571
ABCB11	72	intron18+(5882-5883)	tgcgtattccctcagttcag (C) tttttattcaagccacagca	1572
ABCB11	72	intron18+(5882-5883)	tgcgtattccctcagttcag ttttttattcaagccacagca	1573
ABCB11	73	intron19+10022	tggctaagttaaaaaaaaaa A/Δ gagattcaactataattgct	1574
ABCB11	74	intron21+322	caagattcaatactgccccc C/Δ agggggtgggtgaacagggc	1575
ABCB11	75	intron22+257	ctgttcaatttcctctcgca T/C agtgattcattccacattcc	1576
ABCB11	76	intron22+552	taattaatatcttgtccttg G/C ggggtaaatgagggatggta	1577
ABCB11	77	intron22+569	ttgggggtaaatgagggat G/A gtagcataaacacttctcaa	1578
ABCB11	78	3'flanking+243	aaacaccacagaatgacata G/A aactaaaggcggcaggaatc	1579
CYP4B1	1	5'flanking-333	gaaacattcacagtgcttgt A/T tgagaagacagtggttatta	1580
CYP4B1	2	5'flanking-18	gagcagctgaaggcaggtca G/T atgaaggctaggtggctgga	1581
CYP4B1	3	intron1+341	tccaaaacctctggatagta C/T atagaagtaggcaatccatt	1582
CYP4B1	4	intron1+542	cctatgggtggctcaggagc C/T gtgacaccttcccaggttca	1583
CYP4B1	5	intron1+2856	gaggactttgcacatagtag G/A tgctcagctatattgttggc	1584
CYP4B1	6	intron1+6086	tttggaatctaaagactggg G/T cacgatgctagttgtgtgac	1585
CYP4B1	7	intron1+6598	ttttggggtgtggggagagg G/A cccatagtagggagacagct	1586
CYP4B1	8	intron1+6660	acctaagggtgtccatcctg A/G aggagagcagtcctagggggg	1587
CYP4B1	9	intron1+7242	ccctggtctcccttaactca T/C gctggactgttccctttggt	1588
CYP4B1	10	intron2+107	gcctgtgtactaagtctgcg C/G agctgaggttcccaccctac	1589
CYP4B1	11	intron3+361	atggtgtggtggtaggacca C/T ggctggtcaccagaggctgt	1590
CYP4B1	12	intron4-492	aaaggctttcacatctaaaa C/A gtgtctcctcattttctgtc	1591
CYP4B1	13	intron4-315	ggattacttacatatacacc A/G tgcgggggagctcaccacct	1592
CYP4B1	14	intron4-157	ctacccaccctatcctgata T/C tccagcaggatggagggcag	1593
CYP4B1	15	exon5+22	acaagtgggaagagaaagct C/T gggagggtaagtcctttgac	1594
CYP4B1	16	intron5+125	cccagggagccttagcttgc G/A gggagacaggacctgctcat	1595
CYP4B1	17	intron5+(287-289)	tgtctaagccaatccctcct CCT/Δ accctctgcttagcagggac	1596
CYP4B1	18	intron6+54	gcctgggttcctcctcctgg C/T ccctctatgccccctcccat	1597
CYP4B1	19	intron7+(99-100)	agctcttaagcatttccccc (TC) tttcctcagcaaatataacc	1598
CYP4B1	19	intron7+(99-100)	agctcttaagcatttccccc tttcctcagcaaatataacc	1599
CYP4B1	20	exon8+114	tcctggtttctctactgcat G/A gccctgtaccctgagcacca	1600
CYP4B1	21	exon8+139	tgtaccctgagcaccagcat C/T gttgtagagaggaggtccgc	1601
CYP4B1	22	intron8+247	agaaagttgtcaacaagagg C/T tgatattttgtgtgctaact	1602
CYP4B1	23	intron8+366	tgtgggggtgaacagagctg A/G gacagctgggagagccagtt	1603
CYP4B1	24	intron8+650	cctttgcttgtggtcagaca C/A cctgcctttctctctgggct	1604
CYP4B1	25	intron8+844	tcatatgtgagaatcccccc C/A ccacggggtatccagacaca	1605
CYP4B1	26	intron8+1767	tcccattccaagaatgttct G/T gttgtgttgctggcagggat	1606
CYP4B1	27	exon9+53	tgtgcatcaaggagagcttc C/T gcctctacccacctgtgccc	1607
CYP4B1	28	intron9+652	agtcggatgtggtcatgaac G/T ctctgtcactggcagtggtc	1608
CYP4B1	29	intron9+774	cctggtcaccaacctctgtt C/T tgcccacaggaagcctgatc	1609
CYP4B1	30	intron10+33	tgggctgggagatcagacag G/T gtgggggactgggagggtca	1610
CYP4B1	31	exon12+224	ccagatggctcaggctgtga C/A ctccctgggcaccaccctcc	1611
CYP4B1	32	exon12+270	ctgggtgtggaggagttggg G/A ccccctgccttcaggaggct	1612
CYP4B1	33	3'flanking+129	tctgtgtctcacagtcacgt G/A gtgctccaggcattcagggt	1613
CYP27A1	1	intron1+295	aggagggagctgtcttggga A/G gagagtggcagaggcaaatg	1614
CYP27A1	2	intron1+17503	cagtgcataaagcctctgat C/T ctccttagagaaggagggac	1615
CYP4F2	1	intron1+(145-146)	ccaagcccctggcaacctca CA/Δ gtgattcaggctgggccttt	1616
CYP4F2	2	intron1+193	tttaatcagtctctctctct C/T tttcccattctaagtgctta	1617
CYP4F2	3	intron1+324	ccctgctctacctccggcac T/C gcccgtccctgcctctccac	1618
CYP4F2	4	intron1+367	tccctggaggtccctgggcc G/C ttctctgggcctcaggatct	1619
CYP4F2	5	intron1+402	ggatctcaccgtccatcccg T/C ctgccctgcaggatgtccca	1620
CYP4F2	6	exon2+35	gcctgtcctggctgggcctc T/G ggccagtggcagcatcccct	1621
CYP4F2	7	exon2+166	cggtgtttcccacaaccccc A/G agacggaactggttttgggg	1622
CYP4F2	8	intron2+125	ggcagagaagcagaggaggc A/G tcttactcattcctctgctt	1623
CYP4F2	9	intron2+440	gggccgtctcccacttccac T/C acacccgaaggcacctttct	1624
CYP4F2	10	exon3+48	gttctgactcagctggtggc C/T acctaccccccagggctttaa	1625
CYP4F2	11	intron3+701	agactccaccccagcttggg T/A ccctttccttgacccctgtg	1626
CYP4F2	12	intron3+742	cttcccatcgttggacgggc G/A aggctgagcaggggaatgg	1627
CYP4F2	13	intron3+1020	gctttagctttctccatgtc G/A cttttcctatcaaggtggcc	1628
CYP4F2	14	intron3+1039	cgcttttcctatcaaggtgg C/A cttttcctcatgatgtcaac	1629
CYP4F2	15	intron3+1040	gcttttcctatcaaggtggc C/G ttttcctcatgatgtcaacg	1630
CYP4F2	16	intron3+1920	ccacctgtctaacctctgtt G/C ctgtttgctcatgtctgggg	1631
CYP4F2	17	intron3+1945	ttgctcatgtctgggggctg T/A ctctacaatggctgttatat	1632
CYP4F2	18	intron3+2621	agcattctgtagaatgctga G/A ctgtgctcaggggttgcgga	1633
CYP4F2	19	intron3+2665	tgttggatcgtgtaggaggc A/G tgtcaaggcatgctggaacc	1634
CYP4F2	20	intron6+194	gggtttgaactggtgggtgt G/T gtcagagctctgtaggggac	1635
CYP4F2	21	intron7+67	tgtgaaatgtcagatgaaag G/A atttgaacttgattaagagg	1636
CYP4F2	22	intron7+2811	ttccaagggaaattgccatt T/G aattctcctgtaactcaggt	1637
CYP4F2	23	intron7+(3096-3097)	ggggtgggggttgggggggg (G) ttactgccttctctccagga	1638
CYP4F2	23	intron7+(3096-3097)	ggggtgggggttgggggggg ttactgccttctctccagga	1639
CYP4F2	24	intron8+145	ggtgctgtctaccttcgggt G/A ctgaagcagcccagagaccc	1640
CYP4F2	25	exon9+44	ctctcctgggtcctgtacca C/T cttgcaaagcacccagaata	1641
CYP4F2	26	exon11+48	gaacccatcacaacccagct G/A tgtggccggaccctgaggtg	1642
CYP4F2	27	intron12+108	tggtccaagttccagctctc C/T ttccctcacctcctctggag	1643
CYP4F2	28	intron12+285	gcatggggatccaggcacgg A/T taccccttctctattcctc	1644
CYP4F2	29	exon13+238	aagtgaagcctagaattacc C/A taagaccctgttccacagtc	1645
CYP4F2	30	exon13+342	tgtgcgtgaatgttcatggc G/A gccctattcacagtagccaa	1646
CYP4F2	31	exon13+563	tagtgtactgtccttttata T/C gaaatttccagaacaggcca	1647

Designation of Gene	No.	Location	Sequence	SEQ ID NO
CYP4F2	32	exon13+707	aaatgttccggacctagata G/C tgacgaaggtagcacgacac	1648
CYP4F3	1	intron2+258	cattaatgcacctctgcggg G/T ctcttgggcaggggggttggg	1649
CYP4F3	2	intron2+916	ttagggacatgtcctgagtc C/T acactgctccccacaaacct	1650
CYP4F3	3	intron2+3417	atccaggtctcacacagtgt C/T acttcctctcttggctttag	1651
CYP4F3	4	intron2+4090	gagagcatgaattgggtcct G/A tgtctttctctccagattca	1652
CYP4F3	5	intron3+89	tgtgctgcctccagcgggtc G/A cgtgcccatgtgcagacagg	1653
CYP4F3	6	intron3+243	tcaagtctgctgtacggcta C/T gtcttgtcacctgtatatttt	1654
CYP4F3	7	intron3+502	aggtctgggacccagggtcc G/C taagtgaactgtctgagaca	1655
CYP4F3	8	intron3+755	ttttgtggccatgtcaggac A/T tgtgaacacatgtcagtgtc	1656
CYP4F3	9	intron3+855	gggacagacagggtgtccta G/A gtccttgtgaaggcattctg	1657
CYP4F3	10	intron3+970	cctgacatagctcctacgtg C/T catgttaggcagtgtcattg	1658
CYP4F3	11	intron6+122	gaggagttgttatacctgat C/T gttgaaggactggtatgaat	1659
CYP4F3	12	exon7+159	ggtgcacgacttcacagatg C/A cgtcatccaggagcggcgcc	1660
CYP4F3	13	intron7+2107	caggttgccagtgatttttt T/Δ ctcagaaagttttcatcaag	1661
CYP4F3	14	intron7+2255	gaccaagaagggtctaggag T/A gcaagatgggcttgggtttc	1662
CYP4F3	15	intron8+132	cctcaatgcaaggttgctgt A/C caccctcgggtgctgaagca	1663
CYP4F3	16	exon9+59	taccaccttgcaaagcaccc G/A gaataccaggagcgctgtcg	1664
CYP4F3	17	intron9+13	attgaatggtgagtgcaggt G/A ctggtgccctgttcctgagc	1665
CYP4F3	18	intron9+36	ggtgccctgttcctgagcct G/C tctcattggctctgttcccc	1666
CYP4F3	19	intron9+167	acccatcctgactgtctggg C/G aaaggttataggcccttagg	1667
CYP4F3	20	intron9+369	tccctaattcctacccttcc G/A tccagtccagggatttataa	1668
CYP4F3	21	intron9+458	tcattcatccatccagtcct T/C gttcagcaaatactctcata	1669
CYP4F3	22	intron10+46	ctcctgggtaggaagagggg A/C ccctcaggcagggagcattg	1670
CYP4F3	23	intron10+63	gggcccctcaggcagggagc C/A ttgtcctgactgccccctc	1671
CYP4F3	24	intron11+14	ccctgaggtgcgggcccccc C/G tctctgtttttgtccattcc	1672
CYP4F3	25	intron11+84	gatcaggagaatccaacatc G/A cctccctccaagacacacac	1673
CYP4F3	26	intron11+113	caagacacacaccactgtct T/C tccaaggctggcggactggg	1674
CYP4F3	27	intron11+164	cggcaacccttcttggtctc T/G cctccaggtctatgacccct	1675
CYP4F3	28	intron11+165	ggcaacccttcttggtctcg T/C ctccaggtctatgaccccct	1676
CYP4F3	29	intron12+156	gaaaaggcccacagagtagg G/A ttgggttggtcctagaagga	1677
CYP4F3	30	intron12+253	gagctcggctaggctcgcag G/T atatgcaagcccacatgggg	1678
CYP4F3	31	intron12+346	tgggtgtcccaggccaggtt A/C ccggcttgatggggccagga	1679
CYP4F8	1	5'flanking-61	accatgtttacccatcattg G/T tcctggagctccccagcccc	1680
CYP4F8	2	exon1+67	gtggcagcatccccgtggct G/T ctcctgctggtggtcggggc	1681
CYP4F8	3	intron1+707	tacgcagcaggtattcacca T/G tatttccacattatccactg	1682
CYP4F8	4	intron1+857	acacccccctacccctcacatc G/A tgacacagctgggccagaag	1683
CYP4F8	5	intron1+907	tgccatctccaccctccccc G/A tgcaggggcatcttctttat	1684
CYP4F8	6	intron2+668	tgtggcacttccaccatatg T/C tcattgccctcttgctccag	1685
CYP4F8	7	intron2+818	gccacagagaccatggctca G/A gccccaaaatgctgagtgac	1686
CYP4F8	8	intron2+1079	tatgcttgggtgttgcagaa C/T atgttggaccatgtaggagc	1687
CYP4F8	9	intron2+1194	ccggtccccttttatgccccc C/A accctccttttcttcttctgc	1688
CYP4F8	10	intron5+45	aacatgggatggagtggggg G/T gtgggtgtggggagagcaaa	1689
CYP4F8	11	exon8+(19-20)	ggccatgacaccacggccag (GCCAG) tggcctctcctgggtcttgt	1690
CYP4F8	11	exon8+(19-20)	ggccatgacaccacggccag tggcctctcctgggtcttgt	1691
CYP4F8	12	intron8+222	tttatttccccactaacttg C/G tatgcaagcttagtaaaatc	1692
CYP4F8	13	intron8+334	cttggagaattaacggcaaa A/T accgcaatgacttttggacc	1693
CYP4F8	14	intron8+1999	ttctaagtacatttattctc T/C tgcttttagctatgatctag	1694
CYP4F8	15	intron8+4184	caggagggccgtgtatgctc C/T ctggataattgttgggtgtt	1695
CYP4F8	16	exon9+119	acgtggtgctcccagacagc C/T gagtcatccccaaaggtgcc	1696
CYP4F8	17	intron11+282	gggttgggggttccgggcct G/C gttcctggcgcagtggggcc	1697
CYP4F8	18	intron11+340	tgcagtcagaccttccacct C/T ggccccaggaactgcatcg	1698
CYP4F8	19	3'flanking+35	atcacctacctttgcaccaa T/C tacctttcagatttccggt	1699
CYP4F8	20	3'flanking+83	ctgtgttggcccctgtgcct G/C agtcccgcggatggccagta	1700
CYP4F8	21	3'flanking+90	ggcccctgtgcctcagtccc A/G cggatggccagtaggggcg	1701
ALDH1	1	intron1+564	cattatttcttcagccaagt T/C tgttgccattggagcagatg	1702
ALDH1	2	intron1+710	gttctgagagtaactctgaa C/T tttgcctgtttcacactgct	1703
ALDH1	3	intron1-3868	ccctttttatatccagaata C/G agcctaaacttctttctctg	1704
ALDH1	4	intron2+2933	taagtatgctatactatatt T/C gatagatatactatactata	1705
ALDH1	5	intron2-1646	caatgtgattaactgaatgc C/T gcaaatatgcactgtatatg	1706
ALDH1	6	exon3+54	caggcttttcagattggatc C/T ccgtggcgtactatggatgc	1707
ALDH1	7	intron3+157	taggcccctaacattgaac T/G attctcaaatagtaatctgc	1708
ALDH1	8	intron3+339	tgagtctcctagaatgatat G/A ttaggtttattcaagcattt	1709
ALDH1	9	intron3+655	agcagttagatgagtcagag C/A ataatatagtgggggaggg	1710
ALDH1	10	intron3+735	gaagccaatttaacataaac C/A aataccaagatcaggtttca	1711
ALDH1	11	intron3+863	gcaagtatggttaatcaaag G/A accatttattactcaaatat	1712
ALDH1	12	intron3+1757	agatgacaagatttcttcta T/A ttcaaaaattccctagcaca	1713
ALDH1	13	intron5+90	ttctctaaaacagatggatg C/A ttatgtatttgttaaatgtg	1714
ALDH1	14	intron6+213	caggaagccaaacacaaagg T/C ttggtgtcaaacagtcaact	1715
ALDH1	15	intron6+1323	ttttgaattaaattcttata C/T tgtaacttttaaacttttta	1716
ALDH1	16	intron7+638	gcaaaagaaagtggtggaag C/A atactgtaccatgcaaaaaa	1717
ALDH1	17	intron9+(1462-1463)	aatggaattctatgtttttt (T) gttgtgattatttatctatc	1718
ALDH1	17	intron9+(1462-1463)	aatggaattctatgtttttt gttgtgattatttatctatc	1719
ALDH1	18	intron9+1757	tgatctagaatttagtttct A/G taaatgaatagaatccagtg	1720
ALDH1	19	intron12-1383	aatcccacttattactctcc T/G gagagcttcaagtgcctata	1721
ALDH1	20	3'flanking+40	ttttaagtacaagttttggt T/C acagtgatttcttcttgtca	1722
ALDH2	1	intron3+1766	aaattggtggctcatcctgc C/Δ tggccccctcctcctcctc	1723
ALDH2	2	intron8+52	gaaggtagccctggccacct G/C tgttgtggctccagccgatc	1724
ALDH2	3	intron8+69	cctgtgttgtggctccagcc G/A atcctgtcgccccccagtg	1725
ALDH2	4	intron9+5197	gctttcttatgaccttggtc C/A atttcccagttgtcttgttg	1726
ALDH2	5	intron11+114	gagctgggctcagtttctcc T/C gggtcagggtgtgatgtcga	1727
ALDH2	6	3'flanking+411	ggatatgatttctgcccctc T/C tctgctgtgggtaaacagct	1728
ALDH2	7	3'flanking+(432-433)	tctgctgtgggtaaacagct TC/Δ tgtttcatgcatttacttttt	1729
ALDH2	8	3'flanking+488	ccaataagaatgtgcttgaa G/T gtttcatgcatttaatttgt	1730
ALDH7	1	5'flanking-1455	ctgcctgtccacacccacag C/T agcttgcacatcatccccac	1731
ALDH7	2	intron1+464	catgaatgactctgggaaag A/G atcattcttagcaatggact	1732
ALDH7	3	intron1+2269	aaatggaatccaaacagcaa G/C agacctcccctcaccggtca	1733
ALDH7	4	intron2+1349	actgagcttctgccaccggc C/T gcctgccggccttcatgaga	1734

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ALDH7	5	intron2+1820	tccgtgtggaaggcaccttc C/G cccagcctcagtggctagga	1735
ALDH7	6	intron2+2046	aacctcaggcgctgcctcag C/G cagggagccagcctggcccc	1736
ALDH7	7	intron2+2939	aagcacgcactgaacatgga G/A tgagtgagtgaacgaatgaa	1737
ALDH7	8	intron3+7	tgcccaagaacctggtgagc C/T ggccgggctgaggcgggcag	1738
ALDH7	9	intron4+36	gccccttccggtcacccttc T/C ccgctcgaggcctcagggcc	1739
ALDH7	10	intron6+(116-117)	attctcctctctctctct CT/Δ ggaccaggctgggagcagtc	1740
ALDH7	11	intron6+263	cagaccctcatacgtgaccc T/C gctgccccccaggctcttag	1741
ALDH7	12	intron6+1298	gtagacagagctggactcca T/G ccttgggtgataagggatcc	1742
ALDH7	13	intron6+1411	gccagggtcacaagcagagg C/T gggaggagccaaggggtttg	1743
ALDH7	14	exon7+185	acctgcgtggcccccgacta C/T gtcctatgcagccctgagat	1744
ALDH7	15	exon7+339	tgcgggcattgctgggctgc G/A gcgtgtggccattgggggcc	1745
ALDH7	16	intron7+249	ccagggctccagggctcagc G/A tgctaagatgaactcccatc	1746
ALDH7	17	intron7+277	atgaactcccatcccaccac C/T ggctatcctgaaaggctgta	1747
ALDH7	18	intron7+498	gaccaaggtcgggggattct C/T tgtgtcccacaggccctgag	1748
ALDH7	19	intron8+14	cagccaggtgggggtgcggc C/T gggctgggcagggtcaggag	1749
ALDH7	20	intron8+49	caggagcccgcagtgggcag C/T acaagtggtggcagcagggg	1750
ALDH7	21	intron8+111	tcaggactttgggatggtgg A/T cctcttggctctgtctctgc	1751
ALDH7	22	intron8+3219	atcctgatggggctcaaggc A/G gcctcacgcacatcctgttc	1752
ALDH7	23	exon9+33	gtgctgacccagaccagcag C/T gggggcttctgtgggaacga	1753
ALDH7	24	intron9+946	tcccaggcccccgagctgac C/A cttcttggtggccgtggccc	1754
ALDH7	25	intron9+1067	aggctccccaagcctgggtc C/T ctcttgcccccacccactct	1755
ALDH7	26	exon10+137	ccgcaatcgccgcgccgcct G/A aggatgctgctggtggccat	1756
ALDH7	27	exon10+397	cgctcccaaccatgagagcc G/A aggtgggaggcatgggaaac	1757
ALDH7	28	exon10+1198	ctcttccccatgctgctcat C/T ctcctgggccccatccactc	1758
ALDH7	29	exon10+1475	caggggtggacctgagtttc G/A tctcctgtctctctggctga	1759
ALDH7	30	3'flanking+15	cctggcaatacttacatctc A/G gtgatttgctttctgtgcat	1760
ALDH7	31	3'flanking+60	caacaggactctggaccaag G/C ccctggcgttgggtaacaat	1761
ALDH8	1	intron1+98	agggaaggggatgtgtgccc G/A tggcccgtgggtcagggggc	1762
ALDH8	2	intron1+157	atggctgcaggggccatggg T/C acggggcttgctcaggagag	1763
ALDH8	3	intron1+354	tctgtggacagacaaggatt C/G ggtcgggggcaccagggctg	1764
ALDH8	4	intron1+851	tatgacaggtccatcaggcc T/G caccttcctgtgtgtcttat	1765
ALDH8	5	intron1+894	ctcagcatctgcccccacag T/G gcttttgcacacgttggttc	1766
ALDH8	6	intron1-463	aaagaaccctccgagtccct C/G gtttagtcccagaagggagg	1767
ALDH8	7	exon2+61	gccttcaactgagggcgcac G/A cggccggccgagttccgggc	1768
ALDH8	8	intron2+8	ggacctgcataaggtgggcc A/G tggagagtgggccccggcag	1769
ALDH8	9	intron2+23	gggccgtggagagtgggccc G/C ggcaggggctggagcagcgt	1770
ALDH8	10	intron2+(180-181)	ttcactcctgaacactcaca (A) gccaccctgtgatgcaggct	1771
ALDH8	10	intron2+(180-181)	ttcactcctgaacactcaca gccaccctgtgatgcaggct	1772
ALDH8	11	exon3+72	gactacgctctcaagaacct T/G caggcctggatgaaggatga	1773
ALDH8	12	intron8+375	ctgcagcatcctaacctcac C/T gtcgcgactcaaggctgccg	1774
ALDH8	13	intron8+463	aatcaccccatggcacccc G/A accgtcactgagagggtgct	1775
ALDH8	14	exon9+33	atgctggagcggaccagcag C/A ggcagctttggaggcaatga	1776
ALDH8	15	exon10+428	aggtgtcctcactcacccca C/T cctccccaattccagccctt	1777
ALDH9	1	exon1+121	actgtgtggggtatggcggg G/A tggtggggagaatgtggtgt	1778
ALDH9	2	intron1+67	cgcggatttcccggccagcc C/G ccgtttcctgtgttctgcag	1779
ALDH9	3	intron1+103	tgcagcgttgacttgagcac A/G agacagtgacagtggagagt	1780
ALDH9	4	intron1+1818	gaatttttgagaaaaaaaaa A/Δ tgttcctttagggttgcctt	1781
ALDH9	5	intron2+5891	tcaggaacaggaagtaaaga G/A gtttacatttctaaatttct	1782
ALDH9	6	intron2+6398	atcaaaaacacttgtctgat T/G atcgtgctctgaacctgcct	1783
ALDH9	7	intron2+9677	atgacgctgagtttggtgct A/G ttcttttgtttttcttgcct	1784
ALDH9	8	intron2+9991	gggagaagtgagggacctac C/T cttggcttctaatctttcat	1785
ALDH9	9	intron2+10198	ttgtcagagacatctttgat A/G atccttacgtactatatcag	1786
ALDH9	10	intron2+10256	ttagtagataacttttttt T/Δ gtaaggatggagaataatag	1787
ALDH9	11	intron2+11382	catattcaattcttttatgt T/C ctttagaccaaagaaaggca	1788
ALDH9	12	intron2+11455	taaacctttaagctcatcat C/T ggaccatctattgaatttct	1789
ALDH9	13	intron2+12044	atttaaagtgaaagctattt C/T tagttttaaaaattgagcag	1790
ALDH9	14	intron3+334	ctatttagcaaacttttttt T/Δ gacagtgtataaagttttca	1791
ALDH9	15	intron3+368	gttttcaacaattgatattg G/Δ aaggttggtagggcctagga	1792
ALDH9	16	intron4+191	ccctcaaggagcttatagtt T/A aggttgtacacaatcatgtc	1793
ALDH9	17	intron4+557	tagaaaaaattgtaatgtta A/G aaagcattactgttaggaca	1794
ALDH9	18	intron5+830	agttcaagatgattttgtag G/C ttcagggcctagttgactta	1795
ALDH9	19	intron5+838	atgattttgtaggttcaggg C/T ctagttgacttagcatgcaa	1796
ALDH9	20	intron6+120	agaaaagttgcacaaatagt A/C caaagaattcccatgtacct	1797
ALDH9	21	intron6+2569	attaaaatctgctttaaata T/C ttttttgggggagaggacac	1798
ALDH9	22	intron8+1414	ccgatcttcaaaaaattagc T/C gggggtggtggtgcacactg	1799
ALDH9	23	intron9+664	aaagttcacatttttttttt T/Δ ataacttcatggtcaagagc	1800
ALDH9	24	intron9+2170	taatgcacacatttttttttt T/Δ cttcatagggacatccaacg	1801
ALDH9	25	exon11+587	aaaacaaaaaacaaaaaaaa A/Δ ccttgttcctttataggttc	1802
ALDH10	1	intron1+39	gggtgtggggaaactggccc C/T cgccgcgcacttgtggactg	1803
ALDH10	2	intron3+2491	tgccgcgaagaaattggcac T/A gctgagttctacatgcagtt	1804
ALDH10	3	intron3+2595	ttctgtacatcaacttgtga T/A ggattgaggccagttctggt	1805
ALDH10	4	intron3+2775	taccgctttgcccctgacca G/A gggtaaattcttcaataact	1806
ALDH10	5	intron3+3424	aggcacttctgcacacaccc G/A cgtctcatgcattttccctg	1807
ALDH10	6	intron3+3676	atgttgaagagattgctgat G/A ttagacgttaggatttattt	1808
ALDH10	7	intron4+481	tagaaaataagaggtttcag G/T ttctctctgctaaatccggt	1809
ALDH10	8	intron4+769	atcctgctttatacctgaac G/A tcttgcaggcagagccaaaa	1810
ALDH10	9	intron4+796	aggcagagccaaaagccaca A/G ccaggagagtctgtaccgaa	1811
ALDH10	10	intron5+254	attagttgtggcatatactt T/G ttttaaaaaagttaaataat	1812
ALDH10	11	intron6+137	aatcctgctttctggtatac T/C gtacctgtagcttttgttat	1813
ALDH10	12	intron6+923	aggctaatgaatggtaagag G/A aaggggctatcctgattagc	1814
ALDH10	13	intron7+331	tgcttttctgatgttaatcc A/Δ cagggcattgctgaataaca	1815
ALDH10	14	intron8+643	tttagaacatgacctgcctg C/T ctctcccacatgtgagatga	1816
ALDH10	15	intron8+666	ctcccacatgtgagatgact G/A actcagctttttatttctcc	1817
ALDH10	16	intron9+2129	tgttttcatttttaaaaaaa G/T gtttgactttggaattcatg	1818
ALDH10	17	exon10+(1894-1895)	ttggcttgtctactaataca CA/Δ tctgcttcaaaatgaacata	1819
ALDH10	18	3'flanking+31	gtatttgtcaacttttttttt T/Δ ctcattttaaaattcttagc	1820
ALDH10	19	3'flanking+106	gtgtgttgggggtggtggtt G/A gtagctatagtaaataggtt	1821

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ALDH10	20	3'flanking+1630	aaaagcacgtgggaaacaca A/G ttaatcatgtcttaccgtat	1822
ABCC7	1	5'flanking-834	gctaaaacactccaaagcct T/G ccttaaaaatgcgcactggg	1823
ABCC7	2	5'flanking-729	cctccttgcagatttttttt T/Δ ctctttcagtacgtgtccta	1824
ABCC7	3	exon1+125	tagcagggaccccagcgccc G/C agagaccatgcagaggtcgc	1825
ABCC7	4	intron1+6200	ctatgtgagacgttaagaag G/A tagaggtggcccaagaaggaa	1826
ABCC7	5	intron1+7538	agttctctttcttagcatgg C/A ctacagaggtgcaactacct	1827
ABCC7	6	intron1+13519	gaaacttaaatcttgagtca T/C acaattgtgtctacatactg	1828
ABCC7	7	intron1+14110	attacacagtatttttttt T/Δ aattttggggaaagtcgatt	1829
ABCC7	8	intron1+14293	gccaggcagattcctgactc C/Δ tataacccagagcttatcag	1830
ABCC7	9	intron1+14316	taacccagagcttatcagag C/G atttatgtccccaaagagaa	1831
ABCC7	10	intron1+14433	cagaataacaatgatggctc G/A gaaaaatatgggtatttctg	1832
ABCC7	11	intron1+14824	acgttttgacagttgcacaa G/C tttctttctttaagctttaa	1833
ABCC7	12	intron1+23401	aatatttttgaaaatcacta C/G ggtatcctgcatagtgattt	1834
ABCC7	13	intron3+879	gaaaaatttcagttcataca C/A ccccatgaaaaatacattta	1835
ABCC7	14	intron3+922	acttatcttaacaaagatga G/C tacacttaggcccagaatgt	1836
ABCC7	15	intron3+933	caaagatgagtacacttagg C/T ccagaatgttctctaatgct	1837
ABCC7	16	intron3+13704	tttttccaaataaaaaaaaa A/Δ tcaggtgatatctgtaaatg	1838
ABCC7	17	intron3+13758	tattaaagaacatgatgctt A/G aaacagattagggaaaacta	1839
ABCC7	18	intron4+240	ctctgttgtagtttttttttt T/Δ ctcctaatcatgttatcatt	1840
ABCC7	19	intron4+376	ttatgttcagcaagaagagt A/G taatatatgattgttaatga	1841
ABCC7	20	intron4+586	tgtccagacaagagaccaaa T/C tgccgaggcatcatttaggt	1842
ABCC7	21	intron4+1089	tttcaatctgaacattttac G/A taagtgaagactttgttaga	1843
ABCC7	22	intron4+1615	aaagttaggtggtattgtat C/T tgtcttcctttctcaatgtt	1844
ABCC7	23	intron4+1946	aatacaaacaaacttgagct T/C tgcctatacttttcaagaat	1845
ABCC7	24	intron6+783	tatctaagttttggagtcaa A/G tagcactttgtttgaatccc	1846
ABCC7	25	intron6+(1128-1131)	gattgattgattgattgatt GATT/Δ tacagagatcagagagctgg	1847
ABCC7	26	intron7+(731-732)	gtagcaatgagaccattttt (T) cttcagttgagctccatgtt	1848
ABCC7	26	intron7+(731-732)	gtagcaatgagaccattttt cttcagttgagctccatgtt	1849
ABCC7	27	intron7+1434	gaatgtttggttgtaacctg T/C ataatctggcatgaaattgt	1850
ABCC7	28	intron8+752	catgctctcttctcagtccc A/G ttccttcattatatcaccta	1851
ABCC7	29	intron8+1109	tatggccaagacttcagtat G/A cgtggacttaattcttcctt	1852
ABCC7	30	intron8+1312	atgaagacattcatttttttt T/Δ ctccgtccaatgttggatta	1853
ABCC7	31	intron9+(6521-6522)	gtgtgtgtgtgtgtgtgtgt (GT) ttttttaacagggatttggg	1854
ABCC7	31	intron9+(6521-6522)	gtgtgtgtgtgtgtgtgtgt ttttttaacagggatttggg	1855
ABCC7	32	intron10+2119	gaacactttatagtttttttt T/G ggacaaaagatctagctaaa	1856
ABCC7	33	intron11+3867	tttttcttcaagaaattaga A/Δ gaggggagaaattggtttaa	1857
ABCC7	34	intron11+11844	tgaatcaaaatcatctaaaa A/Δ gctttcagaaaccagacttt	1858
ABCC7	35	intron11+12144	atattaaacagagttacata T/C acttacaacttcatacatat	1859
ABCC7	36	intron11+20975	gtgtggatagtaaatgccag G/A gtaaatcacatagcatctaa	1860
ABCC7	37	intron11+27057	atggaagagaagttttagta G/A aggggaggaaggaggaggtg	1861
ABCC7	38	intron11+27131	gagagagacttttttttttt T/Δ aaggcgagagtttactacct	1862
ABCC7	39	intron13+152	gtattaactcaaatctgatc T/A gccctactgggccaggattc	1863
ABCC7	40	intron13+287	tttgcagtatcattgccttg T/C gatatatattacttaatta	1864
ABCC7	41	intron15+(85-86)	atacatatatatgcacacac AT/Δ aaatatgtatatatacacat	1865
ABCC7	42	intron15+106	taaatatgtatatatacaca T/A gtatacatgtataagtatgc	1866
ABCC7	43	intron15+3341	ggaagtataaatttgtaaat A/C actgagacccaaacttacaa	1867
ABCC7	44	intron15+5556	tgctattgactaatagtaat A/T attttagggcagctttatga	1868
ABCC7	45	intron15+5919	tggtagttctatgtggaaac C/A gtgaggaaataattttatat	1869
ABCC7	46	intron17+2479	caaaaaggtatggaagtcag A/C ggagaaggagacccctatgt	1870
ABCC7	47	intron18-81	aagtatgcaaaaaaaaaaaa A/Δ gaaataaatcactgacacac	1871
ABCC7	48	intron19+751	cattaataaaataacaaatc A/G tatctattcaaagaatggca	1872
ABCC7	49	intron19+820	tgacatttgtgatatgatta T/C tctaatttagtctttttcag	1873
ABCC7	50	intron21+1532	ttacctttaacttttttttt T/Δ agtttgatcagctctcttta	1874
ABCC7	51	intron21+1607	atgcttttggagttgggtct C/T ataaatgtatagaaatgttt	1875
ABCC7	52	intron21+11260	atgtggaacaatcatgacta T/C atgccttttactttctctat	1876
ABCC7	53	intron22+(130-131)	agaatcaatattaaacacac AT/Δ gttttattatatggagtcat	1877
ABCC7	54	intron23+1828	ctgtcctaaagtttaaaaag A/Δ aaaaaaaaaggaagaaggaa	1878
ABCC7	55	intron24+(7100-7112)	cctttacaaactcttagaca (T)12-14 agtttaacatgttacaaaac	1879
ABCC7	56	intron25+237	actcttccccctttgtcaaca C/T atgatgaagcttttaaatac	1880
ABCC7	57	exon27+115	gggtgaagctctttccccac C/T ggaactcaagcaagtgcaag	1881
ABCC7	58	exon27+334	ggatgaattaagttttttttt T/Δ aaaaaagaaacatttggtaa	1882
ABCC8	1	5'flanking-1099	aaaggggctgaaggggtctt T/C cttttgtgttcccctgactg	1883
ABCC8	2	5'flanking-(424-422)	caccccaccaccaccaccac CAC/Δ aaggtaacgttctgccccac	1884
ABCC8	3	intron1+1212	agcctgggcaacatagtgag A/G ccccccccgcccttttctaca	1885
ABCC8	4	intron2+1003	aggaggactgtgaatcccag C/A ctgcatgtttgggtcggatt	1886
ABCC8	5	intron2+1253	catctcactaaggaagaatc C/T agtaaccagcaaggatgaga	1887
ABCC8	6	intron2+1382	cccagactgcactcctgcag T/C gctgcctggctcctgtagtt	1888
ABCC8	7	intron2+2371	tttcagagctgtctggaaat T/A taggggcaggtgggagggg	1889
ABCC8	8	intron3+1957	ccctacccctagcccagggg C/T ccccacatgagtatgaatgg	1890
ABCC8	9	intron3+(2088-2089)	agagaacccttcattaacca (CCA) gggcgtggctgaccagtgtc	1891
ABCC8	9	intron3+(2088-2089)	agagaacccttcattaacca gggcgtggctgaccagtgtc	1892
ABCC8	10	intron3+2204	taaagcacaagttatcaccc G/A tggatggatttgtccttttc	1893
ABCC8	11	intron3+2286	ttatctccccttgaaaggac A/G ctccacagagccagaaattc	1894
ABCC8	12	intron3+2312	cagagccagaaattctagaa C/G agggaaaagtggaggggagg	1895
ABCC8	13	intron3+2356	ctgtgaactgcagggacaga A/G ggaaatgggtattgggagaa	1896
ABCC8	14	intron3+2359	tgaactgcagggacagaagg A/C aatgggtattgggagaatgg	1897
ABCC8	15	intron3+2370	gacagaaggaaatgggtatt G/A ggagaatggccagccctcca	1898
ABCC8	16	intron3+2382	tgggtattgggagaatggcc A/G gccctccaaggggctgatgt	1899
ABCC8	17	intron3+4910	ggggacagccttcagctgtg G/A aattcctccagtcctagaga	1900
ABCC8	18	intron3+4969	cattattccagtcctgaggc A/G tgagagcagaaggccgatgc	1901
ABCC8	19	intron3+5003	ccgatgcttctgccctccat C/G ctaatgtcctcctgcaggga	1902
ABCC8	20	intron3+5019	ccatcctaatgtcctcctgc A/C gggacccaaggtggatggca	1903
ABCC8	21	intron4+14	ggtgagggtaagcaggccac C/T tgggccagggtggggtggga	1904
ABCC8	22	intron4+187	agacactgcatctggcccac G/A tgtgctctaccccagggtcc	1905
ABCC8	23	intron4+204	cacgtgtgctctaccccagg G/C tcccagagggagaggggggt	1906
ABCC8	24	intron4+254	gttcgctgaggttggcggat G/A actttccgtagaaagggaag	1907
ABCC8	25	intron4+357	tgtattcatatcgtcacgct G/C gtaaatgaatgagtaagtgt	1908

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ABCC8	26	intron5+92	ggcattaggtcaaaatcctg G/A tgggacaaaaggggaaactg	1909
ABCC8	27	intron6+4205	tctgtagaaagtacatgggg G/A catgaagatcattggcttga	1910
ABCC8	28	intron6+5519	gattcccagggaatgttaaa A/C aggaccgggtcttcctaaac	1911
ABCC8	29	intron6+5575	tctgacccagtaccagccag G/C ggggcaagtttccatccccc	1912
ABCC8	30	intron6+6587	gttgccatctgagatcttgc C/T ggaagtacacaagagaccct	1913
ABCC8	31	intron6+6747	ttccactggccttttctgct C/T agtaattgctacattacagg	1914
ABCC8	32	intron9+191	gaggaagctgcctcccggtg A/G ggacaggaagcgggcatggc	1915
ABCC8	33	intron10+1963	cccaggagtccaacctccct T/G tgtccagctagaccatggtg	1916
ABCC8	34	intron10+2724	cctgggacatgttttcttat A/G taaacagcatcaaaagatgt	1917
ABCC8	35	intron10+2938	gcccgcccaggactcctcac G/C tgtccaagtcacctagggag	1918
ABCC8	36	intron10+3094	tccgaggatgtgtttttttt T/Δ ccctccgttagtcagcagtg	1919
ABCC8	37	intron10+3368	tcctgctcatatgcggcacc A/G tcagacttctgggcaggcaa	1920
ABCC8	38	intron10+8897	ggtattgattaaaagcctca C/T gggcagagaaattcgccatc	1921
ABCC8	39	intron11+308	tgtgtattgtagaagtgatg G/A gaaatccagaacagaaagct	1922
ABCC8	40	intron11+1171	gccctctcatttcccttcca G/A tgctgagcgtttccagtgtg	1923
ABCC8	41	exon12+7	gcctctgtccacagactttc G/A tgggccacgtcagcttcttc	1924
ABCC8	42	intron12+356	accaagaatgaggccatccc G/T tccccacgtggctgccccat	1925
ABCC8	43	intron12+934	tgggttcaaagatggaatgg G/T gcataactcagcaaaattat	1926
ABCC8	44	intron12+1370	gggagggaggctggacaggg C/G atgaaggcagagcctggtgg	1927
ABCC8	45	intron15+412	ggaggtgggacccaggatgg C/T gtttcttgggaccacaagga	1928
ABCC8	46	intron15+688	actccccccggccccactcac A/G tctgccaccttccctccctg	1929
ABCC8	47	intron16+4464	actcattccaagtattgatc G/A agaagagaggtaggtactgg	1930
ABCC8	48	intron16+4574	ttgaagatcttaagttgttt T/C tggttcactcatttcgcaaa	1931
ABCC8	49	intron16+5011	agctaaaagcaaaacagcct C/T tgacctggcaagcattccca	1932
ABCC8	50	intron16+7608	tgtcctacttttctttttgac C/G cttataacttcctgacttcg	1933
ABCC8	51	intron16+7730	ccagctcctagtgggctgga G/A ggaaggacatgcggttgggg	1934
ABCC8	52	intron16+8369	ttgcaaactgagttagggcc T/C ggagagcttactgtgtgctg	1935
ABCC8	53	intron16+9708	tgcacttgccgcctacttat T/G ccagacccaatgattgggtc	1936
ABCC8	54	intron17+651	tatagattaatgaggctctg A/G gtccctcaaaaccttccctc	1937
ABCC8	55	intron17+692	cccttacctctccaaaaaac A/G cttgagataccctagaggtg	1938
ABCC8	56	intron17+1541	ctcaggatcttcctggagga C/T atggttcactcccatgagag	1939
ABCC8	57	intron18+580	actaagcagatttctaccaa C/T tgcacctccccatccccttg	1940
ABCC8	58	intron18+658	gaacaagcccctgagaatgc C/T ttccgcaccccctactcccg	1941
ABCC8	59	intron18+660	acaagcccctgagaatgcct T/C ccgcaccccctactcccgcc	1942
ABCC8	60	intron19+93	gcccttccatcgatcaccca T/C acccagccatctcactcccc	1943
ABCC8	61	intron19+123	tctcactccccaggtgctta T/C ctgcactccagcctctccat	1944
ABCC8	62	intron19+219	cataggggagagggcaggaa C/T ggagggaagggagagagccc	1945
ABCC8	63	intron19+845	tagtatttaacctgcccaaa C/T gctgtgtgaagtgctgacct	1946
ABCC8	64	intron20+338	tcccctccacaagcttagac A/G aacaggattctcctgtgact	1947
ABCC8	65	exon21+10	tttggtgacagggcatcaac C/T tgtctggtggtcaacgccag	1948
ABCC8	66	intron21+192	caaggatagcacaaatgacc C/Δ attgcagacttcagatggag	1949
ABCC8	67	intron23+17	gaaggtgggtatatccaggg A/G tggccaagcagccacccctg	1950
ABCC8	68	intron23+67	gttctgctagaacctgaact C/T ataaaggtcttcctgtcctt	1951
ABCC8	69	intron26+268	gtgagcgtctgcacatccaa G/C taaagattgttttctcctcc	1952
ABCC8	70	intron26+308	cgataagtgggtgtaatttg C/T ccatccccacccatgagttc	1953
ABCC8	71	intron26+348	cagctccctgccctcccctc A/G ctctctctccctcagccagc	1954
ABCC8	72	intron26+807	gacagctgctgagtcaggcc G/A agccggcagctgagaaaggc	1955
ABCC8	73	intron26+834	cagctgagaaaggcggcagt G/C gtcagatgggcttgagaaac	1956
ABCC8	74	intron28+(118-121)	cctccaaaaaataaaaacaa AAAA/Δ cagaaatgaaggaaatagaa	1957
ABCC8	75	intron28+1348	tggggtaagcggaagacggg G/A ttgaacgctttgagtttggt	1958
ABCC8	76	intron29+1253	ctcttagggatcttgtctaa G/T taaagaagagcagagcaaag	1959
ABCC8	77	intron29+1589	cagatcccagcttcctgtaa A/G cagcctcagatcaggccaaa	1960
ABCC8	78	intron29+2322	gcgcctcacactcctataac G/A cgcacatgccctgatgcaca	1961
ABCC8	79	intron29+2348	atgccctgatgcacacacat T/C ttcaacacgcacttactcta	1962
ABCC8	80	intron29+2418	agacacgtcaccctcccaca C/T gtctccaccctgggggtgtg	1963
ABCC8	81	intron29+2494	tcagtcccctcagacacatg C/A cctctctccacgcagagaca	1964
ABCC8	82	intron29+2735	gcggccaaggagagtgatga C/T ggcagcccaggttgatcaga	1965
ABCC8	83	intron30+386	gctcctggggctccagcctt C/T gcagcccttgtgtgtgtctg	1966
ABCC8	84	intron33+93	ggcttcgcagtcacctcgtg G/T ccctccagggccgaggcctc	1967
ABCC8	85	intron33+358	agggacctgggggcagacag C/T gaggccacccttgtattgag	1968
ABCC8	86	intron38+54	cccagggacaggactggcct G/C ttgtggccgtcatcagtgca	1969
ABCC8	87	intron38+466	aggacattctggccacatgc C/Δ tcatcctcctcctccaagcc	1970
ABCC8	88	intron38+529	tggccccccaccgcgggtggt A/G ttcccaccatcctgacccgc	1971
ABCC9	1	intron3+38	tgttgtttctccttaaagag C/A tatttgtttttccccccaaa	1972
ABCC9	2	intron3+305	gctggccttctggcttgcag T/A agttgtattttaagaatcag	1973
ABCC9	3	intron3+320	tgcagaagttgtattttaag A/G atcagagctcttgtgaggag	1974
ABCC9	4	intron3+631	ttctgtggaaatcagaggct G/C tctaaaatattcctaatttt	1975
ABCC9	5	intron3+8644	tggacgcactcaacattttc A/G agttattactccttcaactc	1976
ABCC9	6	intron4+757	aggatatcatgaaacactga A/C tcttagtaaaaactatcttt	1977
ABCC9	7	intron4+1022	tactgtggaatttttcttgc A/C acagagatatgtatttttca	1978
ABCC9	8	intron5-1217	cagtggtagatgtgttttct A/G ttgccatcatctacaaatat	1979
ABCC9	9	intron6+(106-107)	tatgagttgttcaaataggc (T)7-9 cagagaattgaatgctttct	1980
ABCC9	10	intron6+1347	tcagtcgtattcctactaaa A/Δ caaaattttgtaagttatgt	1981
ABCC9	11	intron6+1618	ctttttatttgctgcttacc G/A ttttactaaggttggatata	1982
ABCC9	12	intron6+1835	cttttaataaatgcaaactg C/T acacctggtctataaaaaga	1983
ABCC9	13	intron7+407	cctatagaatttttctttttc T/G tttttctcaaaaaaattaaa	1984
ABCC9	14	intron7+423	tttctttttttctcaaaaaaa C/T taaatgtttgttatttattt	1985
ABCC9	15	intron8+743	ttctgtagatgaagcttaag A/T gctagatcttatttgaaaaa	1986
ABCC9	16	intron8+850	tttttaacttattgtttgcc T/G tttcatttttttaatagaaaa	1987
ABCC9	17	intron9+585	cgaatttgctgcttttagag A/T aatctttgcaaataataaaa	1988
ABCC9	18	intron9+1394	atttttcttcttgtaagtat G/C agtgatagagctgactgcag	1989
ABCC9	19	intron12+1167	atttgtaagacttttaaaat G/A agataattgtgctggtgtct	1990
ABCC9	20	intron12+1195	tgtgctggtgtctatatctt A/G ctgagaaaactagaatttat	1991
ABCC9	21	intron12+2123	ataagtgctctcccagtgtt G/A attggacttagagcattttc	1992
ABCC9	22	intron12+(2653-2656)	caaaacagaataatgaaaag TAAC/Δ tattatctaaaataataaaa	1993
ABCC9	23	intron13+(3043-3044)	aacatactctcctcctctct (CTCTTT) aagtcaaaatatattagtat	1994
ABCC9	23	intron13+(3043-3044)	aacatactctcctcctctct (CT) aagtcaaaatatattagtat	1995

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ABCC9	23	intron13+(3043-3044)	aacatactctcctcctctct aagtcaaaatatattagtat	1996
ABCC9	24	intron14+85	ttctgtgaaagtgtcccaaa T/A tgtgcctttaaattgttttt	1997
ABCC9	25	intron14+275	agtgtcacatgtatttttttc T/C ggtattcctatgtttatcaa	1998
ABCC9	26	intron14+453	ctcatttcaaacttggctat T/C tggactctccccaggcattg	1999
ABCC9	27	intron14+3709	atcccctagtgatgtacact G/A agcttgcctccatctttcct	2000
ABCC9	28	intron14+3813	ctgatttatatattagctga C/T tttccaagttcagacatcta	2001
ABCC9	29	intron14+4000	ttcttttacttcaatgtagc A/Δ ccaaatcagaaggtgacatt	2002
ABCC9	30	intron16+1466	atcccactggatttaattac A/C ttgtgtagcttgtacaacca	2003
ABCC9	31	intron16+5357	attttggaagagaaattata T/G aaccttccacaactgaattt	2004
ABCC9	32	intron17+1368	aatcctggtgtttttttttt T/Δ ctttttcatttttcagtagg	2005
ABCC9	33	intron20+98	aagtaactcaaggaaagatg G/A tttaacttgtgaaatcgtaa	2006
ABCC9	34	intron22+28	ctcatagttcagaagagttc A/C gagcccaattcagaagagtt	2007
ABCC9	35	intron22+194	tgaacctataaaattctaat G/Δ ccatctttggatgaggtgca	2008
ABCC9	36	intron22+1370	ccagggacaaaagaagatga C/T gtaaacttaaggattgggac	2009
ABCC9	37	intron22+1487	agcaagccaggaagaaagtc C/G attaagttgtatttagaaat	2010
ABCC9	38	intron23+(455-462)	atagccatgaaggataagaa AATTAGAA/Δ tgccatttgt tatgtttcag	2011
ABCC9	39	intron24+(460-465)	aactctttctcttcatctgc TTTAAAA/TTTTAA gcaagccttg aaggagagtg	2012
ABCC9	40	intron24+595	gcatgcaaaataatgaagaa A/G acaatcttgtctgacattga	2013
ABCC9	41	intron28-926	aaatatttcagaatttgggg G/A tgtagagcatttgccgtcat	2014
ABCC9	42	intron29+2692	cttgtaagtctttttttttt T/Δ aaagtaatgaaaatttctaa	2015
ABCC9	43	intron29+5464	agacaacactgctttttgt G/A tgttcacaattcaacgacag	2016
ABCC9	44	intron29-1830	aactggctgaaaggaaaaaa A/T tcatattgctgtaaatattt	2017
ABCC9	45	intron31+102	tgcttttgctttccacttca G/A tatccagaaaactctctcat	2018
ABCC9	46	intron33+877	aacatggaactatagtaaat A/G tagtttttttggggttcaga	2019
ABCC9	47	intron36+1281	aatttacactttttttttt T/Δ gcaggagaatattttgcaaa	2020
ABCC9	48	3'flanking+197	aatggagctcatgcatgtgt T/G ttcaaatatatacatgcaaa	2021
CES1	1	5'flanking-983	tatttccttagccagcggta T/C cacagtgtgtttagtgaatt	2022
CES1	2	5'flanking-814	tcacattgccttgacatcac A/C cctactgctcctccacccta	2023
CES1	3	5'flanking-248	agtcctgcaagggtgacacc G/Δ ttatgccacaagcagttggg	2024
CES1	4	intron1+22	tgagtccttctgaagtcaaa T/Δ atgcggggcacttttgaaa	2025
CES1	5	intron1+30	tctgaagtcaaatatgcggg G/T cacttttgaaatccttgtt	2026
CES1	6	intron1+1662	aagggaatccctgagctgag C/A atgaccagcccagtggtttc	2027
CES1	7	intron1+1726	cctccctgaagtcctcagca A/C tcttagctggttcctcgccc	2028
CES1	8	intron1+2716	tgcttccaaggaagttcatc T/G cagtattatttgtaattagc	2029
CES1	9	intron1+(2747-2749)	tgtaattagcaacaacaaca AAA/Δ gaaaagaagctaaatattga	2030
CES1	10	intron1+3288	ttatttgtccattaaagaaa A/Δ ctcaagcgcttagcctggca	2031
CES1	11	intron1+3691	gagaatatgggacacccctt T/G ttcatcctctcatccagcat	2032
CES1	12	intron1+3819	tccttcttgcatttatttttt A/G gctggatgtttttatgcctc	2033
CES1	13	intron1+3880	aaccagctcaatgggttagg G/A aggacattgatcgtcatccc	2034
CES1	14	intron2+74	gagtcaaggcagtcccctga T/C gggctgatcctttgctctgg	2035
CES1	15	intron2+552	atggaaggtgtgtccattca C/A cctggccaagctgggaagaa	2036
CES1	16	intron2+885	cagtattttagatggtaaag T/C attatgatgtaatatattgt	2037
CES1	17	intron2+2001	ttggcatgtcagggctgcaa G/A actcatgtagaaatcactcc	2038
CES1	18	intron3+2119	cgctgagtgcatgaatagtc T/C aggcttgagggtgatgggag	2039
CES1	19	intron4+127	taaggcatccaagcccctc G/A taattggacactacctaccc	2040
CES1	20	intron4+347	tctgtcatgacacttagcag T/G cagcccagcaggtgaaggtt	2041
CES1	21	intron4+(1984-1985)	tgtggtcctgaaggtcctgc (C) tgacatctctgctccccacc	2042
CES1	21	intron4+(1984-1985)	tgtggtcctgaaggtcctgc tgacatctctgctccccacc	2043
CES1	22	intron5+766	gaggtgggcagagggtcagc T/C cactactggattcctcagtc	2044
CES1	23	intron5+825	ggagtagatctagcctggaa T/G agcgagtgagtcactgaccc	2045
CES1	24	intron5+828	gtagatctagcctggaatag C/T gagtgagtcactgaccccac	2046
CES1	25	intron5+868	ctcctgagcatgaactctcc T/A cccctccactctgctgtcag	2047
CES1	26	intron7+68	acttcttcatttcagctgtc C/G tcttgcccagggacagtttc	2048
CES1	27	intron7+681	cctccaaaatcaacaatcca A/G ttatcgcctgtctgctagtt	2049
CES1	28	intron7+885	aggaactatccaaagagaaa T/C acattcatatacttcgcagg	2050
CES1	29	intron7+2151	gtcgtgtaaactgaaaatct C/G aggagttgatggcttcaggc	2051
CES1	30	intron7+2470	atatagatatacgaattcac G/A gagtgatgcgggaagaacct	2052
CES1	31	intron8+128	cgtgtttgtttctgaggccc A/C gagaggggtagtgactcacc	2053
CES1	32	intron8+2618	cctgatggcaacacatgagt T/C gggctctctctaatctgtga	2054
CES1	33	intron8+2665	aaaaattattcatcaaaggt G/A aaacctaaaattaagacatg	2055
CES1	34	intron8+3785	ccatggcgcatggccatgcc G/A gtctatggtactggtctcac	2056
CES1	35	intron8+3791	cgcatggccatgccggtcta T/C ggtactggtctcaccctcag	2057
CES1	36	intron10+222	gtgggctggagaagctgcat C/T gctcacccggggctggtggt	2058
CES1	37	intron10+230	gagaagctgcatcgctcacc A/C ggggctggtggtcacttttt	2059
CES1	38	intron11+1177	ctagcaggtgccctgacaca C/G ctttgcacaggaaggggcag	2060
CES1	39	intron11+1311	gccctatgctctgcgtctga A/G ctatatatagagttcccatc	2061
CES1	40	intron11+2025	ttctcatttgggatgctaag A/G ttaaaaattagcataacact	2062
CES1	41	intron11+2029	catttgggatgctaagatta A/C aaattagcataacacttcca	2063
CES1	42	intron11+2317	cattcacaaaagctctttct T/C ctatggttggctctgagttt	2064
CES1	43	intron11+3887	caaatatttggctctaattc C/T gcttccacctcagacagcta	2065
CES1	44	intron12+2311	gcgcctctgggcatctcact G/A tgcatgcttaggcgccttgc	2066
CES1	45	intron12+2331	gtgcatgcttaggcgccttg C/G ggctctgttgtttttcagaa	2067
CES1	46	3'flanking+71	aacggtgatgaaagaggcga T/C gtgagaaggaaggtggcttt	2068
CES1	47	3'flanking+362	ttgcatggcacttactgacc G/A ttgcacaggcctgcaacacc	2069
CES1	48	3'flanking+581	atttctggattctgttagta C/T gtagaaagctctaaagcatg	2070
CES1	49	3'flanking+1348	aaatctgctgctgggagaga G/C agcaaagcatgcagatcaac	2071
ABCB4	33	intron22+767	acagtgggctgatgcataga A/Δ cctgtagcaatccaccagca	2072
AADA	23	intron2+46	tgtcactgaggtagttcgca A/G acattttactaagtcttcag	2073
AADA	24	3'flanking+208	aatgctaaaaaaaaaaaaaa A/Δ tcactgtggtactttgggga	2074
ABCA4	1	5'flanking - 1005	tgccatcataagcagaaact A/C tctctctcttcttggaagct	2075
ABCA4	2	5'flanking - 819	gtctagagtctttcaaagag A/T acacattctgagatttgagg	2076
ABCA4	3	5'flanking - 680	agcaccaccccattgcaggg C/A tggaatgacagtaatgggcc	2077
ABCA4	4	intron1 + 208	tgcccttcccaggaagatgt G/A tttctctgtcctcagccaca	2078
ABCA4	5	intron1 + 234	ctgtcctcagccacatgaaa A/G tcttttgcctaccgtgcctg	2079
ABCA4	6	intron1 + 510	agctcacgatcaagtcacag T/C ttaactggacacattatttt	2080

Designation of Gene	No.	Location	Sequence	SEQ ID NO
ABCA4	7	intron1 + 1527	gcttaacaaccagcataaaa G/A agagcagcatgggacacgct	2081
ABCA4	8	intron1 + 2077	caggactgtagctgctggcc T/C aaaatgagcccattcctgtg	2082
ABCA4	9	intron1 + 2174	ccctctcaatctggcctttc G/C ctggcatgggtgggcgactc	2083
ABCA4	10	intron1 + 2246	gctcccagggagatggagcc A/G ctcgggctgagggccttggc	2084
ABCA4	11	intron1 + 2364	ttctgtctggcacgcctccc G/A atggctccccacctgctacc	2085
ABCA4	12	intron1 + 4243	ctccctggggtatgcctgta C/G gcagttaagcgtcaaggaca	2086
ABCA4	13	intron1 + 4287	atgccgctctggggagggga A/C gctgagcatgattttggaag	2087
ABCA4	14	intron1 + 4309	ctgagcatgattttggaagc C/T ggcagaagaggctattgtga	2088
ABCA4	15	intron1 + 4416	tgcagcaaccgcccccgccc C/T ccgccaaaaacaaacacact	2089
ABCA4	16	intron1 + 4996	tttacccctggaacaggcag G/A ccaagctggctggtcccctc	2090
ABCA4	17	intron1 + 5007	aacaggcaggccaagctggc T/C ggtcccctcccctgatacaca	2091
ABCA4	18	intron1 + 5080	gtgtgtggctggtttcttag C/G aagcaccatggttccaagtt	2092
ABCA4	19	intron1 + 5152	gggagatgaacgtaagtgga G/A ggcaggcctacaaggttgca	2093
ABCA4	20	intron1 + 7110	ccactggatctgcttttgga A/G tcaagagtccttaagctcca	2094
ABCA4	21	intron1 + 7290	gatttttgttggctttgcaa T/A ggatcacagtcatttattca	2095
ABCA4	22	intron1 + 7483	tctgagcctctttccttaac T/C gcagagtgagtggctacaga	2096
ABCA4	23	intron1 + 7497	cttaactgcagagtgagtgg C/T tacagagaaatctttactac	2097
ABCA4	24	intron2 + 1067	tcaagcagcagcagcaactg C/A gtggagtcttcttgaactaa	2098
ABCA4	25	intron2 + 1106	aacactcctatgcccctctc G/A gcacaaaatgacgtgtcccc	2099
ABCA4	26	intron2 + 1119	ccctctcggcacaaaatgac G/A tgtccccccttgcttcccct	2100
ABCA4	27	intron2 + 1243	cacccagcacagggactggc A/T cacatgagatgctcctgctt	2101
ABCA4	28	intron3 + 26	tgttgagatccctaccatgc A/G ggggaggaagttgcacaccc	2102
ABCA4	29	intron3 + 101	agcatggagcactgagtgtt C/T ttgtggctttgctgagcccc	2103
ABCA4	30	intron3 + 330	tgcttgggtggagtgaatca T/C tgtaggagaaaaactcagtt	2104
ABCA4	31	intron3 + 470	tgaagtcaggtttacaaagt C/G aagtttacttcttgggagaa	2105
ABCA4	32	intron3 + 634	tgaaaaccaatgacccctct T/C ccaagaaaaatggccacata	2106
ABCA4	33	intron3 + 1016	ccttgggggagctcagtatg A/G ttcttccaggagaagcctgc	2107
ABCA4	34	intron3 + 1554	gaaagttgggtttcatgttt T/C gcactcacattatgagtgaa	2108
ABCA4	35	intron3 + 1686	ctagacattctcacagagcc A/G agggcagcaaggcggggctc	2109
ABCA4	36	intron3 + 1823	ttcacctctctccatggacc A/G gtctcccctgctcctcaatg	2110
ABCA4	37	intron3 + 1938	caaattcctgggaacaaatc G/A ggttgacccagctttattct	2111
ABCA4	38	intron3 + 1951	acaaatcgggttgacccagc T/G ttattctccctgtcccatca	2112
ABCA4	39	intron3 + 2063	ggctgtcagagcctacctgc G/T tgaatgggtggaagggcagg	2113
ABCA4	40	intron3 + 2079	ctgcgtgaatgggtggaagg G/A caggtctcagagaattgggt	2114
ABCA4	41	intron3 + 2186	agacacacagagcatgggac C/T gagaggcgagcagaccctgc	2115
ABCA4	42	intron3 + 2214	gagcagaccctgccaaaact G/A ggagactgaatagatcgctc	2116
ABCA4	43	intron4 + 2717	cgtgcttctgcacagccacc T/C gggaaggtatgccgatggtt	2117
ABCA4	44	intron4 + 2802	attctcagcagggaggatta A/G tggtaaaagcccaggaatgg	2118
ABCA4	45	intron4 + 3182	cccccagagccacagcagcc C/G tgtctcctgggtggtcttgt	2119
ABCA4	46	intron4 + 3515	agtataataaaagcaggagc C/T atagcccccaactctcaaga	2120
ABCA4	47	intron4 + 3907	aggggagtgacagtgggcac C/A actctcagggaacccattac	2121
ABCA4	48	intron4 + 3923	gcaccactctcagggaaccc A/G ttactgtgagagaagccact	2122
ABCA4	49	intron4 + 3952	agagaagccactgtgccact G/C tgtggtcgaacttcaagacc	2123
ABCA4	50	intron4 + 4125	ggctgtccagcacacagggg C/A aggcctcttggccactgggg	2124
ABCA4	51	intron4 + 4637	aatcacttgccccaaggtca C/T cttaactgttaggtgttctt	2125
ABCA4	52	intron4 + 5319	acctctaggggctcccagag A/G ccccaagaacagaaccttcc	2126
ABCA4	53	intron6 + 2266	caccccttgcagacctcagac G/A ggtcctgggggcttgctttc	2127
ABCA4	54	intron6 + 2857	ccagaggagaaagctctgcc G/A tagtcggcctcagttaacca	2128
ABCA4	55	intron6 + 2861	aggagaaagctctgccgtag T/C cggcctcagttaaccacgga	2129
ABCA4	56	intron6 + 3078	gcaggcattaaaatgggact T/G tgcctttattgctcctgggc	2130
ABCA4	57	intron6 + 3375	ttaaatgccaaatgagttct C/G attaacaaagaaagagggaa	2131
ABCA4	58	intron6 + 3412	ggaaaatctcagtaaaccac C/T gtgacggcatctacccactt	2132
ABCA4	59	intron6 + 4635	ctttcgggtggatattgcta C/T gtcaagtgtctgggaaagcc	2133
ABCA4	60	intron6 + 5576	ccactaatatgcattcttta G/C taagcggtctcaatatacac	2134
ABCA4	61	intron6 + 5925	aaaaagcattttgctcttat A/G aaagcacagcctcttttgag	2135
ABCA4	62	intron6 + 6916	cccagacaacccaagcagag A/G cctcttagggccggaatcat	2136
ABCA4	63	intron6 + 6993	agcacaggatcaaggcctaa A/G ggccccttagactgacctca	2137
ABCA4	64	intron6 + 7242	ttgccattttgatctgtgac T/C ttttttttccagaaatagttt	2138
ABCA4	65	intron6 + 7454	atggagggctccctcgggac T/C aggcagtattcagagatgta	2139
ABCA4	66	intron6 - 264	aaacagcaattagaatcact T/C tgaaatagtgatagtattta	2140
ABCA4	67	intron6 - 86	aggaggggggagttttcaa A/G catataggagatcagactgt	2141
ABCA4	68	intron6 - 32	tatacctacaaacatatata T/C atttaaaaaattgttttact	2142
ABCA4	69	intron7 + 828	gatgtgggaaagttagagaa G/C agcccattgtactaatgctc	2143
ABCA4	70	intron7 + 1019	aggcttcttgactgtctaga T/C agcaagtctaatcatttgtg	2144
ABCA4	71	intron8 + 374	gtaaacacggctgtgggatg C/T ttttacaaacacaatatcgt	2145
ABCA4	72	intron8 + 874	tgatgagcttgttattggtg G/A ggtacagcctattaatttag	2146
ABCA4	73	intron9 + 605	tcgtgtctctgtcttgatct C/T tgtctggttttaggccaact	2147
ABCA4	74	exon10 + 1268	aacttttgaagaactggaac G/A cgttaggaagttggtcaaag	2148
ABCA4	75	exon10 + 1269	acttttgaagaactggaacg C/T gttaggaagttggtcaaagc	2149
ABCA4	76	intron11 + 5236	ggcctggcacagatgaaata C/T tattcagagttcacagtgta	2150
ABCA4	77	intron11 + 5270	cagtgtattttcatttcata A/G tatatttgattttcaggtct	2151
ABCA4	78	intron11 + 5687	atcatgtaatgtactttaga C/G tcagatatataaaatatttgt	2152
ABCA4	79	intron11 + 7136	gacttcccaacttaccttag T/C ggagctgtagtcacatagaa	2153
ABCA4	80	intron11 + 7180	acgctcataaatgcttctct G/A ggctgtaaaggttgaatttt	2154
ABCA4	81	intron11 + 7701	gttagacgcaggcattacct C/T gtggctttgccccagtgtga	2155
ABCA4	82	intron11 + 8073	gggatgtttgcccacatcca T/C tggcatttctcaaaaggaac	2156
ABCA4	83	intron11 + 8586	cagctgcctgcgctggagag G/A gctcaaacctcttccgccag	2157
ABCA4	84	intron11 + 8893	agcaaagatgccctttgact C/T cttttcccactagtggtgct	2158
ABCA4	85	intron11 + 9257	gaatgaggtcacttgctgca T/A ggcaggtggcttccccatga	2159
ABCA4	86	intron11 + 11234	cccaaataattttgtttttc G/A ttttaggaattaaatttcag	2160
ABCA4	87	intron11 + 11641	aagaaacaaacatttattga C/G aacttttggtgtgtgacctg	2161
ABCA4	88	intron11 + 11808	tggtatttcttaaagaaata C/T caattccatttccttttaac	2162
ABCA4	89	intron11 + 11923	aagatcattattaatatctc A/G tcagcgtggtgtcacttaag	2163
ABCA4	90	intron11 + 12055	tgagaacattacatgggacc T/C gcccccagggcatggaggct	2164
ABCA4	91	intron12 + 305	tcaccctgtggtcgggaggt G/A tgagtgagctatccaagccc	2165
ABCA4	92	intron13 + 1461	ttgggtttcagtgtcagcat G/A tagctgtctactcagatccc	2166
ABCA4	93	intron14 + 1237	aagggcaccaaagttctaag A/G gatgaggggaggagctgagc	2167

Designation of Gene	No.	Location	Sequence	SEQ ID NO
ABCA4	94	intron14 + 1268	ggagctgagccccttgtcct T/C atctaggtttcccttgttct	2168
ABCA4	95	intron14 + 1309	ttcccatccctcagtctgct T/C cttttcccagtaccaacatg	2169
ABCA4	96	intron14 + 2979	tcacctgtgtgggtagcaaa C/T ctcagaaaatcaagtataga	2170
ABCA4	97	intron17 + 23	gagtcctttaaaacacaaat C/G ttaatgtttgaaatcaactc	2171
ABCA4	98	intron17 + 204	tgctgggccctgtgtgatca T/G gaatggctgatcatggatga	2172
ABCA4	99	intron17 + 715	gggactcccctagagctgaa G/A tactctcccatctgtttgtt	2173
ABCA4	100	intron18 + 1282	ggaagatgaagaacctaagc C/T gcttccagaaattcatgagg	2174
ABCA4	101	intron18 + 1531	gtctacccccttaggaccatt G/A taagagtacattgaggtaat	2175
ABCA4	102	intron19 + 1802	actgctcacccaggaggcaa C/A gcctcgagtcatgcaccgaa	2176
ABCA4	103	intron20 - 195	acagattattccattgtatg C/A atgaactatgtaagccatcc	2177
ABCA4	104	intron23 + 755	ctggctgccgctggggtttc C/T tatgtccatccacggggagg	2178
ABCA4	105	intron26 + 497	ctgagttaggtctagatggg G/A acactttggatgaatgagga	2179
ABCA4	106	intron26 + 702	tatcaaatacaactcagacg T/G cagtctcctggccccttga	2180
ABCA4	107	intron27 + 156	cctgctttccaaacccttat C/T ttgattcttggtaacatgaa	2181
ABCA4	108	intron27 + 385	tttaaagaacagtgagtcac G/A tgacttgctctttgaaatgc	2182
ABCA4	109	intron28 + 299	gacatgccatcagaccactg C/T gagtgttcaggcagcctacc	2183
ABCA4	110	intron29 + 168	ctccttccacacttgtgtgc A/G gggacattcactacctccta	2184
ABCA4	111	intron29 + 497	gctgtcaataaggaccaaaa C/T agactaatttcaaattcctc	2185
ABCA4	112	intron29 + 567	agctgctaggaataaaaagg G/A agacaaaacgatccacaagc	2186
ABCA4	113	intron29 + 577	aataaaaagggagacaaaac G/A atccacaagctagagatggt	2187
ABCA4	114	intron30 - 2494	aatcacagctcatctgctgc A/G tcatagggatcccaaaagaa	2188
ABCA4	115	intron30 - 2169	aatgtaacagccaaagtcct A/G gaaaaaggcaagccagttcc	2189
ABCA4	116	intron31 + 535	ctaactgtgaattatcatct T/G tgatcactgccctttgagat	2190
ABCA4	117	intron31 + 957	gagttctcagcagcaaatct C/A cagtatgaaattttggattt	2191
ABCA4	118	intron32 + 445	tccagaggtttagaacctca C/T caagtgggactctaggagcc	2192
ABCA4	119	intron33 + 48	aggatttttgacttgcttaa C/T taccatgaatgagaaactct	2193
ABCA4	120	intron35 + 129	tgtttagtcaggcacatatg A/C acatccgactttcaaataag	2194
ABCA4	121	intron35 + 209	tctccccaacatttatgtgg C/A aagtaagtttacatttggtt	2195
ABCA4	122	intron36 + 3209	ttgaggcctccacaccccac G/A gcaggttgccccctgaggaa	2196
ABCA4	123	intron36 + 3542	cttggcagggaggtagggca T/C ggggtggggtaggaggacta	2197
ABCA4	124	intron37 + 304	ctgggggcagccattcccca A/G cccctcacccagctctgact	2198
ABCA4	125	intron37 + 525	taaatttgaatgagtaattc A/G tccatctcggcctcagtttc	2199
ABCA4	126	intron37 + 766	tgttgcaggctggagaaccc T/G cctatgaattgtacagggct	2200
ABCA4	127	intron37 + 856	aaaaccccatgaagtggtca A/G ggcaggcatcattatctcca	2201
ABCA4	128	intron38 + 62	tagtagagtatgtgttggtc G/A agcagagccaggggcaagca	2202
ABCA4	129	intron38 + 761	tccttgggcaagttaatctt G/A atgaagagactgggtgttct	2203
ABCA4	130	intron38 + 1315	cagagtcagactctggaaag G/T cgggggataagaacacagc	2204
ABCA4	131	intron38 + 1316	agagtcagactctggaaagg C/A gggggataagaacacagcc	2205
ABCA4	132	intron38 + 1526	ccaacatttgctaagcaccc G/A ccttcaaaaacctggtattt	2206
ABCA4	133	intron38 + 1561	gtattttcatgtaaattatc C/A gatacacagctgctatggaa	2207
ABCA4	134	intron38 + 1562	tattttcatgtaaattatcc G/A atacacagctgctatggaaa	2208
ABCA4	135	intron38 + 1674	ccagctgaacaccacgtgcc G/A ggtgtgtgctgatataaaca	2209
ABCA4	136	intron38 + 2867	tgcctggctagacaaagggg A/C agctcccgcccactagaaac	2210
ABCA4	137	intron38 + 2874	ctagacaaaggggaagctcc C/T gcccactagaaacttgcagg	2211
ABCA4	138	intron39 + 123	gaggggaccttgttgggctg G/A aggtgtcctgccagctggag	2212
ABCA4	139	intron40 + 1904	gacactgtacagccagccca A/C tcctgacccctttcttcat	2213
ABCA4	140	exon41 + 5814	ggaaataaaactgacatctt A/G aggctacatgaactaaccaa	2214
ABCA4	141	intron41 + 122	atttggttcccagttttatg T/G agggtcatcatccctgtgtt	2215
ABCA4	142	intron41 + 287	tctgcagagcatgggtcagc C/T tcgagatgtctcagtactca	2216
ABCA4	143	intron41 + 411	cctcttcccctccttgctct C/A accctgtctcagttctcagt	2217
ABCA4	144	intron41 + 443	gttctcagtccggtttcttc G/A tatcttgcagatttatccag	2218
ABCA4	145	exon42 + 5844	cgtatcttgcagatttatcc A/G ggcacctccagcccagcagt	2219
ABCA4	146	intron43 + 328	tttgtagcctattcctataa A/G aatgcaccattgcttcccat	2220
ABCA4	147	intron43 + 345	taaaaatgcaccattgcttc C/G cattacctccctccacacat	2221
ABCA4	148	intron43 + 370	acctccctccacacattttt A/G caaaacgtttcagggagttt	2222
ABCA4	149	intron43 + 376	ctccacacatttttacaaaa C/T gtttcagggagtttactgag	2223
ABCA4	150	intron43 + 670	ttaaacagactggtccccta T/C gggcaggacagagaggatga	2224
ABCA4	151	intron43 + 701	gagaggatgagctctcactc A/G tctgcctctttcctggctgc	2225
ABCA4	152	intron43 + 822	gttaggtgctgctgacatct G/A tccagcatctgcttgactgg	2226
ABCA4	153	intron43 + 915	ggcaggacgagtcctgagca C/T gcttcactggctcagacagg	2227
ABCA4	154	intron43 + 1242	actgagctggacgctagaaa G/T aaactataggcttaagacac	2228
ABCA4	155	intron43 + 1671	tagagaagtttacttccatc G/A ggcacatcgcatcttttcta	2229
ABCA4	156	intron43 + 2036	ttgaaggatactcagtaatt G/A ctttttttcttgcagtattt	2230
ABCA4	157	intron45 + 176	gtgtttggttcacacagctc C/T ggagaaaaacaagtcacggc	2231
ABCA4	158	intron45 + 193	ctccggagaaaaacaagtca C/T ggcacagccttgacttggga	2232
ABCA4	159	intron47 + 238	cccaagtctctggatggggc A/G tctgatcaggatgcatgcag	2233
ABCA4	160	intron47 + 269	atgcatgcagagcctggctg G/A gatgagggagggctgctacc	2234
ABCA4	161	intron47 + 326	accacttatctcaacagatc C/G gggacctgtggcctatttac	2235
ABCA4	162	intron47 + 715	aagtcactaagctggttggt G/A ggaggaacagcacataaccc	2236
ABCA4	163	intron47 + 734	tgggaggaacagcacataac C/T caccttatctatgctgaggt	2237
ABCA4	164	intron47 + 931	ggacactgcatagatatcta T/C agaaatagcagcatgtcagg	2238
ABCA4	165	intron47 + 1260	acactctctggtggaccatc A/C ctcatccaagagagggtaac	2239
ABCA4	166	intron48 + 1663	tctcgctcttctcttacctc T/C aggtgtttgtaaattttgct	2240
ABCA4	167	intron49 + 127	agagagccccacccacacca C/T ggtccctaccaagtccccac	2241
ABCA4	168	intron49 - 1545	gcagttaattccaaactttt C/A tcccttattggatgagatca	2242
ABCA4	169	5'flanking - (1441-1400)	gtaaatctcagttgaatcag (TCA)14-16 atttttcagtctggttcctg	2243
ABCA4	170	intron1 + (4712-4720)	gaggggcggggactataggc (A)8-10 cagcctaattcaaggatgag	2244
ABCA4	171	intron1 + (7295-7304)	ttgttggctttgcaatggat CACAGTCAT/Δ ttattcactc attcattcac	2245
ABCA4	172	intron2 + (951-952)	cctgtccatcagactcttct TT/Δacctctccccgaggagccca	2246
ABCA4	173	intron3 + (2642-2653)	cctgggtgacagagcgagat (A)10-12 tagcatgagatattattact	2247
ABCA4	174	intron4 + 5202	cacaaagcatctgacacccc C/Δ atccagccctggctaacttt	2248
ABCA4	175	intron6 + (3029-3044)	cactaaaaacaaaaatttac (A)16-18 cctgaaagaaattgcaggca	2249
ABCA4	176	intron6 + (5138-5139)	ttcatgacagatcagatgtt (G) cttttatggatttacaaaga	2250
ABCA4	176	intron6 + (5138-5139)	ttcatgacagatcagatgtt cttttatggatttacaaaga	2251
ABCA4	177	intron6 + 5985	tttccttcttcaaacccccc C/Δagactaggagaaggtctgtc	2252
ABCA4	178	intron6 + 6094	gggacggacagaaaaagacc T/Δagtttctgttgagccaaaga	2253

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ABCA4	179	intron6 - 161	tatttttttcaattaaataaa A/△ gagtttttttgtttctaaaag	2254
ABCA4	180	intron7 + (809-810)	gggccgagtatgcacactga (TG) tgtgggaaagttagagaaga	2255
ABCA4	180	intron7 + (809-810)	gggccgagtatgcacactga tgtgggaaagttagagaaga	2256
ABCA4	181	intron8 + (472-484)	atcttccccacctttcacta (T)10-13 ggtcttctatggggtaaagg	2257
ABCA4	182	intron9 + (48-71)	gtaccctggacctcccagaa (GT)11-13 gagagagatgtgccttcctg	2258
ABCA4	183	intron9 + 554	ataggggcagaaaagacaca A/△ ccaaaagttctctctcactt	2259
ABCA4	184	intron10 + 11	catgatcagagtaaggggggg G/△ ttggaggatggggaggggag	2260
ABCA4	185	intron11 + 4242	ggagaggaaatgatgttagt G/△ cctcctgtaaaataggcccag	2261
ABCA4	186	intron11 + (13743-13753)	tgctcttttgtgggtaatgg (T)9-11 cctcttccaggagaagaaaa	2262
ABCA4	187	intron13 + (636-637)	cggggtggagggttgggagg (G) ctcatttgtcattatagatg	2263
ABCA4	187	intron13 + (636-637)	cggggtggagggttgggagg ctcatttgtcattatagatg	2264
ABCA4	188	intron18 + (569-570)	tgctgccctcatcttctctc TT/△ aaactagttctgtatttctc	2265
ABCA4	189	intron20 - (304-297)	tataacctgacttttttttc (A)7-9 ggattgctttttttaaacata	2266
ABCA4	190	intron22 + (1236-1246)	gctgaattagttcccttggg (T)9-11 agttaactcctgatttttgc	2267
ABCA4	191	intron26 + (4626-4635)	gataatcaatgctgtaaggg (A)9-10 tggcattagagatccagacc	2268
ABCA4	192	intron33 + (115-116)	taaaaccgtcttgtttgttt GT/△ ttacatggtttttagggccc	2269
ABCA4	193	intron36 + 1078	taagcagctatcacttaaca A/△ tacaaaaccagagattatca	2270
ABCA4	194	intron37 + (290-291)	ccttgaccaaagcctggggg (T) cagccattccccaaccccctc	2271
ABCA4	194	intron37 + (290-291)	ccttgaccaaagcctggggg cagccattccccaaccccctc	2272
ABCA4	195	intron38 + 896	ataaaaagaggggaaaaaa A/△ gaaggcagtcgctgcagggc	2273
ABCA4	196	intron38 + (1209-1210)	gtggacccctgagactgact CT/△ ttccagatcttgttagggtt	2274
ABCA4	197	intron38 + 1322	actctggaaaggcgggggg G/△ ataagaacacagccccagca	2275
ABCA4	198	intron38 + 3107	gggccccacctgctgaagag A/△ gggggggtggggtttgcccc	2276
ABCA4	199	intron40 + 152	ttttctccaataatacaagt A/△ gaggatcgggttaaaatagg	2277
ABCA4	200	intron43 + 330	tgtagcctattcctataaaa A/△ tgcaccattgcttcccatta	2278
ABCA4	201	intron43 + 1354	tttaattggcccagccatgc C/△ tttggtggctttttgtcattg	2279
ABCA4	202	intron47 + (1305-1308)	catcctgctgaaggagaaag AAAG/△ caccaatggcccaagcccta	2280
ABCA7	1	5'flanking - 1598	agaatgttggccccctcccc C/T tcctgcatcctctgcagaag	2281
ABCA7	2	5'flanking - 1594	aatgttggccccctcccct C/T ctgcatcctctgcagaagcc	2282
ABCA7	3	5'flanking - 1180	ggccagtgagtgacgggcag G/A tcgcccaaatagcagcgtgc	2283
ABCA7	4	5'flanking - 460	agagctggggtcgtgcctcc A/G gctgggcaactgcctgtctc	2284
ABCA7	5	5'untranslated - 9	ctctgtcccgtcccctgccc A/G gtctcaccatggccttctgg	2285
ABCA7	6	intron5 + 91	ccccgggccaaggacctccc G/A ttccaggcatccaggctgtc	2286
ABCA7	7	exon6 + 563	cagcttgttggaggccgctg A/G ggacctggcccaggaggtac	2287
ABCA7	8	intron8 + 103	gccggagggtcacggaaact A/G tttgaagaagtaggagttag	2288
ABCA7	9	intron8 + 166	tgcggaggatcagaggcaca C/T gcaggagcaaggcagagggg	2289
ABCA7	10	exon9 + 955	accggaccttcgaggagctc A/G ccctgctgagggatgtccgg	2290
ABCA7	11	intron9 + 421	ttttttttttttttttttt T/A taagagatggagtctcactc	2291
ABCA7	12	intron9 + 463	gttgcccaggctggactgca G/A tggcgagatcttggctcact	2292
ABCA7	13	intron9 + 467	cccaggctggactgcagtgg C/T gagatcttggctcactgcaa	2293
ABCA7	14	intron9 + 488	gagatcttggctcactgcaa C/T ctccgcctcctggattcaag	2294
ABCA7	15	exon10 + 1184	cgcacacgctgatgtggggc A/G cctggtgggcacgctgggcc	2295
ABCA7	16	intron10 + 10	gagtgacggaggtgagggcc T/C gtccacctgcggggtctgtt	2296
ABCA7	17	exon11 + 1388	cctgggccccggccacgtgc G/A catcaaaatccgcatggaca	2297
ABCA7	18	intron12 + 115	caggctgcgaactttgcacc T/G ttacaccactccacgtgacc	2298
ABCA7	19	exon13 + 1824	cccttcctgctcagcgccgc A/G ctgctggttctggtgctcaa	2299
ABCA7	20	intron13 + 55	ggtgcgctggagggtgacag A/G caggggcggccccacgtggg	2300
ABCA7	21	intron13 + 78	ggggcggccccacgtgggtg C/A gcgcccccaggccaatccag	2301
ABCA7	22	exon14 + 1851	cgttgcctctcacagctggg A/G gacatcctcccctacagcca	2302
ABCA7	23	exon15 + 2153	cgagggcgcgcagtggcaca A/C cgtgggcacccggcctacgg	2303
ABCA7	24	intron15 + 34	ggcggggctccgggccgggt C/G gcacctgctttgcgggaggc	2304
ABCA7	25	intron16 + 8	ctggacccaaagggtgaggc A/C ctacgaggcttaatagctgg	2305
ABCA7	26	intron16 + 161	tcccgcagcttttataggcc C/T cggcccagcaggtcccggat	2306
ABCA7	27	exon17 + 2385	caccccatctctgcagtgct G/A gtagaagaggcaccgcccgg	2307
ABCA7	28	exon17 + 2421	cccggcctgagtcctggcgt C/A tccgttcgcagcctggagaa	2308
ABCA7	29	intron20 + 166	cgagacagtaagagttgggg A/G tagacagaggttcccctgga	2309
ABCA7	30	exon21 + 3027	ctgctgggagaccgtgtggc C/T gtggtggcaggtggccgctt	2310
ABCA7	31	intron22 + 1386	gggtggggcgtgagccgggg C/T tccctgaagcaccccttttgt	2311
ABCA7	32	exon23 + 3417	gggatctccgacaccagcct C/G gaggaggtgtgaggcctggg	2312
ABCA7	33	intron23 + 147	ggagctctggtggctcagat G/A tcccttgggaaggcctgggg	2313
ABCA7	34	exon25 + 3528	gctggcctagacgtaaccct A/G cggctcaagatgccgccaca	2314
ABCA7	35	exon29 + 4046	cccagcctgccagtgtagcc G/A gcccggtgcccggcgcctgc	2315
ABCA7	36	intron30 + 81	ccccctgggagctctcccgg C/A ccccccggccctcagctccc	2316
ABCA7	37	exon31 + 4239	ctgcctgcatggccccacag A/G tacggaggcttctcgctggg	2317
ABCA7	38	intron32 + 1	caaggagcagctgtctgagg G/C tgcactgtgagtccctccac	2318
ABCA7	39	intron33 + 54	ccactgcttgccactgccct G/A tctggccccttgtaggcagg	2319
ABCA7	40	intron34 + 245	cagtactttgggaggccgag G/A caggaggactgcttgtggcc	2320
ABCA7	41	exon36 + 5057	ggtgagccggatcttgaaac A/G ggtcttccttatcttccccc	2321
ABCA7	42	intron38 + 65	ggcccactcacctttctgaa A/G gacctgcactctcccaggta	2322
ABCA7	43	intron40 + 154	ctctacctcccacacgcgga C/G caggccctgagacaccccctg	2323
ABCA7	44	intron40 + 277	ctgagccccccggcgccccca T/C ccccagcgtggcccgggaac	2324
ABCA7	45	exon41 + 5592	gtggcccgggaacccagtgc T/C gcgcacctcagcatgggata	2325
ABCA7	46	intron41 + 286	ctccttgactctgccttctg T/C ggccctgcccacttgctcct	2326
ABCA7	47	intron41 + 389	tggccgttcccagtttgcag C/T cgtttcactgcctcttccat	2327
ABCA7	48	intron41 + 991	cacactatggccctgcccca C/T acccatcccagctccaccca	2328
ABCA7	49	intron41 + 994	actatggccctgccccacac C/T catcccagctccacccacac	2329
ABCA7	50	intron41 + 998	tggccctgccccacacccat C/G ccagctccacccacaccatg	2330
ABCA7	51	intron41 + 1001	ccctgccccacacccatccc A/G gctccacccacaccatggcc	2331
ABCA7	52	intron41 + 1051	actcatgctggctccaccca C/T accatggccccgccccatac	2332
ABCA7	53	intron41 + 1131	tgccctgccccatgcccatt A/G tgcccctgctccacactcaa	2333
ABCA7	54	exon44 + 5985	gaagcgctctgctcgcgcct G/A gccatcatggtgaatgggcg	2334
ABCA7	55	intron44 + 201	ggcgcaggaccaggaggcgt G/C agccgggggctctgggtgga	2335
ABCA7	56	intron44 + 233	ctgggtggatttagaagaca C/T aatcaggtgtgcgttggagt	2336
ABCA7	57	intron44 + 313	agttaggggagggcctggtt A/G gtgggcggggccataggaaa	2337
ABCA7	58	intron44 + 337	ggcggggccataggaaagtg G/C ggcgggggtatttattgtgt	2338
ABCA7	59	exon45 + 6133	tggcggccgagttccctggg G/T cggagctgcgcgaggcacat	2339
ABCA7	60	exon45 + 6159	ctgcgcgaggcacatggagg C/T cgcctgcgcttccagctgcc	2340

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ABCA7	61	intron45 + 27	acggcgccggggtcgggctg G/C gggaggcaggctgggggcca	2341
ABCA7	62	3'untranslated + 6580	aaggctggagagaagccgtg G/C tggtgaaaccgtgtgcatgt	2342
ABCA7	63	3'flanking + 108	caagctgagtgtgcacatac G/A ggccaagtggcgattcatag	2343
ABCA7	64	3'flanking + 376	cttacaggagcccggtgtcc C/T ggagcacaggccagggccgg	2344
ABCA7	65	3'flanking + 687	cagcagggagacttggggag G/A ggggagagagttcacactgc	2345
ABCA7	66	3'flanking + 688	agcagggagacttggggagg G/A gggagagagttcacactgcg	2346
ABCA7	67	3'flanking + 1169	cctcgacctgacccacttca C/T ggggctgcagggcgggtgat	2347
ABCA7	68	intron9 + (398-422)	cgtgaactaccacgtcctgc (T)22-26 aagagatggagtctcactct	2348
ABCA7	69	intron12 + (175-184)	ggggactctgagggtctggt (G)8-10 actctgagggtctgggggcc	2349
ABCA7	70	intron30 + (81-87)	ccccctgggagctctcccgg (C)6-7 ggccctcagctccccttccc	2350
ABCA7	71	intron34 + (349-361)	agaaagagaaagagagaaag (A)12-14 cagaaatgtgctttgggtga	2351
ABCG1	1	5'flanking - 1772	cctgggcttcagcaggggcc T/C cacacctgcaatgggtgcct	2352
ABCG1	2	5'flanking - 1754	cctcacacctgcaatgggtg C/T ctggggagagggtgcagatg	2353
ABCG1	3	5'flanking - 1450	tccaaagcccagatttggtg T/C ttttggggctcttttggaat	2354
ABCG1	4	intron1 + 4	ctggtggaggaagaaaggta G/A ggagggcggctgctttgtgt	2355
ABCG1	5	intron1 + 576	agctcaggaggtgtctggaa C/T gccacacagtgcaggagttt	2356
ABCG1	6	intron1 + 1426	aattctccttctcaacttaa A/G gaaatattttatagaaaaat	2357
ABCG1	7	intron1 + 2342	agagcctgcaatgggccgcc G/A agggacctgcccatgactca	2358
ABCG1	8	intron1 + 2399	gaggggttgacagacaggat A/G tgtctgctgtgttccagctg	2359
ABCG1	9	intron1 + 2406	tgacagacaggatatgtctg C/G tgtgttccagctgctggttt	2360
ABCG1	10	intron1 + 2911	ccctctctgtgcccactgtt G/C tcccaacaccagcctgttct	2361
ABCG1	11	intron1 + 4363	tataatagattcctagcaga A/G aacataattgtgagaggaac	2362
ABCG1	12	intron1 + 4752	gctttcagagcccattcaca C/T aagggtctcattttattagg	2363
ABCG1	13	intron1 + 5026	ccaggtctgtgggatttcag G/A ccaaaaaggagcgtagcaag	2364
ABCG1	14	intron1 + 5532	gggttaaatattccgggcag C/T gccaagtcagattatctgta	2365
ABCG1	15	intron1 + 5681	gctaaagtgcatggaaggca T/C catgaataaatcctttcagg	2366
ABCG1	16	intron1 + 6290	tcacagcagattcatgagag T/A tgaatgtttagccgccatgt	2367
ABCG1	17	intron1 + 6386	agatgctcccctccagccag C/T acattttctccctgtgagca	2368
ABCG1	18	intron1 + 6758	acctgcatggtgggtgcccc C/G ctgccttcctctactgcctt	2369
ABCG1	19	intron1 + 7029	tgggtcagattaaatatatc C/T tgaaggactaaaccgtaaaa	2370
ABCG1	20	intron1 + 7176	ttgctcacattgtgaaaaaa C/G gcaaaaagatgggttttcag	2371
ABCG1	21	intron1 + 9243	gcctgagagcgctggcagta G/A gaagggtcgccagtgtggac	2372
ABCG1	22	intron1 + 11224	tctggtttagagaggaaaat G/A ggcagcatcattttgtcacc	2373
ABCG1	23	intron1 + 11371	gggctctcttggagcccttt T/G tctctcccagccctgcgtct	2374
ABCG1	24	intron1 + 12420	gggatttcgaatctcaacac T/C ctgagctctgtgctttcccc	2375
ABCG1	25	intron1 + 12484	gagttgtcctccaagagaat C/T tttgtatggttccttttctg	2376
ABCG1	26	intron1 + 12955	ctgggggttggtgggagccac A/G gtctcacacctattggcagg	2377
ABCG1	27	intron1 + 12985	ctattggcaggtcgtgaaca T/C tgttcttggatttgcaaata	2378
ABCG1	28	intron1 + 20041	acatggccggcttcccttct T/C cctcggaatggcctggaatt	2379
ABCG1	29	intron1 + 20046	gccggcttcccttcttcctc G/A gaatggcctggaattcgatc	2380
ABCG1	30	intron1 + 21058	acaagacttagaatttgacc G/A tgattttaaaactattctaa	2381
ABCG1	31	intron1 + 26189	ttcttggatgtggccatgca C/T gggggcaagggtttgatgag	2382
ABCG1	32	intron1 + 27453	atcatgtggtttgggggaaa G/C ctgggaccccacttggtaca	2383
ABCG1	33	intron1 + 28098	caggaaggagacagctgctg G/C tgctgcttagagttaggcgc	2384
ABCG1	34	intron1 + 29670	ccttcagttgtaataggcag A/G aggagcgcacgaggaggctg	2385
ABCG1	35	intron1 + 29810	attgtttctcctggttttgt T/C tgtgttgactttccctttaa	2386
ABCG1	36	intron1 + 36220	cagatcccttggttgctggg C/T aggtagtaggagaggttttt	2387
ABCG1	37	intron1 + 36341	aaacagggcttgagtcctcc G/A taagggacaggagaccttcc	2388
ABCG1	38	intron1 + 36370	aggagaccttcccacatcct G/A gcaagaattcttctttttttc	2389
ABCG1	39	intron1 + 36662	cagactaaatgcacaattct G/A gattgagctgactgtattga	2390
ABCG1	40	intron1 + 36914	tgtaaaagatggagaagaac A/G cagtagtcgcttgctgtgag	2391
ABCG1	41	intron1 + 37029	tgtgactcatggcctctgcc A/G ggggactgggctggcccctgc	2392
ABCG1	42	intron4 + 1196	tgaaaagaaaatggatgagt G/A gaaaccaaaagagagaaaat	2393
ABCG1	43	intron4 + 1200	aagaaaatggatgagtggaa A/C ccaaaagagagaaaatgtgg	2394
ABCG1	44	intron4 + 2041	aagcagaggcttttccaccc G/A gagactcaagaagctgctcc	2395
ABCG1	45	intron4 + 2490	gtggtgaagtagagctgagc A/T cacgggggagccctccatcc	2396
ABCG1	46	intron4 + 2552	atggccttgggccactgcct G/A ctgtgccccgagccgagctt	2397
ABCG1	47	intron4 + 2822	cagcaggctccgtgctgaag T/C cacagcaagccaggcccttg	2398
ABCG1	48	intron4 + 2850	agccaggcccttggcctgcc G/A gagctggaagacccagaaca	2399
ABCG1	49	intron4 + 2919	gcctcccaggagtagctaca C/T gggacccgaaggcagatggc	2400
ABCG1	50	intron4 + 3506	ggcagcctgggctgccgaga T/C cctccctggagcgcccgccg	2401
ABCG1	51	intron4 + 3538	cgcccgccgggaagccccag G/A ggggctggagctacaagtgg	2402
ABCG1	52	intron4 + 3554	ccaggggggctggagctaca A/G gtggccttgcaggttttttg	2403
ABCG1	53	intron4 + 3721	ccagctcatgggcaggggtg C/T ggagggaaaggcacccacag	2404
ABCG1	54	intron4 + 3852	caccagagccactcagtcgg C/T caagagcgtcgcccagtggt	2405
ABCG1	55	intron4 + 3921	gaagaccagcagtcgatgcc A/G gctgggaagagggctctgcc	2406
ABCG1	56	intron4 + 3979	acccaccagccttttccaga C/T agccttccagaagctgtttc	2407
ABCG1	57	intron4 + 4291	gagccgctggagtagggtcc G/A cttgctatggctcccagggg	2408
ABCG1	58	intron4 + 4922	gaaaccaccagaaattgtgc A/G tcctctcatgtgtccattca	2409
ABCG1	59	intron4 + 4968	tattgactggacaccttctc C/T gtatggggcactgggctagg	2410
ABCG1	60	intron7 + 672	atcagtaacgggtcactaac G/A gatgctgctgagtggggcag	2411
ABCG1	61	intron7 + 840	atttcatttcctcaatgtcg T/C ctgaccagagagcgggaggt	2412
ABCG1	62	intron7 + 891	tggcccactgttgagggtgt G/A ggtgaccagaggggcctgga	2413
ABCG1	63	intron7 + 997	tgtgtcctggtttgtggctt C/G atctaggaggtgtggtggcc	2414
ABCG1	64	intron9 + 1616	ctggaggagaagacaggata A/C agtctaagacgtgctgtcac	2415
ABCG1	65	intron9 + 1630	aggataaagtctaagacgtg C/T tgtcacagagttcagggtcc	2416
ABCG1	66	intron9 + 1674	gcttccaaaggccgcatccg G/T gttgttctctgagccgagga	2417
ABCG1	67	intron9 + 1689	atccgggttgttctctgagc C/T gaggacggctttgcgaacgc	2418
ABCG1	68	intron10 + 446	tggctgacagtgaacacagc G/A gctgcttctccagaacttta	2419
ABCG1	69	intron10 + 581	atgcagagtttcagaagagg C/G agactcaggaagagtaaggc	2420
ABCG1	70	intron13 + 243	acccggagagccatggcagg A/C ccaagtgttctggacgttgc	2421
ABCG1	71	3'untranslated + 2370	gcctctcagctgatggctgc A/G cagtcagatgtctggtggca	2422
ABCG1	72	3'flanking + 1124	ctcagaactacatcgagtga G/A gtcagtgttgaaaacgccca	2423
ABCG1	73	3'flanking + 1252	atggggcccacagccctgcc T/C cagaagcagctttggtctcg	2424
ABCG1	74	3'flanking + 1433	gggggaagagcttgggaacc A/G tgagggctgttaggctgcaa	2425
ABCG1	75	3'flanking + 1513	tgaagggtgaactggagtag G/C tgaggattctgcagttgacg	2426

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ABCG1	76	intron1 + (19909-19944)	ccgatgaggaggggatgggg (CACCAGGCAGCAGACTCTGA TGAGGAGGGGAGGGGG) caccaggcagcagactctga	2427
ABCG1	77	intron1 + (19909-19944)	ccgatgaggaggggatgggg ca ccaggcagcagactctga	2428
ABCG1	78	intron1 + (25136-25137)	catgaacttgcctgaccata (G) ccctgtgaggagctagggct	2429
ABCG1	79	intron1 + (25136-25137)	catgaacttgcctgaccata ccctgtgaggagctagggct	2430
ABCG2	1	intron1 + 152	tcatttgaaagtgggtatgc G/A gtttaaaactgacagttcaa	2431
ABCG2	2	intron1 + 614	agctagtcataaaataaatac G/A ccagagtagtaaggaagaga	2432
ABCG2	3	intron1 + 10002	cctcatgaatggtatacatg T/A cccaacatatctctttcgat	2433
ABCG2	4	intron1 + 10123	acagtggtccctttgggtgc G/A tatacccaaatccctgcata	2434
ABCG2	5	intron1 + 10768	ataggaataattgagaacag G/A gtctgaagaactctgcagga	2435
ABCG2	6	intron1 + 10791	ctgaagaactctgcaggaaa T/C gaaaatagttccctgctttt	2436
ABCG2	7	intron1 + 10792	tgaagaactctgcaggaaat G/A aaaatagttccctgctttta	2437
ABCG2	8	intron1 + 14183	tcacttaaggctttgcaggg T/G gtctaggacacagaaagaga	2438
ABCG2	9	intron1 + 14934	aaagtgtctttaaaatttcc A/G tcttgagtcagtgagctatt	2439
ABCG2	10	intron1 + 14955	tcttgagtcagtgagctatt G/T aaattcaagcaataagttat	2440
ABCG2	11	intron1 + 17251	ctgtttgggaacagcaactc A/C atcataggcagagagaaagt	2441
ABCG2	12	intron1 + 17347	atttcaaacctgtttcacaa G/A ttgttaagctcatcttaagg	2442
ABCG2	13	intron1 + 17626	gaaggtgcataacaacttcc T/G acataaagtctggagctata	2443
ABCG2	14	intron1 + 18271	aaatgaagctgctcattgcc A/G cacatttaaaaatggacttg	2444
ABCG2	15	intron1 + 18369	ctattgcttttctgtctgca G/T aaagataaaaactctccaga	2445
ABCG2	16	exon2 + 34	atgtcgaagtttttatccca G/A tgtcacaaggaaacaccaat	2446
ABCG2	17	intron2 + 36	tgtaaaaagacagctttta A/G tttacctacagtgaacctca	2447
ABCG2	18	intron2 + 4230	caaccctaaattggagggcc C/T gggcgtggtgattgagaaag	2448
ABCG2	19	intron2 + 4518	gttgacagacttttatagtg A/C gggacactgacctgcatgca	2449
ABCG2	20	intron2 + 6278	atgtatgtaccacgtcttca T/C attcttaaaggatgacccta	2450
ABCG2	21	intron3 + 10	ggcaaatcttcgtgagtata A/G gagagtataagtaagcgttt	2451
ABCG2	22	exon5 + 421	tgacggtgagagaaaactta C/A agttctcagcagctcttcgg	2452
ABCG2	23	intron6 + 3158	actattctagttgattctag A/G ttgtcaatacaacacactga	2453
ABCG2	24	intron6 + 3203	tcctattctgttttaataaa A/G gcattgaatttaggtttgct	2454
ABCG2	25	intron6 + 3287	gtcaggctgaactagagcaa A/G caatctaaaggcaagaatag	2455
ABCG2	26	intron7 + 179	ttcatttttgtagcaccagc T/C tgttatttaggtatctttct	2456
ABCG2	27	intron9 + 5677	gcacttggactttgctttgc T/C acatacttgcattgctctgc	2457
ABCG2	28	intron9 + 5974	tatactaataaatggtgtgt A/T taagtttttatctctaattg	2458
ABCG2	29	intron10 + 1908	gacgcttatgtgcagcctat G/T ttgatgtctggaaaggctga	2459
ABCG2	30	intron10 + 2094	ccctgagggctgaggtatct G/A gattatttccagacttgcta	2460
ABCG2	31	intron11 + 20	tgtgagtaggtctttgttct A/G ggaacggggctgtccagcag	2461
ABCG2	32	intron11 + 1447	tgttcttcaaggaaagcccc C/T gtcaaagaaggaaaagaagc	2462
ABCG2	33	intron12 + 49	atgtctttagtcttgcctat G/T ggtgaagtcagttgcacctt	2463
ABCG2	34	intron12 + 1566	tatgcagttacatggacaga C/T acaacattggagaccgaggg	2464
ABCG2	35	intron13 + 40	gctctgataaggaattgttt C/T tttccttcatttcttcctgc	2465
ABCG2	36	intron13 + 1823	ttactcaagcaggcctgact C/T ttagtatttgctttttgtag	2466
ABCG2	37	intron14 + 497	ctaatgaaaacaaacaagaa T/C gaaagattgtcactgtaaat	2467
ABCG2	38	intron14 + 815	taactctttggaaacttctt A/G aaatttaaaactgtttacct	2468
ABCG2	39	intron15 + 110	ccaggggcactgaatttttc C/T gagcctacgttttctcatcc	2469
ABCG2	40	intron15 + 566	gccgcatagtcatgtgttgt T/A gtttttaaattaacttggaa	2470
ABCG2	41	intron15 + 639	aacaagaaacacttgaataa G/A ttgagaaaaaaccccgtttt	2471
ABCG2	42	intron15 + 1197	tgagtagctgggattacagg C/T gcccaccaccacacctggct	2472
ABCG2	43	intron16 + 520	catcaattcaggtcaagaaa T/C agaagattgtagcacacaaa	2473
ABCG2	44	5' flanking - (998-995)	gttgggatggctacactcac TCAC/△ aaagcctgatggcccgtttc	2474
ABCG2	45	intron13 + 405	ctgctagtttatttttttttt T/△ aacatttttaatttatgttt	2475
ABCG2	46	intron13 + (692-702)	tcaatatgtttctgcttatc (T)9-11 aatggttacttaatcctaat	2476
ABCG2	47	intron15 + (645-650)	aaacacttgaataagttgag (A)7-8 ccccgttttcacataatgtt	2477
ABCG4	1	intron1 + 84	ggcctgggtgtcccatgttc G/A gaaagtcctgcaccagtggg	2478
ABCG4	2	intron2 + 77	gaacacagaaggtattctga A/G agggcattgacccccatcct	2479
ABCG4	3	exon6 + 679	tggtgtccctcatgaagtcc C/T tggcacaggggggccgtacc	2480
ABCG4	4	intron7 + 95	ggcctcctaggggtagagat C/T tcaccgtcgcctgccttccc	2481
ABCG4	5	intron7 + 158	cttgcccttgggaagtgagt G/A tgaatctaaactgagctctc	2482
ABCG4	6	intron8 + 106	ccccagaggcattgcaacca A/G tgggtgctaggaagaaccta	2483
ABCG4	7	intron8 + 1089	aggtacacaacttaatggta C/G aagattctctgtagacctgg	2484
ABCG4	8	intron11 + 1113	acgtgagacgagataagtga T/C ggtcatatggccagggagga	2485
ABCG4	9	intron11 + 1120	acgagataagtgatggtcat A/G tggccagggaggaaggggac	2486
ABCG4	10	intron11 + 1173	gggggacagcttgaacaaga A/G tgtggaggcaggatggacac	2487
ABCG4	11	3' untranslated + 2758	gagtgacaggcacatacatg A/C gaacaggccatctcagccct	2488
ABCE1	1	5' flanking - 158	aactcagattctcggcacct C/T cagcagctggcttcgccaac	2489
ABCE1	2	intron9 + 237	ctgaaattatatgcaaattc C/T gtagctttataggaagcaga	2490
ABCE1	3	intron9 + 4203	ttgtgtaggaagctgataca T/G taatttgacatatgagatgt	2491
ABCE1	4	intron10 + 1811	ccaagaaacttcagctttct C/T ttcacttaaatataggaaac	2492
ABCE1	5	intron17 + 2301	atatccagaaacagatggta T/C gtgcagaacaggttgtacag	2493
ABCE1	6	3' untranslated + 1810	tggatgattagactgactct G/C agaatattgataagccattt	2494
ABCE1	7	intron1 + (5349-5363)	tttgtctgggttggttgggg (T)13-16 gagactgggtctgactctca	2495
ABCE1	8	intron1 + (5845-5854)	tacatttgtcaaaatttata (T)9-10 gcagataatcatttcatctc	2496
ABCE1	9	intron5 + (836-851)	taaattcacatgattctgta (T)14-16 aggatcctcctgactggcag	2497
ABCE1	10	intron8 + (1153-1169)	tctttcaaacttatatttgc (T)13-17 catagtttcatgtttgatga	2498
ABCE1	11	intron9 + (1023-1024)	ttgctctgtttcaaatctct (T) attcatgggccagcagctcg	2499
ABCE1	11	intron9 + (1023-1024)	ttgctctgtttcaaatctct attcatgggccagcagctcg	2500
ABCE1	12	intron9 + (2338-2346)	agtgtagatggacctcgggg (A)8-9 ctagttaaggaaaagtaata	2501
ABCE1	13	intron9 + (3213-3221)	ttccaattttccattgttac (T)8-9 cttgccagattactcctgaa	2502
ABCE1	14	intron10 + (284-299)	tcctctgcattttggcttct GCAGTATTACTGTAGT/△ atttg tcattttcaaattaa	2503
ABCE1	15	intron10 + (840-853)	ttttttggtttctttctttc (T)13-14 aatcttggaggaatcttttt	2504
ABCE1	16	intron16 + (1163-1172)	gattagaaatccaggttaaa (T)9-10 gttttgcacaaaaatattac	2505
ABCE1	17	intron16 + (1372-1382)	taaaatttaatcaaaattga (T)10-11 ctcttagtcctcaaaccctt	2506
CHST1	1	intron1 + 2475	taaatggagaaaataacacc G/A acctgatagcattgttgtga	2507
CHST1	2	intron1 + 2612	aaactccccaagcatgctca C/A ctagatccttaccctaggtc	2508
CHST1	3	intron1 + 3900	gccctgccccccactcccaga C/G ttgcggccctccagccccctt	2509
CHST1	4	intron1 + 6520	cctcccccagaggagctggg C/T acactggggccttgtgttgt	2510

Designation of Gene	No.	Location	Sequence	SEQ ID NO
CHST1	5	intron1 + 7534	attgtgtgttggcatactgc T/C cacatggaaggatgctctag	2511
CHST1	6	intron1 + 7911	ttttccttaggaagaaaaac G/A ccttgctgttttatgcattt	2512
CHST1	7	intron1 + 7963	aaaacattcatgggggatta G/C tgctggctacgtcagagtca	2513
CHST1	8	intron1 + 9173	gcgctgccacagatcaggcc G/A aggtgggggacagaaatgcc	2514
CHST1	9	intron1 + 9701	cccagaattctgaatacagc A/G gcgatgacgggactacgagg	2515
CHST1	10	intron1 + 12132	aacagatccacaggaccaga C/A agcaaaggggaggaacatgc	2516
CHST1	11	intron1 + 12465	atgcagggaaggggcttggc G/A caaaactgtcaactgagata	2517
CHST1	12	intron1 + 12561	atgctccctggtccactttc G/A ctttgagtttcaggtagctg	2518
CHST1	13	intron3 + 529	ccatggtctgcaggggtcct T/G catgctcaggggattggggt	2519
CHST1	14	intron3 + 617	agaggacagaggaaagagga C/A cacctggagaactgggcgcc	2520
CHST1	15	intron3 + 796	aagaggcttccgcagctgtc C/T gcaggttaaatcctggggtg	2521
CHST1	16	intron3 + 818	caggttaaatcctggggtgc A/G aggaatgtttgttcagctcc	2522
CHST1	17	3'flanking + 762	ataactggtacaggtttact G/C gtgtctacactggcagagaa	2523
CHST1	18	intron1 + 7874	gttttccccttgccttgcct T/△ cattttcatcacctcatttt	2524
CHST1	19	3'flanking + (335-349)	cacactgccacacctggcta (T)12-15 ggattttagtagagacgggg	2525
CHST3	1	5'untranslated - 294	tccagcgtgccgaccggccc C/G gcagcgcctccatccctccg	2526
CHST3	2	intron1 + 96	gcgtccaggcgcgcgcgcca G/A actttggagggagaaggggg	2527
CHST3	3	intron1 + 4467	agagaagaatggggcagagc C/G ggagcagccaggggaggtga	2528
CHST3	4	intron1 + 4853	ggatgagcactgcccagctg A/G tccctgcccaccttccacag	2529
CHST3	5	intron1 + 4965	tccactgcagaggggacaca G/C tgaccaggacggaagttggg	2530
CHST3	6	intron1 + 5046	gggctgtccatctttgtacc C/T ctggttccatcccagtgcct	2531
CHST3	7	intron1 + 5300	ccttttcttctctaaggcct A/G aagagatgacagaatgctgc	2532
CHST3	8	intron1 + 5354	agcgcgtggactccacagcg G/A ggtgtggggtggcccctggc	2533
CHST3	9	intron1 + 5428	gacacgcttcagccctctgt C/G tctattgccccaaatctggc	2534
CHST3	10	intron1 + 5621	ctgtggcttccctgggccct A/G ggaaatttatcactgaggtt	2535
CHST3	11	intron1 + 6555	gagtggggcactgctggaag G/C ttctggttcctgctttgttc	2536
CHST3	12	intron1 + 6990	aaacacactgggccaccccc G/A tccccgcactgtgactacac	2537
CHST3	13	intron1 + 7133	ctgagggcctgtcctgcagg T/G ttgatgtgtctgaagaggcc	2538
CHST3	14	intron1 + 7161	gtctgaagaggccccgagaa T/C agaaatctagaacctgccag	2539
CHST3	15	intron1 + 7199	cagtcacgaagcagtgtcac C/T caccagaggatgaagaactg	2540
CHST3	16	intron1 + 7316	cttgcatctggtgtaggtgc C/T tgggggtagcgtgcccagga	2541
CHST3	17	intron1 + 7967	gacaggaaccccaccccgag T/G gatgtctggccctgtgacct	2542
CHST3	18	intron1 + 11412	gcttgcacttctgattcatt C/T tgcagtcactggctctttgt	2543
CHST3	19	intron1 + 11591	ccctggaagggcctcactgc G/A gtgactcattacccagcatg	2544
CHST3	20	intron1 + 12541	acccacacagcatgaatggg G/C ccagccccagcctgcccgct	2545
CHST3	21	intron1 + 12672	gtagccacagctggggctgt G/C gggtcagggcatggcaaggg	2546
CHST3	22	intron1 + 14809	ggatgtgtagggtttgggct C/T ggccttaagggatgggtgga	2547
CHST3	23	intron1 + 16161	gatgctggtcaggcattgtc G/A ttgggatctttaacaccacc	2548
CHST3	24	intron1 + 16385	tatttagcatgtgggtttca A/C ctttctgtttttttcaaaggg	2549
CHST3	25	intron1 + 33638	gacttgggccacgtccttgg G/C catgaatcttggtctatgtc	2550
CHST3	26	intron1 + 33878	agcaagaaagtgtgctcccc C/T acagccccactcaggcataa	2551
CHST3	27	intron1 + 34690	agcacacatggagctttccc G/A cagtgggtttcagcgctccc	2552
CHST3	28	intron1 + 35145	agggaagccgaagcctcact T/C gctggggcttgcctggcctc	2553
CHST3	29	intron1 + 35340	tgtgaagttttgcccacagt T/C ggtggccatggttcgcaccg	2554
CHST3	30	intron1 + 35436	gccactcatgtatggagcaa T/C tgccttttttttcttcctctt	2555
CHST3	31	intron1 + 36150	ccatagaagaggctgggcct G/T aggaagccagggaagcagga	2556
CHST3	32	intron1 + 36194	ggtgtggggaggccagcagg G/A gtgtgggcctcagcggggag	2557
CHST3	33	intron1 + 36561	ctctggtgtttgctgtcaat A/G tgcagagtgctggacaaaac	2558
CHST3	34	intron1 + 37602	ctggaacagcaacttaaaaa A/T agaaatagtccctggaaggg	2559
CHST3	35	intron1 + 37725	gggtagccagggcagctccc C/T gacccgcacctgccttttt	2560
CHST3	36	intron1 + 37734	gcagctccccgacccgca C/G ctgccttttcacccctctcc	2561
CHST3	37	intron1 + 38208	gccattctagatgcgagtcc C/T gactttggggtgcttgca	2562
CHST3	38	intron1 + 38219	cgagtcccgactttgggg T/C gcttgcattctgggaaggga	2563
CHST3	39	intron2 + 255	ctacagctgtgaaaggttag A/G caagatacttaacatttctg	2564
CHST3	40	3'untranslated + 2202	acacctcagaggagcctgtg C/A ttaacatttgtaggattatt	2565
CHST3	41	3'untranslated + 2569	aggcctcatctggggtaggg C/G caagaggaaagtacagagtg	2566
CHST3	42	3'untranslated + 2717	ctggaattcctccttagggc C/T ctgggaagagtattgcttaa	2567
CHST3	43	3'untranslated + 2753	cttaacgcaggatgtgctgg G/A tgttttgtttcgggctttta	2568
CHST3	44	3'untranslated + 2800	gcttggtgtctttcttgttt C/T atggctgtgtttttgctttt	2569
CHST3	45	3'untranslated + 3283	ccgagggctgcccagctctg C/T ttctggtttcctggacaatt	2570
CHST3	46	3'untranslated + 3327	ctgtcagatacggcccattg T/C aaacccagagggctgcattt	2571
CHST3	47	3'untranslated + 3787	gttccccatgtggaggtcgg A/G ggggctgggactggggaggg	2572
CHST3	48	3'untranslated + 3860	ggccctgctaatgtggacag T/C agactttatccctccttctt	2573
CHST3	49	3'untranslated + 4915	ccagatgtgcatagaagcca G/A tctctgtcacatacaccgca	2574
CHST3	50	3'untranslated + 4993	taaagcaaatttaggctttt G/A tccttctgcaatacatgcac	2575
CHST3	51	3'untranslated + 5223	ggaaggagcttcagcaggag G/A tccttcccagaaggttgatt	2576
CHST3	52	3'untranslated + 5370	tcatacctgtaatcccagca G/T ttggggaggccaaggtggga	2577
CHST3	53	3'untranslated + 5545	ccattcccaaagtcagaaag T/C gaagccagatctcaagggct	2578
CHST3	54	3'untranslated + 5859	caaaagcacaaagcagaatt G/C gcaacttcacttgtctca	2579
CHST3	55	3'untranslated + 5870	cagaattggcaacttcac T/A tgtctcaagagctccaagat	2580
CHST3	56	3'untranslated + 5971	ttccaaggctacagacatgg C/T gccatcctcacaggcctagc	2581
CHST3	57	3'untranslated + 6208	atttcatgtctgcatggtac G/A agacacccctcacggca	2582
CHST3	58	3'untranslated + 6223	tacgagacaccccttcac G/A gcatacactgccatggtatg	2583
CHST3	59	3'flanking + 281	agacaggagtgttgggccag C/T ggtcagggggcctggggatg	2584
CHST3	60	3'flanking + 997	acctcttaaagtatttgagc C/T ggtgcctgtcatcccaacct	2585
CHST3	61	intron1 + 22595	cgggagcaggaaaaaaaaaa A/△ gaataagaagaaaagaggct	2586
CHST3	62	intron1 + (35423-35424)	gctcatgctcacagccactc AT/△ gtatggagcaattgcctttt	2587
NDUFV1	1	intron3 + 670	ctgggtggagtggggtggca T/C ggagttgaagacccagtcct	2588
NDUFV1	2	intron6 + 160	tgtgccggccccagccctga C/G catgcatccctttggggacc	2589
NDUFV1	3	intron9 + 27	accaccctctgcgtagcac G/A gagggtgggtggcatcaagg	2590
NDUFV1	4	3'flanking + 1111	tgtaggctgaggtcagcccc A/C atccagtccaaagcccaccc	2591
NDUFV1	5	3'flanking + 1658	gaatgcggaagtgctctgtg G/A gcacccaccatgctccgggc	2592
NDUFV1	6	3'flanking + 1713	gatctggggcggagggtaca C/T ggggctggcgctgggtgaag	2593
NDUFV1	7	intron4 + 214	tggtgtaaatttttttttt T/△ gcttcaaaaatatagtattt	2594
NDUFV1	8	3'flanking + (772-774)	tgaactcggggttcagggtc TTC/△ ctgtgaacactggttttgaa	2595
NDUFV2	1	intron1 + 526	ggaaatgctggctaaataaa C /T ggtatcaaactaactctgaa	2596
NDUFV2	2	intron1 + 6689	tcgttggatggtagtattgt T/G tgaacaacagaagaaattca	2597

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
NDUFV2	3	intron1 + 14767	ccaaatgcatgccagcagag C/T gtggcaggaaggtacacaag	2598
NDUFV2	4	exon2 + 86	aaggaatttgcataagacag T/C tatgcaaaatggagctggag	2599
NDUFV2	5	intron2 - 29	cagaagatcttactctctaa T/G gaagctggataacacttttt	2600
NDUFV2	6	intron2 - 168	tttactttggtaatcatact T/C atcaaatgtgtgtttagaca	2601
NDUFV2	7	intron4 + 677	aaaccacatactatttgatt C/A tgatgagaatcacataacca	2602
NDUFV2	8	intron4 + 2295	tatgattcaactttcaaaag A/T gtattgtgatatgaaataga	2603
NDUFV2	9	intron5 + 102	caacttctgccatcttattg G/A atctgtacttacctagtaat	2604
NDUFV2	10	intron7 + 5466	tggtaagaggctttaagata A/C caaatgctcagctttcagga	2605
NDUFV2	11	intron1 + (13562-13563)	tactcttaaaattaatcctt (CTT) ttattataagtatacagtct	2606
NDUFV2	11	intron1 + (13562-13563)	tactcttaaaattaatcctt ttattataagtatacagtct	2607
NDUFV3	1	5'flanking - 606	aattacgactaacgttgggg A/G cgaactctttgctaaataaa	2608
NDUFV3	2	5'flanking - 222	cgccgcgcccccgccacagc G/A cccaggcgcccgcagggcac	2609
NDUFV3	3	5'flanking - 111	tggccccaagggaggcactt A/G gccctactggggatgcgcgc	2610
NDUFV3	4	intron1 + 137	ttgggccgctgaccccgctc C/T ctgggcccaggactgaccgc	2611
NDUFV3	5	intron2 + 152	tatacaagacacaagatcta T/C aacagattttagaccaaaca	2612
NDUFV3	6	intron2 + 6304	ttcacagatgaaggggttcc G/A aaatttttgtcaagaaagac	2613
NDUFV3	7	intron2 + 6433	tcgccttcgtcttcatcctc T/G tccagctcctctgattctga	2614
NDUFV3	8	intron2 + 6563	cctttgaaaacagagccccc C/T gagttacagtatcagcaaaa	2615
NDUFV3	9	intron2 + 9619	actatcttctgtgcgcatgc G/A cagagcccaccttgcagagc	2616
NDUFV3	10	intron2 + 9858	aggatgcagctctttaaat G/A agacatcgtttttgcttaac	2617
NDUFV3	11	intron2 + 11673	cttggtaggtaagcgcctgt A/G tgtgagccaagtcattcata	2618
NDUFA10	1	5'flanking - 1734	tgcaccttgaactgtttact T/C tcctgtaaccatttaccctt	2619
NDUFA10	2	5'flanking - 1492	aaaacatccacgcaaacagg T/C tgtgagaagttacgtctgcg	2620
NDUFA10	3	intron3 + 370	aagactgtgcatgtgccatg C/A agacagagatgtggatgcca	2621
NDUFA10	4	intron3 + 2485	ttgttattttcttttctctg G/A aatgcagtgatcagttgaca	2622
NDUFA10	5	intron4 + 236	ctgtgaaagcagattggagc C/T ctggacctcaaacacacgca	2623
NDUFA10	6	intron4 + 1742	tgtcggcatctgctgagtgt C/T tgctgaagtctgaggactgg	2624
NDUFA10	7	intron4 + 2090	ggctgggggaaagcagatca T/C gttggctaaaggacaggtgg	2625
NDUFA10	8	intron4 + 3054	cagctgattatactactgaa A/C cgggataaatgcagcttgat	2626
NDUFA10	9	intron4 + 3066	ctactgaaacgggataaatg C/T agcttgatgattttcagctg	2627
NDUFA10	10	intron4 + 3377	gtcacagtttaaatgctgct G/A ttttactctgtgtaagtagc	2628
NDUFA10	11	intron5 + 46	aagcatctctattttgaatg T/C agatcagcactaaaagccct	2629
NDUFA10	12	intron8 + 1465	gcaacgcccagttcctggta C/T aggcctcatatccagcgtgc	2630
NDUFA10	13	intron8 + 1809	cctggaggcacaaggatggc C/A ggggcactcaacttccctct	2631
NDUFA10	14	intron8 + 11226	gttgtgtgactgtgtggggc A/G tctcacctctcgggctgcag	2632
NDUFA10	15	intron8 + 11319	atcttgccttccctcctgcc G/A tctgttcaggcttgaatcct	2633
NDUFA10	16	intron8 + 11386	ccataatcctagcttgaacc C/T tcctttttccctgctgaccc	2634
NDUFA10	17	intron8 + 12301	acataattattgtaaacatg C/T cgcttaccagtgacattcat	2635
NDUFA10	18	intron8 + 13361	ccaggccactgattgctttc G/A cattttctagcattttctta	2636
NDUFA10	19	intron9 + 183	tttctgtgtggaaagctgat G/A aagtcctcagatgacagccc	2637
NDUFA10	20	intron9 + 6669	aataataatgaccatttctg G/T aaattcatagaattcctttt	2638
NDUFA10	21	intron9 + 8028	gaggacattccacagaacgt G/A tgactattagagcagaaggt	2639
NDUFA10	22	intron9 + 10742	ctggaggagaggggtggagc C/G agttcagccagcactggggt	2640
NDUFA10	23	intron9 + 10985	agaaagggttacacaggagc A/G cacttctcagggagtggtgt	2641
NDUFA10	24	intron9 + 10989	agggttacacaggagcacac T/C tctcagggagtggtgtgacg	2642
NDUFA10	25	intron9 + 12601	ctgtgaatcctctcacctgc G/A tgaagggcctggctgcctct	2643
NDUFA10	26	intron9 + 13908	cacattgttatgtaaccaag C/T ctggaattgcagtgtgaaga	2644
NDUFA10	27	intron9 + 13911	attgttatgtaaccaagcct G/T gaattgcagtgtgaagaact	2645
NDUFA10	28	intron9 + 14064	tcttgactattagaaaccct A/G tcagataaatttaaaacag	2646
NDUFA10	29	intron9 + 14184	tggctttggttgggaacagc G/A agagatacagaaccgacggt	2647
NDUFA10	30	intron9 + 16487	cttgaagctgatcgttccct C/A cttgaagctgatcgttccct	2648
NDUFA10	31	intron9 + 16779	gccagacgtgactgctttag G/A ttcctcatgacattcagacc	2649
NDUFA10	32	intron9 + 17663	ttccaaatcaccccagaact T/G tgcagtattttgaagctcct	2650
NDUFA10	33	5'flanking - (1668-1659)	gtaaaattgttttaactaga (C)9-11 ttcctaaaccaaggtataaa	2651
NDUFA10	34	5'flanking - (1355-1334)	ctgtatccattggaaggcac (A)15-21 tgcaaaggaaacaaggcaaa	2652
NDUFA10	35	intron1 + (46-61)	tggcggggtggcagggtggc GGGGTGGCGGGGTGGG/△ gag cagttccacatctcccc	2653
NDUFA10	36	intron4 + 2486	ctcactggaacttttttttt T/△ aatttaatttttaaaatttt	2654
NDUFA10	37	intron7 + (1600-1601)	cacttccattctgactgtta (A) cggtgtgattcttcctgcca	2655
NDUFA10	37	intron7 + (1600-1601)	cacttccattctgactgtta cggtgtgattcttcctgcca	2656
NDUFA10	38	intron9 + 1054	gcgcgtgctgtttctcccttt A/△ tctgtccttgtacacgtgtg	2657
NDUFA10	39	intron9 + (8161-8172)	tttctcgctttctgggagac (T)10-12 aatgttgaaaatatgtgttt	2658
NDUFA10	40	intron9 + (8646-8647	aattcccccattgcttctct (TT) ctgtagacattttaaaccta	2659
NDUFA10	40	intron9 + (8646-8647)	aattcccccattgcttctct ctgtagacattttaaaccta	2660
NDUFA10	41	intron9 + (16503-16523)	ccctccttgaagctgatcgt TCCCTCCTTG AAGCTGATCGT/△ gtccaagatagttgctagga	2661
NDUFA10	42	intron9 + (17905-17936)	caaatatatgtatacatgta (CA)12-18 tccttcatgaaaactctttc	2662
MGST1	37	5'flanking - 1376	ttaataaatgtttattcaat T/G aaaccaactgctaatattct	2663
MGST1	38	intron1A + 147	cctggagattttaactttct G/A cgaagtttttaaaaacaact	2664
MGST1	39	intron1B + 36	ggagaaggggaccgcatgca A/G agggtggcaggcagggaggg	2665
MGST1	40	intron1C + 456	ccccttgggacggttctcac C/T tgtgccccacttccccagtc	2666
MGST1	41	intron1C + 719	gcccgcaagcattgctgtat A/G gcacccaggcctccagtgag	2667
MGST1	42	intron1C + 985	cgagtaaaatttttctaccg C/G tttgttttagagtggtgtct	2668
MGST1	43	intron2 + 3083	aaaaaatttgtagatatggg T/G actccctatgttgcccaggc	2669
MGST1	44	intron2 + 3106	tccctatgttgcccaggctg A/G tcttgaattcttgggctcaa	2670
MGST1	45	intron3 + 1703	ttctcttctaagaagaagtc T/C gtgcagatacttagcacaaa	2671
MGST1	46	intron3 + 2557	tccagcatcttcccctttcca T/C ttttaagttagactttttttt	2672
MGST1	47	intron3 + 3032	agagacatttagaatatatt C/A cctttaaaggtagagaataa	2673
MGST1	48	intron3 + 3045	atatattcccttaaaggta G/C agaataacccttcactgaga	2674
MGST1	49	intron3 + 3289	ggtttatagtgttccccccc T/A ccccgcccccaaaagaccca	2675
MGST1	50	intron3 + 3885	gaagctgccgctccaggaag G/C agtctgtcgttggagaagag	2676
MGST1	51	intron3 + 3976	ggaaagctggggaactgttt G/T cctggaacagagtctcaaaa	2677
MGST1	52	intron3 + 4298	tgtcaactgcgtaacacagg C/T gtagaagtggacattgtttt	2678
MGST1	53	intron3 + 4519	tttaatagaaaatggtattc C/T tgtcttttcttccatctc	2679
MGST1	54	3'untranslated + 603	gggtaaacccattttgaata T/C tagcattgccaatatcctgt	2680
MGST1	55	3'flanking + 147	tatttgctttccttctctct C/T tgttttctttttctctgaaa	2681
MGST1	56	3'flanking + 237	cagcacgtttttcctatgaa C/T aagacattctccaaataact	2682

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
MGST1	57	3'flanking + 1318	tggctctgtgtgcatgaaca T/C gcacgcgtgcacgcgcacac	2683
MGST1	58	3'flanking + 1331	atgaacatgcacgcgtgcac G/A cgcacacacacacacacaca	2684
MGST1	59	intron1C + (904-923)	tgcgattatctttggtaatt (A)18-20 ggcaaatcagtccaaatttg	2685
MGST1	60	intron1C + (3433-3434)	ccccttcaatactagaacaa (AA) gcagacacattaaatgttac	2686
MGST1	61	intron1C + (3433-3434)	ccccttcaatactagaacaa gcagacacattaaatgttac	2687
MGST1	62	intron1C + 5146	actatttcaatttttttttt T/△ ggaggggggagacagagtctc	2688
MGST1	63	intron2 + (552-563)	cccagcattataagaatgac (T)9-13 aagtgcagatgtggggaggg	2689
MGST1	64	exon3 + (172-173)	tagcatttggcaaaggagaa AA/△ tgccaagaagtatcttcgaa	2690
MGST1	65	intron3 + (152-158)	agaaaactggatgtctgaaa TTGACA/GTCCAATAT cactg cacttgtatgtgttg	2691
MGST1	66	intron3 + (2198-2200)	ggattttagattcctcccta CTA/△ ttctttccgaccttccaccc	2692
MGST1	67	intron3 + (2571-2580)	tttccatttttaagttagac (T)9-10 cacctctctcgttacttcag	2693
MGST1	68	intron3 + (4682-4683)	tcctcttcatgtctctatgt (GAGATGTTG TGGCTCACAT) agtcatcctctttgtgagac	2694
MGST1	69	intron3 + (4682-4683)	tcctcttcatgtctctatgt agtcatcctctttgtgagac	2695
MGST1	70	3'flank + (1359-1360)	acacacacacacacacacac CC/△ tgctctggagttgggcaact	2696
MGST1	71	3'flank + (1889-1891)	ttagaatagtttctaactat ACT/△ tttactcccaagagaagctt	2697
HMG17L1	1	3'untranslated + 864	ctttctgatttttgatagtc G/C gttgaagaagggagtttgaa	2698
UGT2A1	1	5'flanking - 1602	ataacatcttctgcagagaa A/C cttcaatggaaatacactca	2699
UGT2A1	2	5'flanking - 1480	tacagattatctttggtgat G/C ggagagcttagaagagacat	2700
UGT2A1	3	5'flanking - 1406	atttcagaagatttattaac A/T tgaaaaggatcactctgctt	2701
UGT2A1	4	5'flanking - 1388	acatgaaaaggatcactctg C/T ttattcacagacatatgcat	2702
UGT2A1	5	5'flanking - 935	aaattattcaatctctttgg G/A cagtggtttctttttctttg	2703
UGT2A1	6	5'flanking - 287	cctgaatgtagagttgagat G/A tacagaagctttatccaatt	2704
UGT2A1	7	5'flanking - 128	gagaagtaagacacattacc C/T ataaatctgtaaatatccta	2705
UGT2A1	8	intron1 + 535	cattgatcagggtgatttat C/T catgctaagcttatttaatt	2706
UGT2A1	9	intron1 + 642	tatattgatcatgttgatac A/C tttatacacatatttgtcta	2707
UGT2A1	10	intron1 + 1221	ttttaatctaataagcaatt C/G aggaccatctaaagggaaat	2708
UGT2A1	11	intron1 + 1448	aggtgcttacaggcaacatc C/T acatagcagtctgtggctgg	2709
UGT2A1	12	intron1 + 2000	gacacattagcttcttttct A/G cagatctctgttctaaaaca	2710
UGT2A1	13	intron1 + 3118	cttaaaattctttaatgaaa T/G cattgcaacaaatttatatc	2711
UGT2A1	14	intron1 + 3191	ataaatagaacaactcccta A/T gtttacttctctgcagtgga	2712
UGT2A1	15	intron1 + 3770	atcaccagataatttactat C/T cattaaggagtaggtcatca	2713
UGT2A1	16	intron1 + 4584	tgattggttagaatctttga A/C aaatcttctagtatcattcc	2714
UGT2A1	17	intron1 + 4854	tactctgtgcattgttaata G/A cctatcacttgtggtctgcc	2715
UGT2A1	18	intron1 - 19146	ctgtttaaattctcattcaa C/T ggccacatggttaaaataaa	2716
UGT2A1	19	intron1 - 18346	atggcaatatttttagaaat G/A ttaactcccaataatgaata	2717
UGT2A1	20	intron1 - 18218	tatatcattattttaactta T/G agatagcactagccctaatt	2718
UGT2A1	21	intron1 - 17937	ctcctaataatttggactca C/T catacttattcagcactatc	2719
UGT2A1	22	intron1 - 12585	ttccacacagggacaagtca A/G cagaggaaatttttcttgct	2720
UGT2A1	23	intron1 - 11430	aacaaaggtttattttctta C/G agttctgatggctagacgtc	2721
UGT2A1	24	intron1 - 10761	tttaaaatatgcatgtattt T/G ccacttttaaaaactatatc	2722
UGT2A1	25	intron1 - 381	aaatcctccctccttccttc C/T tttcccaggccccactctac	2723
UGT2A1	26	intron1 - 329	ttcccttttctccttttctcc A/G tctctctctcttcctctctc	2724
UGT2A1	27	intron1 - 41	ttttctcctcagcaaacata T/A aagctaatttcctccatcca	2725
UGT2A1	28	intron2 + 263	caccttgatactggacttgg T/C gggacagaaaaccagatcat	2726
UGT2A1	29	intron2 + 454	agaaagcccattgaaataag G/C cagggtttttaggttttaat	2727
UGT2A1	30	intron2 + 554	aaaaactttttgagttgac A/T atggtgagtttagtttctga	2728
UGT2A1	31	intron2 + 1113	ctgcaggcaagctctagtga A/T tgtttattataggaaataat	2729
UGT2A1	32	intron2 + 1304	gacaaatcagccatgtttta C/T aatagcagacattatgccat	2730
UGT2A1	33	intron2 + 1305	acaaatcagccatgttttac A/G atagcagacattatgccatt	2731
UGT2A1	34	intron2 + 1367	atcgatataggctttgggaa A/C tatgaataccaaccatgggt	2732
UGT2A1	35	intron2 + 2074	aaatttttttcttagacctat G/T aatcaaaggaggcatacagt	2733
UGT2A1	36	intron2 + 2164	attttattagatataactgg A/C atgctaacaattttaaaagc	2734
UGT2A1	37	intron2 + 2298	taacaatttcagttagcatg A/C gaagagttgtcccttattta	2735
UGT2A1	38	intron2 + 2346	tttctgtaatggttttgctt T/C catgcttggacttgtaatca	2736
UGT2A1	39	exon3 + 922	gtgttgtggtgttttctctg G/A gatcaatggtcaaaaaccttt	2737
UGT2A1	40	intron3 - 217	aagcttagaagtgataaata T/C caaaacaataatactatact	2738
UGT2A1	41	intron3 - 194	aaacaataatactatactgg G/A tagactattagtacaagact	2739
UGT2A1	42	exon5 + 1171	acggagtccctatggtggga G/A ttcccatgtttgctgatcag	2740
UGT2A1	43	intron5 + 1546	tttttaaaattcagaaactc A/G gttatggtgtattcttacaa	2741
UGT2A1	44	intron5 + 1547	ttttaaaattcagaaactca G/A ttatggtgtattcttacaaa	2742
UGT2A1	45	intron5 + 2013	atcatattcattaccctccc G/T ctattattgtattttgaatc	2743
UGT2A1	46	intron5 + 2318	aatttagtgctttttcttaa C/T ggaagtaacctgcttaaaaa	2744
UGT2A1	47	intron5 + 2505	taattgacttttattaatac G/A tacatgttgtataagtcata	2745
UGT2A1	48	intron5 + 2639	tagactattacaaagttgtt A/G gttgctgacaattttgttca	2746
UGT2A1	49	intron5 + 4009	gaatccaggctggaactttt C/A ttccagacacaaaccaaaat	2747
UGT2A1	50	intron5 + 4311	atacagacactgtccttttc G/A tcacaaacatacagatgtgt	2748
UGT2A1	51	intron5 + 4545	agctcacacagtatcaaaat T/C atttttggaaaaattatgct	2749
UGT2A1	52	intron5 + 4616	actttttttatgtctacattt G/C atcatactgtgttaagcata	2750
UGT2A1	53	intron5 + 4717	tgcaagaattatattttctc C/A acgtaactatggccttaaac	2751
UGT2A1	54	exon6 + 1524	gctatatttttggtcataca A/G tgttgtttgttttcctgtca	2752
UGT2A1	55	3'untranslated + 1683	aaggagtttaacaaaaacac G/A tctcccatcctgtttccaaa	2753
UGT2A1	56	3'flanking + 685	aatctagaaaataattatca T/C ttttataaaatttttagtca	2754
UGT2A1	57	intron1 - (18967-18965)	ctcccaattagattgattag TAT/△ gagttcctggggttactggt	2755
UGT2A1	58	intron1 - (18862-18803)	aatacattcttccccccttca (AC)14-17 atgcttactggcctatttat	2756
UGT2A1	59	intron1 - (17463-17447)	aaacttagaaacctctattc (A)16-27 gtaaagaaaatggcagagaa	2757
UGT2A1	60	intron1 - 10860	attcaatgcaacttttttttt T/△ gtaatggcagaattagaaca	2758
UGT2A1	61	intron2 + (528-538)	ctgttaggaaacaattggtt (A)8-10 ctttttttgagttgacaatgg	2759
UGT2A1	62	intron2 + (1514-1533)	ttgtgtgtatgtgtatgttt (GT)9-11 tattttaatgaattaatatc	2760
UGT2A1	63	intron5 + (916-917)	gcttagtatattatatatat AA/△ gtctatatatagcttagt	2761
UGT2A1	64	intron5 + 1163	caatatttatgtcatttttt T/△ ctcacatttactctgtttcc	2762
UGT2A1	65	intron5 + (3819-3838)	agacagacagacacacaaac (AC)8-12 tcaacacatgtaaactactc	2763
UGT2A1	66	intron5 + 4785	tatcttcaatgaaaataaaa A/△ caaaaattgtctaatttctg	2764
OATP1	1	5'flanking - 916	acagagtagatgttcaataa G/A tatttgttgtatctgtgaga	2765
OATP1	2	5'flanking - 843	tagtgcagcgactatgcctt G/A atgtgtgtgtgtttgggatt	2766
OATP1	3	5'flanking - 526	aaatgtgtgcctgtatgtta T/C acatctgtacatatatttcc	2767

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
OATP1	4	5'flanking - 172	acaaacacaactcaaagtat G/A tgtgttattaaaagtagcta	2768
OATP1	5	intron1 + 206	ttgattcaggcaagttagtc C/G taaatggctttgagagactt	2769
OATP1	6	intron1 + 454	caacataacaataatttcct G/A taagaaaaatggccattttg	2770
OATP1	7	intron1 + 999	gtttagcaaggttagatatt A/G atgtggatgttaagacaaaa	2771
OATP1	8	intron1 + 1223	ttgctagaagctagtaggac C/T agctttataaatacagagat	2772
OATP1	9	intron1 + 1326	aactagttaggcaacccatg T/C gttttaggggaaaagcaatg	2773
OATP1	10	intron1 + 1336	gcaacccatgtgttttaggg G/A aaaagcaatgaggtcatgat	2774
OATP1	11	intron1 + 1498	atagtttgctcttaagaata C/T actctgagaaggtttatagt	2775
OATP1	12	intron1 + 5041	ttatgctcccgaggagttag C/T tctctaaatgcataaggaga	2776
OATP1	13	intron1 + 9532	aaagactgggagcacttccc A/G atgacaaatactagactaga	2777
OATP1	14	intron2 + 198	ttacctcatattaacaccta A/C atattgccacatatcctacc	2778
OATP1	15	intron2 + 961	aaaaagttatatagaaatat A/G agtgtcactcctttctagtt	2779
OATP1	16	intron2 + 1110	gtctactagtgttcaactcc T/C ttagatcttagcctgtatca	2780
OATP1	17	intron2 + 1419	aaagcctaagaaggatgcag T/C gcaatagcctatgtgagaag	2781
OATP1	18	intron2 + 3339	tatggtttgcaaaaaactta T/C tcgtatatttgtttttttca	2782
OATP1	19	intron3 + 66	caggaaatgaagttgcactt T/C cctctctaggagcaatgctt	2783
OATP1	20	intron3 + 205	tcagttttgtcaatttacac A/G atggggatttgggacctttt	2784
OATP1	21	intron3 + 6377	aatgaatagactttgagtta C/T tggatttttagtggataaat	2785
OATP1	22	intron3 + 7238	tgaatgtcacatttttttaaa G/A tttgtgttccttatctcata	2786
OATP1	23	intron4 + 1016	ttttattctggattcatgtt T/C gtggaaattgcagtagtcca	2787
OATP1	24	intron5 + 110	tccacaatgatgagtagagt A/G tcttggcacagttggccttc	2788
OATP1	25	intron6 + 496	agtgtctgaattataagcca A/G ttttatagttggttgggacc	2789
OATP1	26	intron7 + 1934	aaagtgaaaggaaattaaaa G/C tgagaacttgagcctgaatg	2790
OATP1	27	intron7 + 2140	tagaatgtaccaaatgaatc A/G gcatctctgaggatgggacc	2791
OATP1	28	intron7 + 2365	tgaaatcttctttatcaact C/T gattttcctccagactttac	2792
OATP1	29	intron8 + 88	gcaaactcctaagttgaagt G/C ttttaggatatttttttgact	2793
OATP1	30	intron9 + 534	tcatattttgtattttaaag G/A ttatctgggttttactgaaa	2794
OATP1	31	intron9 + 1286	tattcttctgagataaatca T/C tgaaggagtggctatgtggt	2795
OATP1	32	intron11 + 215	ttcactcctattcctcgcta C/T ttttcttccttatttcttag	2796
OATP1	33	intron11 + 663	ttcttcttctttttggagctc T/A aaagtagagttcagttaatc	2797
OATP1	34	intron11 + 999	atcatcactgcatgagagtt A/G gaattatctaactttgtgat	2798
OATP1	35	intron11 + 16727	tttcttttatttacaaactt A/G tttacttttcaggtgtatga	2799
OATP1	36	intron12 + 48	ctatcagaacaatattatta T/G tattatttttattacactt	2800
OATP1	37	intron12 + 686	tatgttttgataaactttgc C/A gtacaaataaagaaaattga	2801
OATP1	38	intron12 + 708	tacaaataaagaaaattgaa A/G tatttccaaataaatcaagt	2802
OATP1	39	intron13 + 418	tctctggtctccaaaatcat A/G tattttctccctctttacat	2803
OATP1	40	intron13 + 436	atatattttctccctcttta C/A attttgctgaaacaatcttc	2804
OATP1	41	3'untranslated + 2130	gtctttaagaacctaaaaaa C/A ctcttaactcaaaataataa	2805
OATP1	42	3'flanking + 57	agtgactaaagtttttctta C/A aaacaagtgtctgaatcaaa	2806
OATP1	43	3'flanking + 572	aatacactatggttatttat G/A tgtactataaatggagtgag	2807
OATP1	44	3'flanking + 788	atttcctaaatgatcagatg C/T atcatatgaaaaaagaaagc	2808
OATP1	45	3'flanking + 1356	aggtgactgacataaatggg G/A gcagaggacataatgaggtt	2809
OATP1	46	5'untrnslated - (189-188)	attttctaatctgtattaaa (A) gcgttccaggtatttttgta	2810
OATP1	47	5'untrnslated - (189-188)	attttctaatctgtattaaa gcgttccaggtatttttgta	2811
OATP1	48	intron4 + (725-726)	tgatctttaatagcggggaa AA/△ caggcaagtacgctatagtt	2812
OATP1	49	intron4 + (1082-1083)	attgagtcaggaaaccaaaa CA/△ gtttcaaaaatttgaaaaat	2813
OATP1	50	intron4 + 2301	aatgtcatgtctttttttt T/△ aatgcagagtgtacaaagga	2814
OATP1	51	intron9 + (241-246)	attgtatgtgcatgtgggtg TGTGTG/△ catgattgtctttgtgatat	2815
OATP2	1	5'flanking - 2574	ggataaggcaacccctatgt A/G tcactgctgcaggagaggga	2816
OATP2	2	5'flanking - 2366	aacataggaatgtgcagagc C/T ctgtggggattagagaagag	2817
OATP2	3	5'flanking - 2244	tgatgatgccagagctttga T/G cattggtgggtatagaaaca	2818
OATP2	4	5'flanking - 1723	tctttcagacttcaaaggcc A/G tgatatttcatcagagctgt	2819
OATP2	5	5'flanking - 1180	tgcttatttaacaggcataa T/G ctttggtctcctgagccaga	2820
OATP2	6	5'flanking - 811	tatgtgcatatgtgtataca G/A gtaaaagtgtgtatatatgt	2821
OATP2	7	intron1 + 7188	aatcatttgaaatttaagaa A/G aaaatatgttcagagaaaaa	2822
OATP2	8	intron1 + 7331	gtgaaatgaggaacaaagtg T/C ccacctttttttcctgaata	2823
OATP2	9	intron1 + 7391	agagagatgtgaaatagtat T/G tttctggggaagtaggggaa	2824
OATP2	10	intron1 + 7886	ttgttagtagaaagaaaatc G/A aagcctaaaactaaaggaag	2825
OATP2	11	intron1 + 7958	ttgctattatataatttttt T/A aaaaaaagatttcctaatat	2826
OATP2	12	intron1 + 7959	tgctattatataatttttt A/T aaaaaagatttcctaatatt	2827
OATP2	13	intron1 + 8036	ggaaaaaatggggtgaaatt A/T atcaaagggcagcttattac	2828
OATP2	14	intron1 + 9164	acattatattctatataaaa G/T agtcagttgaagtaaaaagt	2829
OATP2	15	intron1 + 10123	tctgtctttcctacttttgt T/G tccagcattgacctagcaga	2830
OATP2	16	intron2 + 193	tgattaagtatttctttggc G/A aaatttttgatgcttaatag	2831
OATP2	17	intron2 + 1020	ttgagtaacatttaggccaa G/A tggcagtcataaggaaaaag	2832
OATP2	18	intron2 + 14865	agaggaattaatcataagag G/T tttatttggctaaagtgaca	2833
OATP2	19	intron2 + 14931	gttagttaataacagaaaaa A/T tatcagaaattttaaaaaat	2834
OATP2	20	intron2 + 15417	ttctaaaataagtaagctaa A/T tattctatattatactacta	2835
OATP2	21	intron2 + 20823	ttgtataagagatacaaaac A/C aattcctactaggggaaata	2836
OATP2	22	intron2 + 20852	ctaggggaaataaagcttca G/C taaggaggtggcattaagct	2837
OATP2	23	intron2 + 20930	atggagagaagcagcagtgt A/G ccacagataaatgaagtgag	2838
OATP2	24	intron2 + 21360	ttcaaaagctgtatttctca T/C tagtgctttttgtgaataaa	2839
OATP2	25	intron2 + 21467	tatatacacaatacctgtcc A/G gaagatgtggtataagccaa	2840
OATP2	26	intron2 + 21621	tatcaatacttatgaagaga A/G ctaactattctaactaggga	2841
OATP2	27	intron2 + 22760	ttccccacctcctgttggtt C/G tcctcttaaacttctccttg	2842
OATP2	28	intron2 + 23199	cctatctgcacataacatta C/T aaacttatggcaattataaa	2843
OATP2	29	intron2 + 23218	acaaacttatggcaattata A/G aactcaatacatattatact	2844
OATP2	30	intron2 + 23330	gcccttgttcctgttcctct G/A tacctgcctcaactacatag	2845
OATP2	31	intron2 + 23673	ctggagacggtagctcaaac T/C gaggatgaaaatagacattt	2846
OATP2	32	intron3 + 89	ggttatcaactggggtaaat T/G tatctctcacaggcaatttg	2847
OATP2	33	intron3 + 224	tgctaaatattctataatgc A/G caaagaatgatgtaactgaa	2848
OATP2	34	intron4 + 97	ccctttaaataggcagttac C/A ttttgagaagatacccacta	2849
OATP2	35	intron4 + 568	ttcatgatccaaattgtggc A/G acgtatttccaggcaacaag	2850
OATP2	36	intron4 + 599	aggcaacaagatagaagaag A/G aaagaataagaagcaacaaa	2851
OATP2	37	intron4 + 753	aaaatagacattattccaag T/A taccaagttcccggttaaaa	2852
OATP2	38	intron4 + 781	ttcccggttaaaaatcccaa G/C tataattactgtggaaggaa	2853
OATP2	39	intron4 + 1196	aaggaccacaatctagatca G/T cattgctctaaatatgccat	2854

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
OATP2	40	intron4 + 1229	tatgccataatatgtgacac T/C tttgcacctggtatttctac	2855
OATP2	41	intron4 + 1623	catctagttgaaatggatta G/C attttatttttactacattt	2856
OATP2	42	exon5 + 388	attctaaagaaactaatatc A/G attcatcagaaaattcaaca	2857
OATP2	43	exon5 + 452	taatcaaattttatcactca A/G tagagcatcacctgagatag	2858
OATP2	44	intron5 + 165	ttaatatacacagttcgccc A/T ttaacaacacaggtttaaac	2859
OATP2	45	intron5 + 189	acaacacaggtttaaactac G/A cgttttcacttctatgcaaa	2860
OATP2	46	intron5 + 191	aacacaggtttaaactacgc G/A ttttcacttctatgcaaatt	2861
OATP2	47	intron5 + 507	atataactttgctttcattg C/T aaaaggcaaactgttatatc	2862
OATP2	48	intron5 + 520	ttcattgcaaaaggcaaact A/G ttatatcatttaaagacttt	2863
OATP2	49	intron5 + 856	agtcatgataaacctaatag A/G ataaaacaacaaaaaagaaa	2864
OATP2	50	intron5 + 1157	acagataatttttacttgtt T/C gtgcttttctgtatgatatg	2865
OATP2	51	intron5 + 1226	ccttgattgtaataatctcc A/C catgccaagagtggggccag	2866
OATP2	52	intron5 + 1228	ttgattgtaataatctccac A/C tgccaagagtggggccaggt	2867
OATP2	53	intron5 + 1304	actgttctcgtggtaatgaa G/T aagtctcacaagatctgatg	2868
OATP2	54	intron5 + 1348	ttataaatgagagttcccct G/A caaaagctctcttgcctgcc	2869
OATP2	55	intron5 + 1407	ttgctcttccttcatcttcc G/A ccatgattgtgaggcccccc	2870
OATP2	56	exon6 + 521	gtcatacatgtggatatatg T/C gttcatgggtaatatgcttc	2871
OATP2	57	exon6 + 571	gggagactcccatagtacca T/C tggggctttcttacattgat	2872
OATP2	58	exon6 + 597	ctttcttacattgatgattt C/T gctaaagaaggacattcttc	2873
OATP2	59	intron7 + 33	agaacaaggtaccatgataa C/T gtctttctaagcacacatgc	2874
OATP2	60	intron7 + 267	caaaataaccaaatgtaaaa T/A gtctccctcccaaactgact	2875
OATP2	61	intron7 + 1260	gtaatctcacatttctctgc A/G tttacacttggtaaaacttt	2876
OATP2	62	intron7 + 1386	agtctcaaattaatagccaa G/A agcatgcctttattgtaacc	2877
OATP2	63	intron7 + 1472	ctttaccacatgacagaatg G/A catgttcttagcaaataata	2878
OATP2	64	intron7 + 1697	tttacatgttcaattttaga C/A atatgccttagagtagctac	2879
OATP2	65	intron7 + 2273	ttctcacgtcctatctagcg C/T gattatgacccttagttact	2880
OATP2	66	intron8 + 207	gtggaagagaattaggtttg T/C acttttagcagggagaaac	2881
OATP2	67	intron8 + 546	tcgggagaagtttctcccta T/C gtaattagagtaatatttat	2882
OATP2	68	intron8 + 565	atgtaattagagtaatattt A/C ttttggtaattatctatcta	2883
OATP2	69	intron8 + 668	taagtaatgtaaattaggat G/T catcagcatttgacagtgcc	2884
OATP2	70	intron8 + 739	tggagaaccattgagagtca A/G taaacaaagagaatgacttg	2885
OATP2	71	intron8 + 2193	tgatcacagatccaaatgac A/G taatttctaccatgaacaga	2886
OATP2	72	intron9 + 112	attttagtaatacaggataa G/C tataattttcttgtattctt	2887
OATP2	73	intron9 + 266	ttagaggtagtatctgtata A/G ttggatcttataatttagtg	2888
OATP2	74	intron9 + 305	tgctaagatctgagacaaac C/G cttttgtaattataatcatt	2889
OATP2	75	intron9 + 888	aggttctgtatgttttttaa T/C aaatgacaaagatatattaa	2890
OATP2	76	intron11 + 10224	tacacttgttccataaaaaa T/C tcctctatattattcctagt	2891
OATP2	77	intron11 + 10359	attaatagattcaacgtgag G/C ttcccttaaactttagccta	2892
OATP2	78	intron11 + 10916	cttatatagaaagaaatcca C/G aaaactattttacctttttat	2893
OATP2	79	intron11 + 10997	aatatattagtttgaacaag T/C gagacttcactaaatataat	2894
OATP2	80	intron11 + 11018	gagacttcactaaatataat G/A caatgtatttgcagcactgt	2895
OATP2	81	intron12 + 442	aacattccaaaactttaat C/T gactcacagcatgacttta	2896
OATP2	82	intron12 + 445	attccaaaactttaatcga C/T tcacagcatgacttttataa	2897
OATP2	83	intron12 + 447	tccaaaactttaatcgact C/A acagcatgacttttataata	2898
OATP2	84	intron12 + 907	aatgaaaagaagctggcaga T/C tgaaacatactgaatgagag	2899
OATP2	85	intron13 + 65	tatatatatatatatatata C/T acacacacatacatatatta	2900
OATP2	86	intron13 + 870	aattctgagtatcctatttc G/A atgtatccaatctgtggcac	2901
OATP2	87	intron13 + 1935	taaaaaaaaaaaaagtctgc T/C tttacagcaattgagccaag	2902
OATP2	88	intron13 + 2261	aacgaatcctccaaatttttt G/C aacttttatttaatcaaaat	2903
OATP2	89	intron14 + 248	tcaaggataataaccaactt G/A tcaaaaatcagagataataag	2904
OATP2	90	intron14 + 2463	atttgtttactaatatggaa C/G cttcttcaagacatattttt	2905
OATP2	91	intron14 + 2857	tcatcatgtatttccaggac A/T cctggcaagatgctcctcag	2906
OATP2	92	intron14 + 11458	atctccagaggtcctgctgt C/T tccccaaagtccactgaccc	2907
OATP2	93	3'untranslated + 2243	ataataaaacaaactgtagg T/C agaaaaaatgagagtactca	2908
OATP2	94	3'untranslated + 2404	tcttaataaaacaaatgagt A/G tcatacaggtagaggttaaa	2909
OATP2	95	3'untranslated + 2515	cagagtttgaactataatac T/G aaggcctgaagtctagcttg	2910
OATP2	96	3'untranslated + 2539	gcctgaagtctagcttggat A/G tatgctacaataatatctgt	2911
OATP2	97	intron1 + 457	taattggcaaacataaaaaa (A) caggtgtctcaaagtcacat	2912
OATP2	98	intron1 + 457	taattggcaaacataaaaaa caggtgtctcaaagtcacat	2913
OATP2	99	intron1 + (7537-7538)	gatcagcattacaaccaaga (G) atggagaatgacattcagga	2914
OATP2	100	intron1 + (7537-7538)	gatcagcattacaaccaaga atggagaatgacattcagga	2915
OATP2	101	intron1 + (10032-10035)	tgtgtgattctatattactt ACTT/Δ gtttcaaatttctctccaca	2916
OATP2	102	intron1 + (10058-10061)	ttcaaatttctctccacaaa TTTA/Δ tttttctattaaattgtaat	2917
OATP2	103	intron2 + (413-423)	acttatttaaaaattctttt (A)11-13 caaaaaacaggatttaaaaa	2918
OATP2	104	intron3 + (1595-1603)	ttgccaagtaattcaagtgc (T)8-10 gtatttaaaacaacttttca	2919
OATP2	105	intron4 + (10-23)	ttcatgggatagtaagtgtt (A)12-14 cctctgtgccactatcagta	2920
OATP2	106	intron5 + (1567-1572)	gtgaatataaattacttgta CTTGTA/Δ aattaaaaaaaaaataagtag	2921
OATP2	107	intron5 + (1577-1585)	attacttgtacttgtaaatt (A)9-10 taagtagaataattaagagt	2922
OATP2	108	intron8 + (1939-1941)	ttctctaactccttctactc CTT/Δ atttcaagcagatgcaactg	2923
OATP2	109	intron10 + (3077-3078)	aaattctttatctacttttt (CTT) ttccctctttctctgctttc	2924
OATP2	110	intron10 + (3077-3078)	aaattctttatctacttttt ttccctctttctctgctttc	2925
OATP2	111	intron11 + 11011	aacaagtgagacttcactaa A/Δ tataatgcaatgtatttgca	2926
OATP2	112	intron12 + (1160-1169)	agcatgacatggtagagatg (A)9-11 gcatttttaacatttgttaa	2927
OATP2	113	intron12 + (1310-1312)	tccatcttaatataaaatgt TGT/Δ ctactcaaaaggagaagtct	2928
OATP2	114	intron13 + (9-34)	tacgagcactaggtatgatg (A)24-27 tatatatatatatatata	2929
OATP2	115	intron13 + (35-64)	aaaaaaaaaaaaaaaaaaaa (TA)10-21 cacacacacatacatatatt	2930
OATP2	116	intron13 + (1379-1387)	aaaattattcaccacaatac (A)8-10 caaagtaaagttatgaacac	2931
OATP2	117	intron13 + (1916-1928)	aattctcttaaaataatgtt (A)11-13 gtctgcttttacagcaattg	2932
OATP2	118	intron14 + (588-596)	caattatactttacctcttt (A)8-10 ctaatttcaaattcatatat	2933
OATP8	1	5'flanking - 1413	aataggggcttaataactct G/C aaacttatgatttctcatat	2934
OATP8	2	5'flanking - 1345	gaatttatcctacagatatg A/G ccacacagaaaatgacatat	2935
OATP8	3	intron1 + 38962	atgaaattagtttaaaaata G/A caaccttaactatactcctc	2936
OATP8	4	intron2 + 253	acagacttaccaacaaagaa T/G tatccttcccaaaatgtcta	2937
OATP8	5	intron2 + 329	actcatggtttgcaaattaa C/G tttttaggaaactttatctc	2938
OATP8	6	intron2 + 2568	ccattctggtgctttctttc G/A tgaaactattttccatcagt	2939
OATP8	7	intron2 + 2679	ctcttattgctcttcttcca T/C gttttaatctaaataattta	2940
OATP8	8	intron2 + 2753	caggaaactttcacaaagcc C/A ctaattaatttaagctccct	2941

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
OATP8	9	intron2 + 3132	tggtttaatgtaggagagtt T/C accttcacagttaaattaca	2942
OATP8	10	intron2 + 3193	aatgtcttgggcatatttgc A/G ttcatttggggcattcagtt	2943
OATP8	11	intron2 + 3207	atttgcattcatttggggca T/C tcagttctactagatacaaa	2944
OATP8	12	exon3 + 334	gaactggaagtattttgaca T/G ctttaccacatttcttcatg	2945
OATP8	13	intron3 + 76	agaattttatttttatactt G/A taagtgggcagttacctttt	2946
OATP8	14	intron4 + 2443	tcaatttcatgttgctctta C/T agttataggtattctaaaga	2947
OATP8	15	intron4 + 67	taatcacgtctataaagttt C/G tgatattctttaacaaaatt	2948
OATP8	16	intron4 + 91	tattctttaacaaaattgat T/A taagaacaaataggaagaac	2949
OATP8	17	intron4 + 197	ggtttgaactgcacctgttc G/A cttatatgcagcttttgtcc	2950
OATP8	18	intron4 + 813	tttaacagaataaaaaaaaa T/A attttgtaacgacaaaagaa	2951
OATP8	19	intron4 + 974	atatgcaccttaaaaataac C/G tggatttttaaatatgtaat	2952
OATP8	20	intron4 + 1003	taaatatgtaatgtacataa G/T gaatattatgcatattttgt	2953
OATP8	21	intron6 + 155	cattaataatcagaataaaa A/G agaaatttagctcctattta	2954
OATP8	22	intron6 + 750	atccaactggggtttagatt T/G cctctttctgcctctcctcc	2955
OATP8	23	intron6 + 780	gcctctcctccatctgcacc C/T tctcttttcctcagcaaaca	2956
OATP8	24	intron6 + 1248	ctatgccctgtaatctcaca C/T ttccctttatttaaaattgg	2957
OATP8	25	intron6 + 1500	tcgtgtctgtgttagcatat A/G ataactcatcagggtttgtg	2958
OATP8	26	intron6 + 2008	ataacataaatgagtaaaga A/G tatcaagggcaggaaattag	2959
OATP8	27	intron6 + 2087	actactctccccatacacac T/C aaaactcatgtgctccccag	2960
OATP8	28	intron6 + 12305	tcatctatggaggactgcaa T/C cattatcattatttcccaga	2961
OATP8	29	intron7 + 363	taacaaatgataccagccat C/G atactattctctggtaatag	2962
OATP8	30	intron7 + 411	cctttatttttttgagaacct G/A gtggatgatattaagacgta	2963
OATP8	31	intron7 + 428	cctggtggatgatattaaga C/A gtatatagatcactgtaata	2964
OATP8	32	intron7 + 634	aaaattatatatatacatat A/G taatcttacctaagtattca	2965
OATP8	33	intron7 + 1791	tgtttttttaagggtagtga T/C gtgaatagtaaagcgaattt	2966
OATP8	34	intron7 + 2000	agttgagcaaattgctctca G/A gtagcataatgtcacttgaa	2967
OATP8	35	intron7 + 2043	gtttattgatccatttttta A/G tggatcaacattgtagtgag	2968
OATP8	36	intron7 + 2171	atttattttgagcaaaggtc G/A cgactctcttagaaagcctc	2969
OATP8	37	intron7 + 2173	ttattttgagcaaaggtcgc G/A actctcttagaaagcctcac	2970
OATP8	38	intron7 + 2179	tgagcaaaggtcgcgactct C/T ttagaaagcctcacaaatca	2971
OATP8	39	intron7 + 2219	atttgtaactttaagtctta T/G ataacttatatttacaaaat	2972
OATP8	40	intron7 + 2261	cagatattaatatatatttt A/T ttattgaaatatgttatttt	2973
OATP8	41	intron8 + 150	acaaaatttctccatcttgt T/C atatcatcgttgttctgcat	2974
OATP8	42	intron8 + 154	aatttctccatcttgtaata A/T catcgttgttctgcatttga	2975
OATP8	43	intron8 + 1303	tttttttttgagatggagtct C/T gctctgttgcccaggctggg	2976
OATP8	44	intron8 + 1372	aagctccgcctcccaggttc T/G ccacccttctcttaaagaaa	2977
OATP8	45	exon9 + 1272	tccttcttgtttcaacttct A/G tatttccctctaatctgcga	2978
OATP8	46	intron10 + 63	tcacagatttgatttaataa A/T tacttatcaaatcttcctat	2979
OATP8	47	intron10 + 911	cttgcccaatatcctaccaa C/T gtattattaaacggcatgga	2980
OATP8	48	intron10 + 972	tcctagtttccttgaagata G/A gctacaactttagtaaactt	2981
OATP8	49	intron10 + 1101	tccctggtcctgtgttgtcc A/T gtagtgaagacctgaaagag	2982
OATP8	50	intron10 + 1103	cctggtcctgtgttgtccag T/C agtgaagacctgaaagagag	2983
OATP8	51	intron10 + 2027	cccattttcatgagtggcta A/G gttttgtccgtttcaaact	2984
OATP8	52	intron10 + 2028	ccattttcatgagtggctaa G/A ttttgtcccgtttcaaacta	2985
OATP8	53	intron10 + 2148	gtattttggaaagaaaatgt A/G ggtggaagagaaatatttta	2986
OATP8	54	intron10 + 2214	atatacagaatttcatacac T/C aatttcttaaattcctaaat	2987
OATP8	55	intron10 + 2316	taaatattttagtttgagac T/G tctttaaatataatggaatg	2988
OATP8	56	intron10 + 2372	tgtatttggcaaatgtattt G/T ttaatatttcaaaaactatt	2989
OATP8	57	exon11 + 1557	cagaacagaaattactcagc A/G cacttgggtgaatgcccaag	2990
OATP8	58	intron11 + 147	tttcttagaattattttgat A/C tttcaataacatcattaata	2991
OATP8	59	intron11 + 10339	aaaaaactgcattttagtgg G/C ttagctagaaaagatttgtc	2992
OATP8	60	intron11 + 10358	ggttagctagaaaagatttg T/G ctcatatacacaataaatta	2993
OATP8	61	intron11 + 10538	caacagaggatcaatgtaaa T/G gaaatctcttaaattaaaca	2994
OATP8	62	intron12 + 55	ataaatattaatgttaaata C/T taaagactgaatgcaattaa	2995
OATP8	63	intron12 + 1802	taaaatgaatcggtaaaaca T/G tcatgtataaatcactgtca	2996
OATP8	64	intron12 + 2612	ataggcatataatactcttt C/A ttccctctgtatatagggag	2997
OATP8	65	exon13 + 1833	aacagctgtggagcacaagg G/A gcttgtaggatatataattc	2998
OATP8	66	5'flanking - (1590-1587)	atatacataacatatacctaTATC/△ tatgttatgtgtctgcttat	2999
OATP8	67	5'untranslated - (11-28)	agcatcagcaacaattaaaa ATATTCACT TGGTATCTG/△ tagtttaataatggaccaac	3000
OATP8	68	5'untranslated - (4-7)	tattcacttggtatctgtag TTTA/△ ataatggaccaacatcaaca	3001
OATP8	69	intron4 + (213-214)	cctgttcgcttatatgcagc (T) ttttgtccaaccaaacagaa	3002
OATP8	70	intron4 + (213-214)	cctgttcgcttatatgcagc ttttgtccaaccaaacagaa	3003
OATP8	71	intron4 + 505	tataactttctctttataaa G/△ atgcaaaatgttatagcatt	3004
OATP8	72	intron4 + 616	aaaaataaatgaagtggagg A/△ aaaaaaatgatttcaagttt	3005
OATP8	73	intron4 + (804-812)	acatccatgtttaacagaat (A)9-11 tattttgtaacgacaaaaga	3006
OATP8	74	intron4 + 855	gagattgtttaaccaaatta G/△ gaaactattattcaacacac	3007
OATP8	75	intron7 + (619-628)	ttttatatatgaattaaaat (AT)4-5 catatataatcttacctaag	3008
OATP8	76	intron7 + (1773-1779)	attttctatattatgaactg (T)7-8 aagggtagtgatgtgaatag	3009
OATP8	78	intron8 + (1270-1290)	tagtgtgccacccttctctc (T)19-23 gagatggagtctcgctctgt	3010
OATP8	79	intron10 + 665	ttctttcttaactcaaaggc T/△ ttttttttccatgtgacac	3011
OATP8	80	intron11 + (247-250)	aaaaatcttaaggcacacac TGAT/△ tgacagttgccttgattgta	3012
OATP8	81	intron12 + (1622-1630)	aaataaattgttggcatcta (T)8-10 atttttctaagggtcgctgt	3013
OATP8	82	3'untranslated + (2464-2465)	gagaaaagcctgatgccttt A/△ aaaaaaaatgaaacactttg	3014
OAT1	1	5'untranslated - 127	gcagctcggactcagctccc G/A gagcaacccagctgcggagg	3015
OAT1	2	5'untranslated - 20	gaaggcctcagccccagcc A/G ctgggctgggcctggcccaa	3016
OAT1	3	intron3 + 150	caatagaacaaccttttctc G/A ggctcatgccgccctgaccc	3017
OAT1	4	intron4 + 211	ttctctggcttcccccactc A/C gttctccagcctgcctgctc	3018
OAT1	5	intron5 + 33	gagacttcccatgataacct C/T ccagggcttcaccccccaaac	3019
OAT1	6	intron6 + 168	gaaccagatgcccccagcct C/T gactcagtcccagtctccac	3020
OAT1	7	intron1 + (58-71)	ggaagatgggggcctttgtt (A)13-15 gtacatggagaaattaactg	3021
OAT1	8	intron3 + (1306-1319)	aataggttgaggaggagcag (A)12-15 tcaagagtgtggaggggca	3022
OAT2	1	intron4 + 842	ttgacctccaaaagtgtttg G/A attacaggcatgggccattg	3023
OAT2	2	intron5 + 33	gtgtgtgtgagcatgcatat C/A tgtgtgtggtggggagtggg	3024
OAT2	3	intorn5 + 183	ccacatccatcattcgagac A/C aactcgtctcagctgccatg	3025
OAT2	4	intorn5 + 184	cacatccatcattcgagaca A/C actcgtctcagctgccatga	3026
OAT2	5	exon7 + 1269	actagactgctagtgtcctc C/T ggtgagcccagtcccatagg	3027

Designation of Gene	No.	Location	Sequence	SEQ ID NO
OAT2	6	3'untranslated + 1792	ataaatgtgtacatgagtgt A/G tgaacacaaatacataaggt	3028
OAT2	7	3'flanking + 1386	tgtagcagcccacatcgcca G/A tgttcacacctgagagagag	3029
OAT3	1	5'flanking - 580	ctgtgtcagagacacagaca C/G ggaggtcctggctgccccag	3030
OAT3	2	5'flanking - 463	ttcctgagaggcaaatcccc T/C tcccctactcgggaggtgcc	3031
OAT3	3	5'untranslated - 16	cctgcccacagctctggctc G/A tcttgccccagtgccatgac	3032
OAT3	4	exon2 + 153	cctgtccaccactgtcgccc G/A ccccacaatgcctccacagg	3033
OAT3	5	intron2 + 177	gcaccaagacccttggcttc T/C tcccactcagagtccaagca	3034
OAT3	6	intron2 + 6201	gctcatcctctctggtcctt T/G tgccccagcacaggttcctc	3035
OAT3	7	intron3 + 79	tctgctccacccgtgcaccc G/C caaagaggcaaagagctggg	3036
OAT3	8	exon5 + 723	tggcgttggctgcagttaac T/A gtgtccattcccttcttcgt	3037
OAT3	9	intron5 + 524	tcgaagtacaaaggaaagtt T/C aaagagaagcctgagcctgg	3038
OAT3	10	intron7 + 386	gaccaatgggtttcagactc G/A aagacaaaaattatgtttat	3039
OAT3	11	intron7 + 754	gcccacgtcagacatgacca G/A tcaatcacagcactttctcc	3040
OAT3	12	intron9 + 81	attgtcctgtcctctaccca G/A gggagccatcctttatgaac	3041
OAT3	13	5'flanking - (661-660)	tacatttggtccccaggggg (G) agcggctgatcaggagagaa	3042
OAT3	14	5'flanking - (661-660)	tacatttggtccccaggggg agcggctgatcaggagagaa	3043
OAT3	15	intron8 + (211-212)	tctgacttggactgggcaaa AA/△ gtatggtggtatctggatag	3044
ALDH1A2	1	5'flanking-716	cagggatcctcattctgagc C/G cgaggcgaggggactcgca	3045
ALDH1A2	2	intron1+314	cggtcccgactgccgcgggg G/△ aaggcgtcggaaccgcttag	3046
ALDH1A2	3	intron1+(664-675)	ttttgaactgaagaacttac (T)11-13 ataacgaacgttgacatctt	3047
ALDH1A2	4	intron1+1370	gcatgcagcttagaagtttt A/G ttttatgagggtctctaacc	3048
ALDH1A2	5	intron1+1557	ggtacgtttttcagaattta A/△ tttggaagctcttccagttc	3049
ALDH1A2	6	intron1+1934	tcagctctttagtgagactt C/G taaattttctaagacaagca	3050
ALDH1A2	7	intron1+(1971-1980)	agcatagtggacaagcagta (T)9-11 aaacgtgaagagcagaagct	3051
ALDH1A2	8	intron1+2295	tactgtaagacaatatgtta T/C tgttttttgtcttgctaaac	3052
ALDH1A2	9	intron1+2387	ttgggacccacatagagtca C/T tacttaaaataaatgaccag	3053
ALDH1A2	10	intron1+2841	aggaatgtgctttttaaaac T/△ agatggtgttagtcaaggag	3054
ALDH1A2	11	intron1+3035	gacttttataattttgtata A/G ctgatattatagaatacac	3055
ALDH1A2	12	intron1+3319	aaagagttatgttttttttt T/△ ctgcatctgatattatatgg	3056
ALDH1A2	13	intron1+3474	ttgtctttttatttattcat T/C taaacttctgttttctgggg	3057
ALDH1A2	14	intron1+4186	ccttccaaaccctttacttaa G/C attgtctgttttggtcataa	3058
ALDH1A2	15	intron1+4222	cataaattgtcagtcaaact A/G catgttaatagaggacttca	3059
ALDH1A2	16	intron1+4254	aggacttcaggttttttttt T/△ aaatacttttttcataactat	3060
ALDH1A2	17	intron1+4397	cccttccactacatgggcct A/G tgttaccatgtggaattatc	3061
ALDH1A2	18	intron1+5935	aactccaggttgcaaataga T/C gtttctggtattttaagtag	3062
ALDH1A2	19	intron1+6206	ttttgaaagccctcctagca T/G ttctttaatttctttattga	3063
ALDH1A2	20	intron1+9559	agataaattgatgaattatt C/T actctgtgctgctgatagat	3064
ALDH1A2	21	intron1+(9631-9632)	taaaaagaatttctaaaaga (AAGA) ccttttttttgaataactct	3065
ALDH1A2	21	intron1+(9631-9632)	taaaaagaatttctaaaaga ccttttttttgaataactct	3066
ALDH1A2	22	intron1+12731	ctgaaatagaaaccctttcag T/A gtaccttgcagagcagtgaa	3067
ALDH1A2	23	intron1+13442	cagtgtcataaagatccagc G/A gaaatcaaaatgtttcatat	3068
ALDH1A2	24	intron1+(14173-14176)	tctaaaaaaaataaataaata AAAA/△ gagaaaattaagtttaagat	3069
ALDH1A2	25	intron1+14586	actcatttattggttcaaag C/G cttcttcaaccttaggatat	3070
ALDH1A2	26	intron1+14595	ttggttcaaagccttcttca A/G ccttaggatatgcattgagg	3071
ALDH1A2	27	intron1+14711	gtttgagacattaacttcta A/G ttcaactgaagatgctagtt	3072
ALDH1A2	28	intron1+(15327-15337)	gaagagcacagtagaaagac (T)9-11 aaccctagcaatactattga	3073
ALDH1A2	29	intron1+17258	atcagtacaatgtgttgggc A/G tacaacacttaatttaaaat	3074
ALDH1A2	30	intron1+18277	taatacaaatcatttgaagc A/G tttactattaaaaaaacaaa	3075
ALDH1A2	31	intron1+18734	ctttgagcacctactgcatt T/A taagtgctgttaagatgtgg	3076
ALDH1A2	32	intron1+19081	ttaatcacctcaatctttaa C/T gaatttcttgatttttcttt	3077
ALDH1A2	33	intron1+21514	aatcaggatatgggggttc G/A ttctttattctgccacaaat	3078
ALDH1A2	34	intron1+21732	cattttaaaatagtgcttta A/G taggacttggctgttaaagt	3079
ALDH1A2	35	intron1+21865	tggcataggtttaaaaatgt C/T tgttgtaggactcttttcca	3080
ALDH1A2	36	intron1+26282	taaagaaggagaaaaaaaaa A/△ ctaatctgagactttgcagg	3081
ALDH1A2	37	intron1+27805	ggatgatgctacccaaggaa T/C tgcacacttccagacagtac	3082
ALDH1A2	38	intron1+28204	tcactccatttttttaactgt C/G cttcctaaatgtgtggttaa	3083
ALDH1A2	39	intron1+28521	tctttgttacacttcttaaa T/C cggggtatcagataatcttc	3084
ALDH1A2	40	intron1+49478	gaataaaaggatagggacat G/T ggtaagaccacttttttccct	3085
ALDH1A2	41	intron1+49834	gcctctcaatttttctcatgt G/T taatagagagaaaaccctgc	3086
ALDH1A2	42	intron1+50351	gactgactggttcataagtt C/G agaaatttcactgtggtgct	3087
ALDH1A2	43	intron1+51181	tgttattaccatagtagttc C/T gtaacacttggccgttgact	3088
ALDH1A2	44	intron3+654	ttaacctctcttgagtaaaa G/A gaatccttcagaaccagagg	3089
ALDH1A2	45	intron3+668	gtaaaaggaatccttcagaa C/T cagaggggatggtacggacc	3090
ALDH1A2	46	intron3+712	catacacttctgctccgttt G/T ccctgtcattctgtgagcca	3091
ALDH1A2	47	intron3+1273	tattcatactgtgaaaaagg T/A gtttcatggtgaagaaattc	3092
ALDH1A2	48	intron3+1743	ccacacctaaatgagattcc C/T gttttaaacactctcaagct	3093
ALDH1A2	49	intron3+2891	tgcacatatatactcattgt A/G gtttttactaggaactagac	3094
ALDH1A2	50	intron3+2919	ctaggaactagaccaaactg G/A cagtactagaaatcttttta	3095
ALDH1A2	51	intron4+290	cattgtgctagattaggtgc T/C ggggtaggtatgaaggggca	3096
ALDH1A2	52	intron4+380	ctccttgccctcctgaaaca T/C ataagatctactctttggaa	3097
ALDH1A2	53	intron4+461	gattatggctgattttcagt G/T tctttttaatatttttctct	3098
ALDH1A2	54	intron4+506	tctatatttctcgaacggcc G/A tgaattactttcataatcta	3099
ALDH1A2	55	intron4+1952	ttggtccccactccacctgt C/G atttcattattaaaacaaca	3100
ALDH1A2	56	intron4+2079	ctctatttggcctaacggta C/T cttggttttctttttacttcc	3101
ALDH1A2	57	intron4+2519	ttgggtcataagagctctct C/G catggtgtctcaaacagatg	3102
ALDH1A2	58	intron4+(2840-2851)	tttgtctctgcatacttggc (T)11-13 cacagtgaagtctggaatat	3103
ALDH1A2	59	intron4+7231	aataggatacaaatacacaa A/T gatagtgattcagatcctaa	3104
ALDH1A2	60	intron4+7958	taaaatcgtttttattgtta C/T taggtatataaaatttgcta	3105
ALDH1A2	61	intron4+8090	tctgattttatcactgttta C/T agattgcttagtcatactca	3106
ALDH1A2	62	intron4+12823	tgttagcctgtagctaaatg C/T ttttcaaatatgtgaacggt	3107
ALDH1A2	63	intron4+12939	atgaggtccgacttttaaga T/C ttttgtctacattttcttcc	3108
ALDH1A2	64	intron4+14935	tattgatggagttctttttta T/G aaatggacttttaccttctt	3109
ALDH1A2	65	intron4+15321	gcatttgggtgtctgagaga C/T atatccagaaatatgctatg	3110
ALDH1A2	66	intron4+15412	tttcaagtttatttctgttt T/G ttttttttttttttttttg	3111
ALDH1A2	67	intron5+1888	aatccaaacatctgtacttt G/T tagtggacaagatttatgtc	3112
ALDH1A2	68	intron7+9166	gaaaagctactttattcaaa G/A ataaaagtattttaagaaaa	3113
ALDH1A2	69	intron7+9914	aagctggagaaaatactagg C/T tttcctcaacagtgatttcc	3114

Desig-nation of Gene	No.	Location	Sequence	SEQ ID NO
ALDH1A2	70	intron7+18942	tttggaggggaactaatccc G/A tgacttctaggttatctctt	3115
ALDH1A2	71	intron7+19820	ttcacccctcattttaggtt A/G ggggaggtggcttgctacag	3116
ALDH1A2	72	intron7+19826	cctcattttaggttagggga G/A gtggcttgctacagttttag	3117
ALDH1A2	73	intron7+19913	cgtgaatcattcagtatttt A/G tttaaaaataccagtttgaa	3118
ALDH1A2	74	intron7+(20110-20111)	catgatttattctctaacta (ACTA) tgctaagtcaaagattctgc	3119
ALDH1A2	74	intron7+(20110-20111)	catgatttattctctaacta tgctaagtcaaagattctgc	3120
ALDH1A2	75	intron7+21857	acaatgaaaattaagaaagg A/T gaagagggaagaagcagaga	3121
ALDH1A2	76	intron7+21929	tacaagacacaggcatctttt A/G actagtttactgggatctct	3122
ALDH1A2	77	intron7+23308	ggctttgacttcggaaacct G/T tgggttataacaaagtactg	3123
ALDH1A2	78	intron7+23554	gacattggtgaaaaccaggg C/T tgtttaggagtgtcctgtcc	3124
ALDH1A2	79	intron7+(23701-23703)	catctgagatttgccttgtg GTG/△ tttaccgagttagtgggtgc	3125
ALDH1A2	80	intron7+26479	gatacatgaacaatttgttt T/C atcctcatgatatctttcaa	3126
ALDH1A2	81	intron7+26561	taaaggccacaatgcagtga T/C tgaaatctccagttacattt	3127
ALDH1A2	82	intron7+26662	tttccttagtccttccatca C/T gaaactaaagctgtcttcca	3128
ALDH1A2	83	intron8+76	tttatatctccacttttgat G/A ggacactagcaaaagatatt	3129
ALDH1A2	84	intron8+(700-711)	accatctcattcagtgattc (T)11-12 ccctccacttgttgccaggc	3130
ALDH1A2	85	intron8+724	ttttttttccctccacttgt T/C gccaggcagagctgctttcc	3131
ALDH1A2	86	intron8+800	cagattgcttgaatttcagc C/A ccagcttggaatttgcagag	3132
ALDH1A2	87	intron8+1251	gatttctgtgaaaattgaga G/A gatctggcaacctggggctc	3133
ALDH1A2	88	intron8+1627	ggcccctccccaggcaaagc G/A gtgagaacatggctgtttcc	3134
ALDH1A2	89	exon9+141	tggagcgggccaagaggcgc G/A tagtggggagtccctttgac	3135
ALDH1A2	90	intron9+778	aaccagtctggacagatccc T/C tgtagcttgtgaaagtgtag	3136
ALDH1A2	91	intron9+801	tagcttgtgaaagtgtagga A/G gtgaagggctggctcacttc	3137
ALDH1A2	92	intron9+868	tctgaaggcctcgtgtactt T/C agtggggtggggagggccac	3138
ALDH1A2	93	intron9+1338	aatttttgcctctttttact A/G tcaatacaacttgctaagtt	3139
ALDH1A2	94	intron10+(227-229)	ctatgtgcttatgattatta TTA/△ gccaacagaacaatcagaat	3140
ALDH1A2	95	intron10+316	ctaaatgtgggtcactggga T/C gttaaccaggagagagaatc	3141
ALDH1A2	96	intron10+368	ctttacatctgtgcaagaga G/A ggacaaggagcaaatcagcc	3142
ALDH1A2	97	intron10+660	gtaaacttgcattgaaatgt G/A gaaagcaggtaaaggaatga	3143
ALDH1A2	98	intron11+104	tggggaataccaaaagcaac C/T aaagttcaccagaaaagggg	3144
ALDH1A2	99	intron11+229	aaacttctaaaagaaatacc A/G tgccagtcagattatgtgct	3145
ALDH1A2	100	intron12+117	catacattcaacaaacattt C/T gtggagcacatgctactata	3146
ALDH1A2	101	intron12+691	gatagggaagatcactgtga A/G ctggaaaaatctgggaaacc	3147
ALDH1A2	102	intron12+1934	catcttgtctagattgcatg T/C ttgtttgtttgtttgtctct	3148
ALDH1A2	103	intron12+1973	ctacttacccccaaaacatg T/A tttctctttcttaaatgacc	3149
ALDH1A2	104	intron12+2722	ccagagtgactccagtatac C/A tcactgcccaggacccacag	3150
ALDH1A2	105	intron12+3855	cacttgaaagcaaccataat T/C gtgaggtttctgatgctgta	3151
ALDH1A2	106	intron12+4185	ttgctttaagcgaaatgaac T/C atacggacaggagaacagcc	3152
ALDH1A2	107	intron12+4991	acaggaacacttagacatgc A/G acccactcccaccctccgtc	3153
ALDH1A2	108	intron12+(5018-5019)	cccaccctccgtcttggggg (G) aggaaagcacactactgtcc	3154
ALDH1A2	108	intron12+(5018-5019)	cccaccctccgtcttggggg aggaaagcacactactgtcc	3155
ALDH1A2	109	intron12+(5051-5052)	actgtcccaaagaactaata (A) ctgaaccagtgctgccttgt	3156
ALDH1A2	109	intron12+(5051-5052)	actgtcccaaagaactaata ctgaaccagtgctgccttgt	3157
ALDH1A2	110	intron12+(5300-5302)	ttaaagttttaaaaaaactt CCT/△ taaaaactactcatgagatg	3158
ALDH1A2	111	intron12+5405	catcccaggacttgctgttc G/C caggtgataaactgcacctc	3159
ALDH1A2	112	intron12+5435	aactgcacctccccaggact C/A ccgctgcactcacatgcagc	3160
ALDH1A2	113	3'flanking+449	tttgggccgggaacaatttt T/C caaggttgtaaagccaaatt	3161
ALDH1A2	114	3'flanking+597	acctgggatattcctgaccc A/C atctggttttctttttaccca	3162
ALDH1A2	115	3'flanking+669	atagagactggaagtcatca T/C gtgcagttcaccgcttctga	3163
ALDH1A2	116	3'flanking+1122	cgtgctccactgagctcctc T/G gtcacaccccattcttgccc	3164
ALDH1A2	117	3'flanking+2214	tgcagctgtaaaaagaaatc T/C gtaaatggtgaccgtactac	3165
ALDH1A3	1	5'flanking-1425	cagtgttagccagccgatat C/T ggtcaaggctgccccgctcg	3166
ALDH1A3	2	5'flanking-1379	ccattatccccttccccgg C/T ctcagctgtgcactccaggc	3167
ALDH1A3	3	5'flanking-1270	aacttacccctctatccagc T/A ctatccagaaggacaccagg	3168
ALDH1A3	4	5'flanking-(1214-1213)	acggaggcctcaaaacagga (GGA) aaataaggagacccctcccc	3169
ALDH1A3	4	5'flanking-(1214-1213)	acggaggcctcaaaacagga aaataaggagacccctcccc	3170
ALDH1A3	5	5'flanking-1103	gcacagcttttgtcaggagt C/T cgtgcctccggtctttgttc	3171
ALDH1A3	6	intron1+986	gccttaactttccccacctt T/G ggcttctcttgatttttgct	3172
ALDH1A3	7	intron1+1462	gtacaggatttcaaaatact G/A tatatagaaaccagacagta	3173
ALDH1A3	8	intron1+1661	cctgttgtcttggtgggtgc G/A caaccttgccagttaaagg	3174
ALDH1A3	9	intron1+2360	agaggatagaagtcccttct A/G atttagagggcctctttctt	3175
ALDH1A3	10	intron1+2516	tgaaaacatattctttttga G/A tttagctgagtggcctgttg	3176
ALDH1A3	11	intron1+2624	cctgagacaccttacagctc C/T gtcctgcttccatgtcattc	3177
ALDH1A3	12	intron1+3255	tttcatctttctacaaatgg G/C cccctcttcctggctgcact	3178
ALDH1A3	13	intron1+(3643-3656)	gcttcagaggtttttgtggg (T)12-14 aacattctatcaacttttaa	3179
ALDH1A3	14	intron1+4265	ccaaaagccctctcttttaa T/C atgacattaataagacaatt	3180
ALDH1A3	15	intron1+5187	caagatggataagacgtcac C/T taaggtccttagcatgttga	3181
ALDH1A3	16	intron2+43	ctctaagtaattcaattatg G/T atgaccaaaggataaggaaa	3182
ALDH1A3	17	intron2+127	cagggcctgggctagctgcg T/C gaattggcatgtggttctca	3183
ALDH1A3	18	intron2+(285-300)	aggaaaggttttctttttttc (T)16-17 atcaattatttggacctgga	3184
ALDH1A3	19	intron2+778	cgtgtgcagagtaggcttgg A/G ttttatcttgcccatgagtt	3185
ALDH1A3	20	intron2+1216	actcggtagagtcactcctg A/C ctggtgtcccacatccactc	3186
ALDH1A3	21	intron3+81	accatggggtatgggaaaaa A/C gatcacggtcctggtttttgt	3187
ALDH1A3	22	intron3+236	gctcagcttcttgaccaagt T/G gttgtctataggcagttgag	3188
ALDH1A3	23	intron3+1467	ggcccggttgtaggggagga G/T atctccttttctggccttga	3189
ALDH1A3	24	intron3+1725	ccacatgttccccgggtgag A/G gtagctccctcccagggtaa	3190
ALDH1A3	25	intron3+3777	gccagaagtagatgccccca A/G ttcagctgctgcattactgg	3191
ALDH1A3	26	intron3+3829	caagtcactgggccgttagc G/C tccgtgcctgcaccttgaag	3192
ALDH1A3	27	intron3+4299	tcactttccacagccacact G/A gccagcctggccgagaagga	3193
ALDH1A3	28	intron4+84	agagccccccctgactgttt C/G cctaaggcaccattcccaac	3194
ALDH1A3	29	intron4+126	ccactccctctccaaatggt A/G ctgccaattcttcttctaag	3195
ALDH1A3	30	intron6+(290-291)	tagagaattttcagggggg (G) tcaaccaagagggagccaaa	3196
ALDH1A3	30	intron6+(290-291)	tagagaattttcagggggg tcaaccaagagggagccaaa	3197
ALDH1A3	31	intron6+705	aacagctggtgatgagccaa T/G tttccactttccttggtga	3198
ALDH1A3	32	intron7+56	ggggcgtgttatttgacacc C/T gtgagcttttcctttgacag	3199
ALDH1A3	33	intron7+1107	gatgctgttactctccttgg A/G gacagacactgccctgtgga	3200
ALDH1A3	34	intron7+1610	aagagccacacagaaccacc C/G ccctactgggctgttggaat	3201

Designation of Gene	No.	Location	Sequence	SEQ ID NO
ALDH1A3	35	intron7+1820	cacctgtaagtggagcggct T/C agaccaaggatcccaggatg	3202
ALDH1A3	36	intron8+963	gagaaaggacaggaggagga C/T acaggctctcaggaaggaaa	3203
ALDH1A3	37	intron8+1824	accattcttatccactaagc G/A tgtcccccaagatcttattc	3204
ALDH1A3	38	intron8+2384	cgcctccctcgcccctcccc C/A tccagtggacttggcagtgg	3205
ALDH1A3	39	intron9+24	atccccctggtgtgtgtgaa A/C ccatggtgcttgtctagggg	3206
ALDH1A3	40	intron9+91	gcctacagggtccctctccg T/C gaaaggaatgctgacctgtc	3207
ALDH1A3	41	intron9+219	actgaggcatgggaggaggg C/G gctattcccagggcagaagg	3208
ALDH1A3	42	intron9+435	ccagacggagagagcctggg G/A caggagaatgtatctccagg	3209
ALDH1A3	43	intron9+1472	ttgacttttgaggccagata C/T accgatttcttccaagagaa	3210
ALDH1A3	44	intron9+2038	taaacaatgtgttcctacgg G/A ctctccagggagtgtggagt	3211
ALDH1A3	45	intron9+2124	caaacagggtctgccagatg G/A catatgcccagcagccaggg	3212
ALDH1A3	46	intron9+2154	agcagccagggaggacctgc G/C gttgggcgaagcccctgtgt	3213
ALDH1A3	47	intron9+2197	cttttggcccctcagggagg G/A gaagagcagctcagcagcat	3214
ALDH1A3	48	intron9+2466	ttcttagttcctcatgtttc C/T ctctagaatgttttcgtgtg	3215
ALDH1A3	49	intron9+3655	gattggtcaagtggcatgca C/T ggtttatgccctctctcctg	3216
ALDH1A3	50	intron9+3954	gggtgcgcttttgacaactg C/G tcagtagcgtgttcacaagc	3217
ALDH1A3	51	exon10+88	tggaatgcgggggctcagcc A/G tggaagacaaggggctcttc	3218
ALDH1A3	52	intron10+8	tgccaaagaggaggtacaag G/A gggctgtggcaaggctacga	3219
ALDH1A3	53	intron10+307	ctctctgattttctaacaca A/C ccggtccccgagtcagtcat	3220
ALDH1A3	54	intron10+378	gtgggttttgccaggaatca G/A ttcaagaacctgtggattca	3221
ALDH1A3	55	intron10+975	aatattgtgtcattccttcc C/G ctggtagttattatggaaac	3222
ALDH1A3	56	intron10+1088	cagtgccaggagccaggggg C/T cttctccagatgactctgag	3223
ALDH1A3	57	intron11+105	ttgtttacattgtatattat A/G taccaagccctgtctcagtg	3224
ALDH1A3	58	intron11+274	agggctccagtacctgtgcc T/G gtggccccgtgctgtactg	3225
ALDH1A3	59	intron11+1088	cagtgccaggagccaggggg T/A cttctccagatgactctgag	3226
ALDH1A3	60	intron12+96	ctccaatctgctgacacccc G/A tccccccacaccgccgctc	3227
ALDH1A3	61	intron12+5642	tctgtgctaacgtctgcttc T/C ctcatgcccctaggctggc	3228
ALDH1A3	62	exon13+104	gggctccttcctcaaacatc G/C gacggcggaatgtggcagat	3229
ALDH1A3	63	exon13+281	ataggttgtctgtgaaatcg C/T agtcctgcctggggagggag	3230
ALDH1A3	64	3'flanking+743	gtgagcaggaaactgtagga G/A aaggatattttccctcattt	3231
ALDH1A3	65	3'flanking+1145	gcctcccagctaccccaccc A/G cctcaggaggggtcattcca	3232
ALDH1A3	66	3'flanking+1185	aacctagggtgctgagaatc T/C gggtgggattaccagcaaaa	3233
ALDH1A3	67	3'flanking+1600	acaccacgccctgcaaattg T/C tgggaacttgtcggtggcaa	3234
ALDH1A3	68	3'flanking+1847	caggagccctgcggctgccc C/G ggttctgtgaaatggcagtg	3235
ALDH1L1	1	intron1+252	cgcagcgccaggactggccc G/C ccgaggatctggccggccgc	3236
ALDH1L1	2	intron1+544	ctcaggggctgcgctggagt C/T ccagctccagccactgcgct	3237
ALDH1L1	3	intron1-6596	cagatttttcttaaggtgca C/G tagccactgaggatattttt	3238
ALDH1L1	4	intron1-6513	caattatggtttatcttagg G/A acatgtttatagagatagta	3239
ALDH1L1	5	intron1-6478	atagtattcttacttagctt G/A cattctaaattttgttccct	3240
ALDH1L1	6	intron2+240	gtggcattagggtcctggag A/G agggctatagagaagcccag	3241
ALDH1L1	7	intron2+1326	gaggaggagaccggagagga G/C agccagtccagtcagggccc	3242
ALDH1L1	8	intron3+386	gtcctactctaacttccact G/A ccgctgctctgggcagcaca	3243
ALDH1L1	9	intron4+271	gggcccgttcaatagacaag G/C aaggctaaaggcagggactg	3244
ALDH1L1	10	intron4+356	taggattctatttctctctc C/T ttcactcgttgattctcctt	3245
ALDH1L1	11	intron4+608	gtgctctgataggctgtctc A/C gtcacatgcttcctgctggg	3246
ALDH1L1	12	intron4+664	ggtcacatggcctgagcggc A/G gggcggctcagtcacctggg	3247
ALDH1L1	13	intron4+785	gagggctgcttgcccctgcc C/G gaggacaggctggcagggac	3248
ALDH1L1	14	intron4+874	ccctggggagcccttgctgt T/G tgggcgcagcaggaagagca	3249
ALDH1L1	15	intron4+1349	tccctcaggctcttgctcac G/A tgggcccagactccttggct	3250
ALDH1L1	16	intron4+1799	ctggggctgggaaggaggca G/A ggtcctattgctggggatag	3251
ALDH1L1	17	intron4+1815	ggcagggtcctattgctggg G/A atagcaacccactggatctc	3252
ALDH1L1	18	intron5+272	aaagcccacagggagataag A/G gtgggagttaggggcaaaa	3253
ALDH1L1	19	intron5+301	taggggcaaaacgtcagcc G/A tagtgcgagcagtcttcaag	3254
ALDH1L1	20	intron5+343	caaggtgtgagggacagtgc G/A ggtctctggagcaatagcca	3255
ALDH1L1	21	intron6+926	cctgcctgggctactggctt C/T gggggcttcttctcacccac	3256
ALDH1L1	22	exon7+41	aacgctgaacacttcaggcc T/C ggtgcccgagggagacgctt	3257
ALDH1L1	23	intron7+305	cctagaatcagagagaagcc C/T tcccagggagcctgggttca	3258
ALDH1L1	24	intron7+837	gtccggacaaaccccatggg C/T gtggtacccccagccgtgtt	3259
ALDH1L1	25	intron7+866	cccagccgtgttgctgtgtc C/T ggcctaccagagtgaggcgt	3260
ALDH1L1	26	intron7+884	tccggcctaccagagtgagg C/T gtggcagtatggggcctggc	3261
ALDH1L1	27	intron7+1118	aatgttccagaaaatcatgc G/C aggcagtaagggcagaggaa	3262
ALDH1L1	28	intron7+1168	aaagtaaaggttcaggagaa G/A tctagcctggggctgctccc	3263
ALDH1L1	29	intron7+1451	cagggcacccacagcatctg T/C ccagagacctgcaaagacag	3264
ALDH1L1	30	intron7+1489	caggaatgcaaagaaggcaa T/C taagtgtcttaagaggaagc	3265
ALDH1L1	31	intron7+1579	tcagggtgggaggggagtga G/A gagagaccagctgagcacac	3266
ALDH1L1	32	intron7+1691	ctggctgggctttagcttgc A/C gaaagctccagaacatcttt	3267
ALDH1L1	33	intron8+2627	aaagaggagagccgggggtg C/T ttgtgccaggggttgggggа	3268
ALDH1L1	34	intron8+2646	gcttgtgccaggggttgggg G/A aactggttctgattgggcct	3269
ALDH1L1	35	intron8+2925	ctgctgccctccataggtcc C/G agactgaatccttcagagga	3270
ALDH1L1	36	exon9+4	caggtcttgctttgcagagt G/T tttggcagcggatcctcccc	3271
ALDH1L1	37	exon10+109	cagctgttagtgaggaagct G/T cgaggggacgatgaggaggg	3272
ALDH1L1	38	intron10+(671-672)	tggcattttcctctgtctga (AG) gtcctcttagcccaccctaa	3273
ALDH1L1	38	intron10+(671-672)	tggcattttcctctgtctga gtcctcttagcccaccctaa	3274
ALDH1L1	39	intron11+8	caccgatggaagtgtgagtg C/A aggcccagcaccccttctcc	3275
ALDH1L1	40	intron11+447	atgagccaaagcacgcctat G/A gtagatacacacgtgaacat	3276
ALDH1L1	41	intron11+601	ctcaaaatgagtcatttgag A/G ggagttaatgaaagactcat	3277
ALDH1L1	42	intron11+639	catctgcaaagggagaggga G/A ggggtagggacacagacagg	3278
ALDH1L1	43	intron12+684	tcctgggagaagagagggtg C/T ggccagatgagccgagaaca	3279
ALDH1L1	44	intron12+767	cgtctaggggtgcgaagcca A/G gttatggcgtggtcccaacg	3280
ALDH1L1	45	intron12+1014	tcataggttccagtcccctt C/T gcaagcccctcaattctaga	3281
ALDH1L1	46	intron12+1359	ctggttctgcctcagctcag C/T acagcagaggctgggtctag	3282
ALDH1L1	47	intron12+1734	ggtggtccaggctgctggtg G/T tcagtagggccggccgagcc	3283
ALDH1L1	48	intron12+1901	ttcagcagcctaactgaatt G/A acaatagaatagtcctgcaa	3284
ALDH1L1	49	intron12-470	gggatggggccacctctcca T/C ctctggagatgccaggctca	3285
ALDH1L1	50	intron12-334	aaggggcagcctcttgggcca T/C gacccctttgctgtctgcag	3286
ALDH1L1	51	intron12-325	ctcttgggccatgaccccctt T/C gctgtctgcagcaagtgggt	3287
ALDH1L1	52	intron12-221	gaaggaagcgagggaagatc G/C aggaaaggagagagggacag	3288

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ALDH1L1	53	intron12-4	cccgcttcccctcaccctgg T/C caggttggcagatctcatgg	3289
ALDH1L1	54	intron13+34	tcccacccagtgtgagcaca T/C gcagactggcccagccatat	3290
ALDH1L1	55	intron13+58	gactggcccagccatatagg A/G gaactccaagggcagcacag	3291
ALDH1L1	56	intron13+125	ccacaactggtggcttggaa T/C gacacctgtttattagcttg	3292
ALDH1L1	57	intron13+126	cacaactggtggcttggaat G/A acacctgtttattagcttgt	3293
ALDH1L1	58	intron13+281	acctgcatccagacgagttc T/G ggtgttgacagagttcagtt	3294
ALDH1L1	59	intron13+299	tcgggtgttgacagagttca A/G ttccgtgtggatgcagggct	3295
ALDH1L1	60	intron14+121	catttatcaaacagccatcc A/G tgtgcttcttgagcacctgc	3296
ALDH1L1	61	intron14+167	gccaggcattgttgtaagga C/T ttgaggacaattgtatttaa	3297
ALDH1L1	62	intron14+205	taatctcccagtaacactgg A/C tcagtcaggtccacggtggg	3298
ALDH1L1	63	intron14+219	cactggatcagtcaggtcca C/G ggtgggaaacaagagtaaac	3299
ALDH1L1	64	intron14+2275	tctcatctgtgatgcatccg T/C cagacctctgctcccagcct	3300
ALDH1L1	65	intron14+2431	agaatgactgagtgatcaga C/G ctagagagccccagccccgg	3301
ALDH1L1	66	intron14+2660	agccaagcatttcttgggga C/T accaagaaaccttgcttggt	3302
ALDH1L1	67	intron14+2740	aactccaccctcaccgtcca T/C gcagctccccaggagcgtca	3303
ALDH1L1	68	intron14+2756	tccatgcagctccccaggag T/C gtcagagggcagaggaggag	3304
ALDH1L1	69	intron14+2805	ccgcacagcaggagaatggc T/C ccaagggagggagggacggg	3305
ALDH1L1	70	intron14+(3636-3637)	tctcctgggtgtgtgtgggg (G) tgtggggcagctcccctatc	3306
ALDH1L1	70	intron14+(3636-3637)	tctcctgggtgtgtgtgggg tgtggggcagctcccctatc	3307
ALDH1L1	71	intron14+4347	tccaggacagaaacagcagg C/T gtgagctgcctctcagaggg	3308
ALDH1L1	72	intron15+380	atgtcccttatgtggcttcc A/G agaccagaagtcctggagag	3309
ALDH1L1	73	intron15+(1055-1056)	gccacaatctgcagctactc (C) tcccagcttgctgctgggct	3310
ALDH1L1	73	intron15+(1055-1056)	gccacaatctgcagctactc tcccagcttgctgctgggct	3311
ALDH1L1	74	intron17+15	gaaaaggtgcgtggctgggg G/C tggagcagaggaggggctgc	3312
ALDH1L1	75	intron17+44	aggaggggctgctgtgagtg C/T gcctgggacatggcagtgct	3313
ALDH1L1	76	intron17+51	gctgctgtgagtgcgcctgg G/A acatggcagtgctgtccaca	3314
ALDH1L1	77	intron17-(2224-2223)	ctggtgtcatctcccagact CT/△ gtcactaaaccacaatatga	3315
ALDH1L1	78	intron18+140	agcgtcatcacaagcatagc G/A tggcaggcagcaggcttagg	3316
ALDH1L1	79	intron19+(51-52)	tggttcactgggacagcagc GC/△ ctggctggaggggttggag	3317
ALDH1L1	80	intron19+399	tcaggtcagcctgggcctga C/A catggacaggggccctggag	3318
ALDH1L1	81	intron19+1794	gtcctgtctgggggtcttaa G/C ggagtcatgagacttccaca	3319
ALDH1L1	82	intron19+1969	tgatcggggtgcggtttggg G/T cgacaggacaggagcagaga	3320
ALDH1L1	83	intron19+1972	tcggggtgcggtttggggcg A/G caggacaggagcagagaata	3321
ALDH1L1	84	intron19+2083	tgagaagagcagaggggtgt G/T ccgggtgctcgagtcacacc	3322
ALDH1L1	85	intron19+2119	acacctgtgtctgattaggg C/T tgattaggggtgcagagttt	3323
ALDH1L1	86	intron20+1388	ttaccctcttcccactcccg C/T tggactgtgagttccatgag	3324
ALDH1L1	87	intron20+1564	cccaggaaccaggaacagtg G/A ggagccatcaccccgccctg	3325
ALDH1L1	88	intron20+1873	tcagtgttaaaacatcattt G/A tgtatgtatgaaaaatattg	3326
ALDH1L1	89	intron20+2427	actaggattggatggacttg G/C gatcaggtctcagctctgtc	3327
ALDH1L1	90	intron20+2458	cagctctgtcacctgccaac C/T ggcggcccctttccctcaa	3328
ALDH1L1	91	intron20+2544	ccaggtgggagagccatctg C/T agcgtggtgacacccatcac	3329
ALDH1L1	92	intron20+2573	gacacccatcacacgggtgc C/T gtgacccggtgcttatgtcg	3330
ALDH1L1	93	intron20+2574	acacccatcacacgggtgcc G/A tgacccggtgcttatgtcgg	3331
ALDH1L1	94	exon21+33	agccaactgttttcacagac G/A tggaagaccacatgttcata	3332
ALDH1L1	95	exon21+87	ccttcgggcctgtcatgatc A/G tctctcggtttgctgatggg	3333
ALDH1L1	96	intron21+323	ccatgcattaaaccaccccc C/G acactgagtggcttggaata	3334
ALDH1L1	97	intron21+361	ataatcagagatttatttta C/G tcacggtctaggttcaatga	3335
ALDH1L1	98	intron21+478	gtcttgcgggaggcttcctc C/A gcgtggcagcctcgggttg	3336
ALDH1L1	99	intron21+1086	caacccaatcttgcccccgg C/T gctgcagcccggcacatttt	3337
ALDH1L1	100	intron22+235	gggcctggaggagacactcc A/C gccaggaggcactgggggcc	3338
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ALDH1L1	102	intron22+1214	tgggcccacttatgaatcct G/C cccgagttccctcagctccc	3340
ALDH1L1	103	intron22+1226	tgaatcctccccgagttccc T/C cagctccctcctaaccctag	3341
ALDH1L1	104	intron22+1623	ggggcttcccactgtccaga C/G aaggcggtgggagctgggga	3342
ALDH1L1	105	intron22+1698	attctggggagtcctggccc A/G ctatccactgccagggataa	3343
ALDH1L1	106	3'flanking+145	gagagacaggaggaaatggg C/T gtgggtcatctcaggcccca	3344
ALDH1L1	107	3'flanking+239	tgggaaacaggtgggaagac G/A gggattgagctgggtgagcc	3345
ALDH1L1	108	3'flanking+288	ggaagcagctcagactccct C/T agcagatggggccgggccct	3346
ALDH1L1	109	3'flanking+1513	agggtcggctcagaccccgg A/C gtgctcctggcatgtccagc	3347
ALDH1L1	110	3'flanking+1707	cggtgggacttgccctagca C/T gtgccacttataccagaaca	3348
ALDH1L1	111	3'flanking+1709	gtgggacttgccctagcacg C/T gccacttataccagaacaga	3349
ALDH1L1	112	3'flanking+1745	acagatgagtccatgtcaac C/T gcttcctgagttccctttgt	3350
ALDH1L1	113	3'flanking+1843	ctgcctctcagcccacagcc G/A ggccgctcacactcctccca	3351
CYP3A4	1	intron2+(754-763)	cacaaaatgagtttgtgggg (T)9-11 acacaaaggcggaatcacat	3352
CYP3A4	2	intron7+258	accactaatcaactttctgc C/T tctatggatttgcctattct	3353
CYP3A4	3	intron7+894	tgctgatctcactgctgtag C/T ggtgctccttatgcatagac	3354
CYP3A4	4	exon9+(32-33)	ttccttcagctgatgattga (A) ctctcagaattcaaaagaaa	3355
CYP3A4	4	exon9+(32-33)	ttccttcagctgatgattga ctctcagaattcaaaagaaa	3356
CYP3A4	5	intron10+12	cccaataaggtgagtggatg G/A tacatggagaaggagggagg	3357
CYP3A4	6	intron10+459	agacatgtgactttttttttt T/△ gaaaggtaacaatcactttc	3358
CYP3A4	7	intron10+608	agccgtctcgaatgtctccc C/T acttcataactcctccacac	3359
CYP3A4	8	intron12+2467	ttttttgcccattactccat A/G gagatcagaatatcactctg	3360

[Document Name] Drawings

Fig. 1

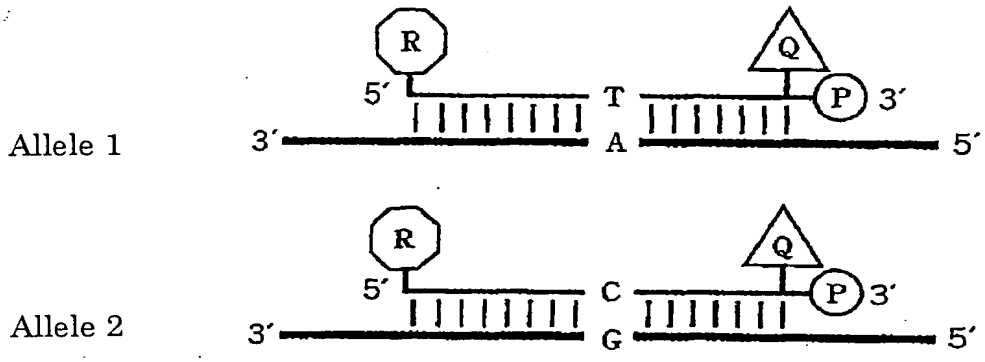


Fig. 2

a. Hybridization



b. PCR Reaction



c. 5' Nuclease Activity

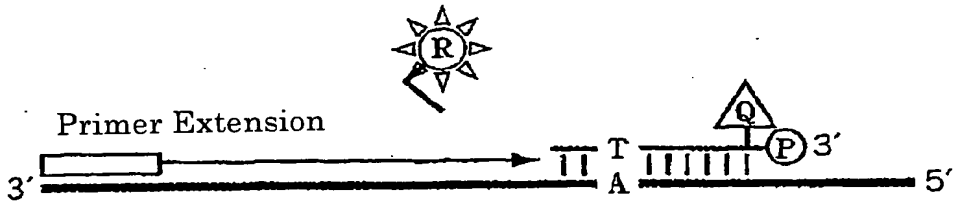


Fig. 3

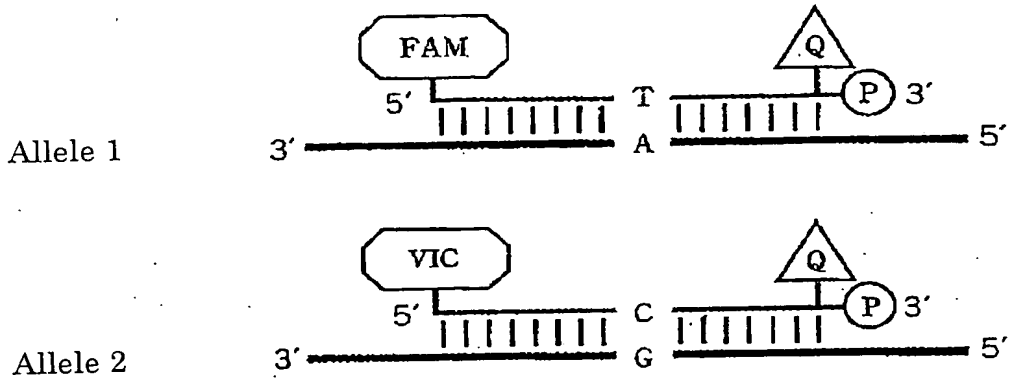
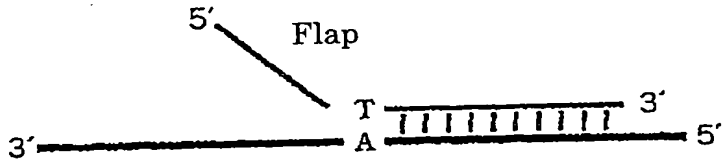


Fig. 4

a. Allele Probe



b. Invader Probe



c. 5' Nuclease Activity

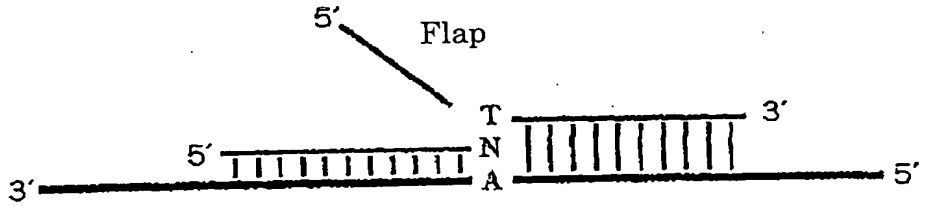


Fig. 5

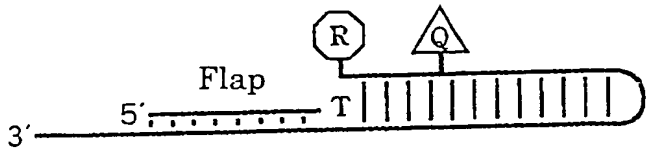
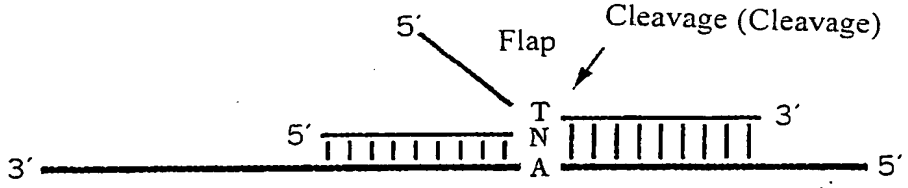
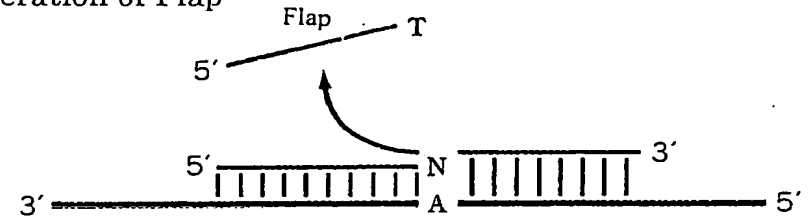


Fig. 6

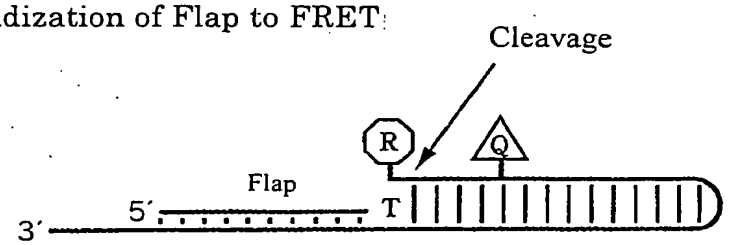
a. Cleavage of Allele Probe by Cleavage



b. Liberation of Flap



c. Hybridization of Flap to FRET



d. Liberation of Fluorescent Dye

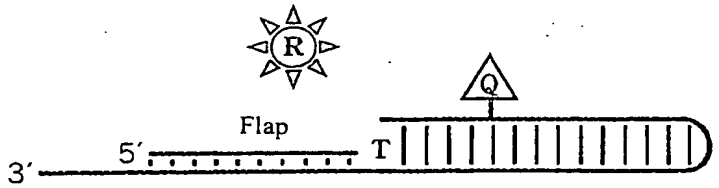


Fig. 7

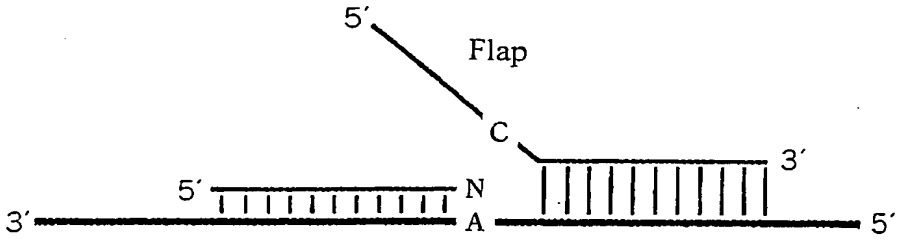

5′
Flap
C
3′
5′
N
3′
A
5′

Fig. 8

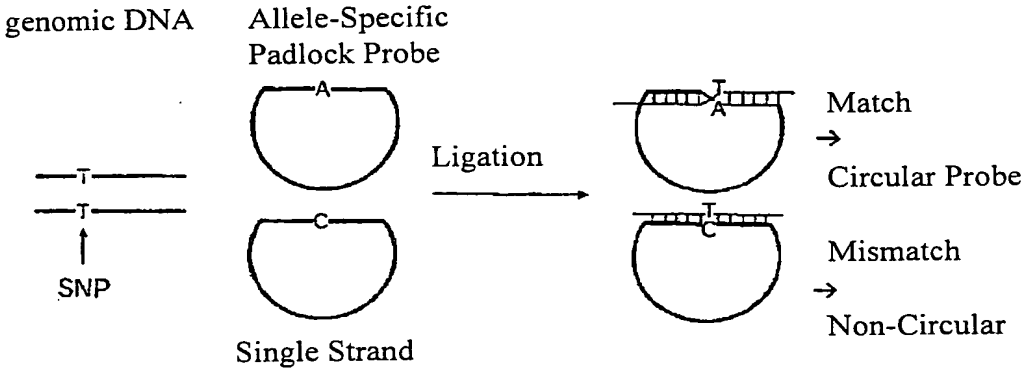
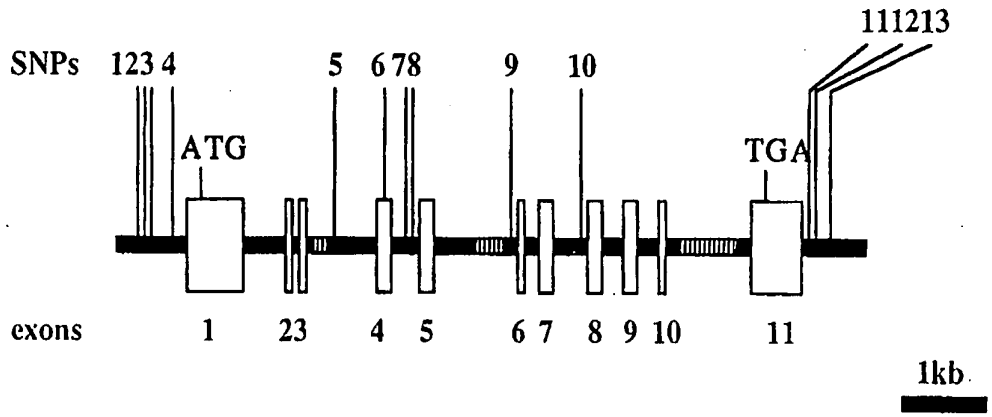

genomic DNA
Allele-Specific
Padlock Probe
A
T
T
SNP
C
Single Strand
Ligation
T
A
Match
→
Circular Probe
T
C
Mismatch
→
Non-Circular

Fig. 9

ATP binding cassette, sub-family B, member 2 (ABCB2)

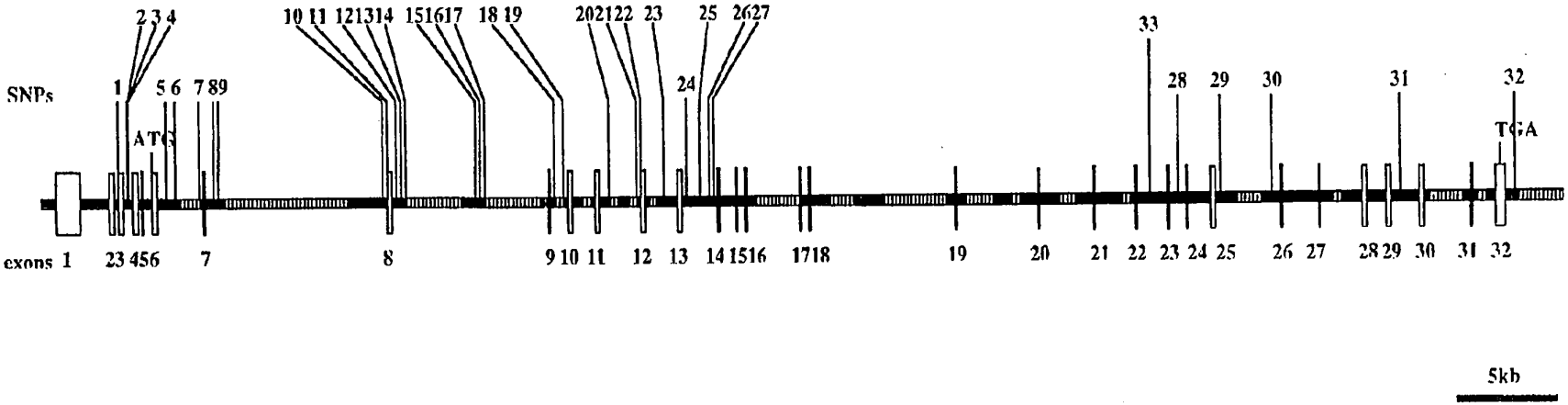
ACCESSION X66401



ATP-binding cassette, sub-family B, member 4 (ABCB4)

Fig. 10

ACCESSION AC079591
AC079303
AC005045



Epoxide hydrolase 1, microsomal (EPHX1)

ACCESSION AC058782

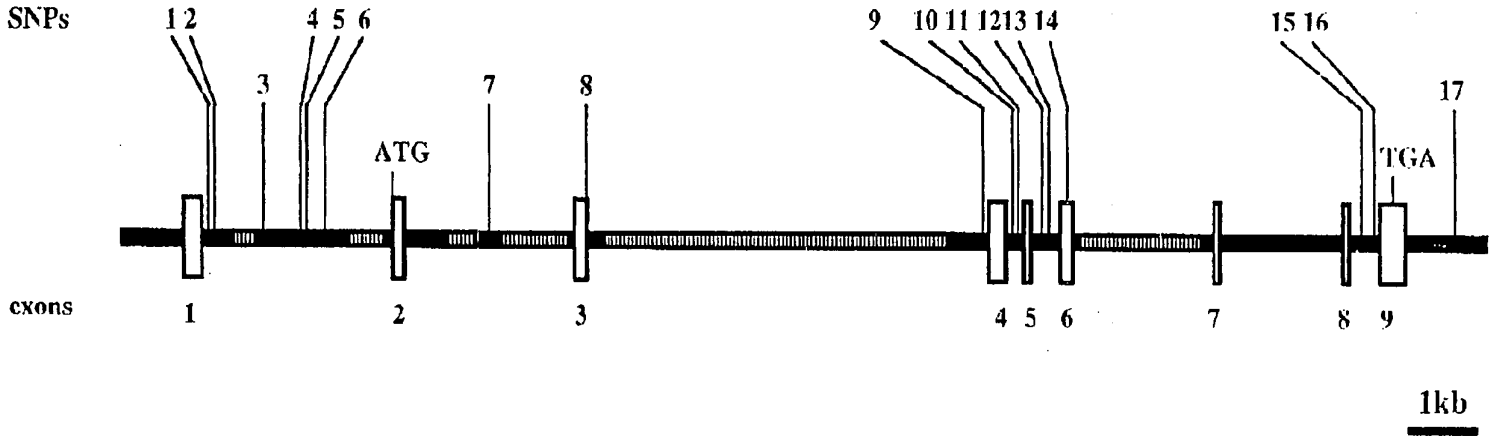


Fig. 11

Epoxide hydrolase, cytoplasmic (EPHX2)

ACCESSION AC010856

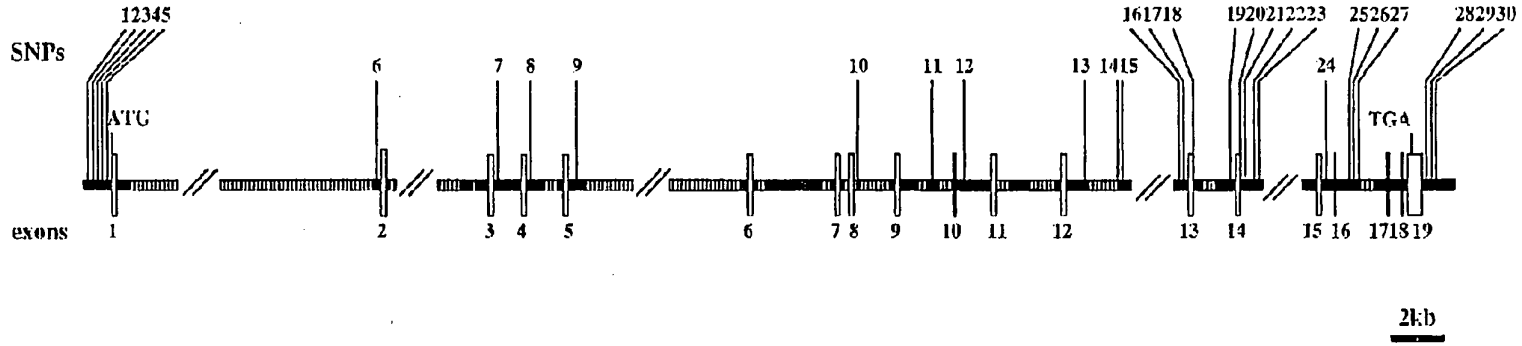


Fig. 12

Fig. 13

Guanidinoacetate N-methyltransferase (GAMT)

ACCESSION NT_000879

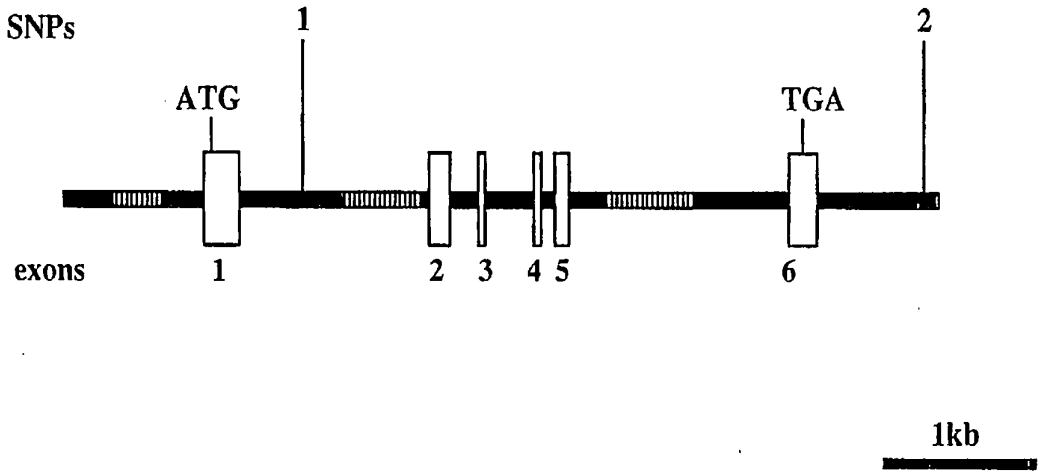


Fig. 14

Nicotinamide N-methyltransferase (NNMT)

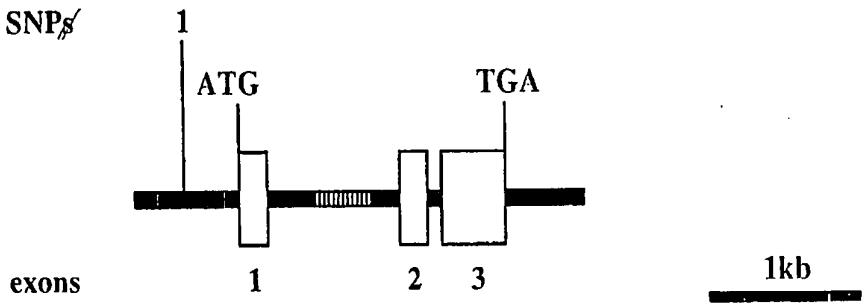
ACCESION AC019290



Fig. 15

Phenylethanolamine N-methyltransferase (PNMT)

ACCESSION AC040933



Phosphatidylethanolamine N-methyltransferase (PEMT)

ACCESSION AC020558

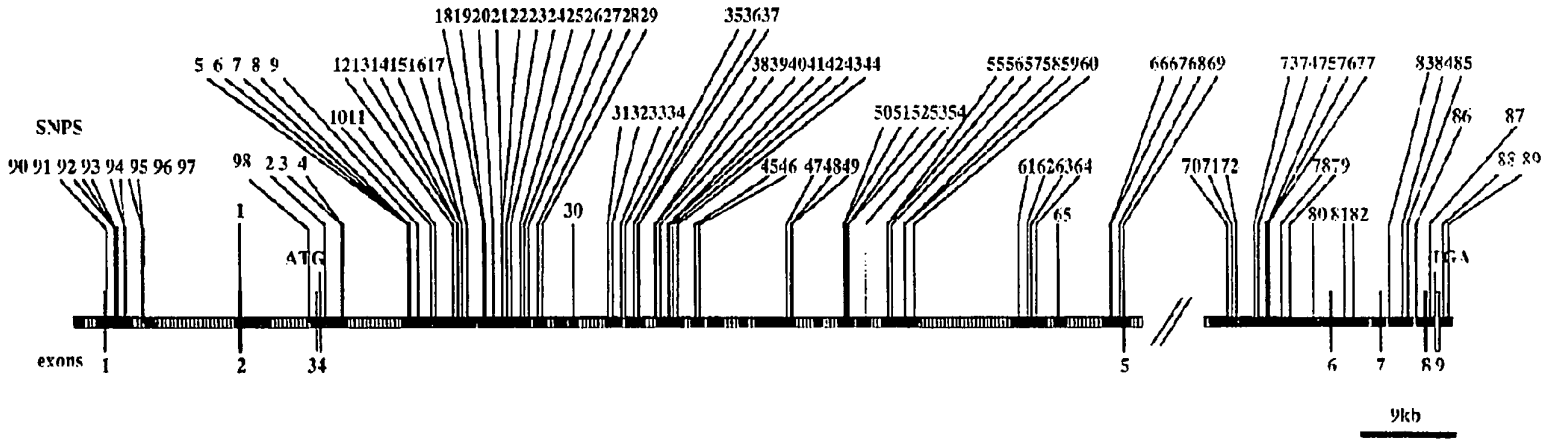


Fig. 16

Fig. 17

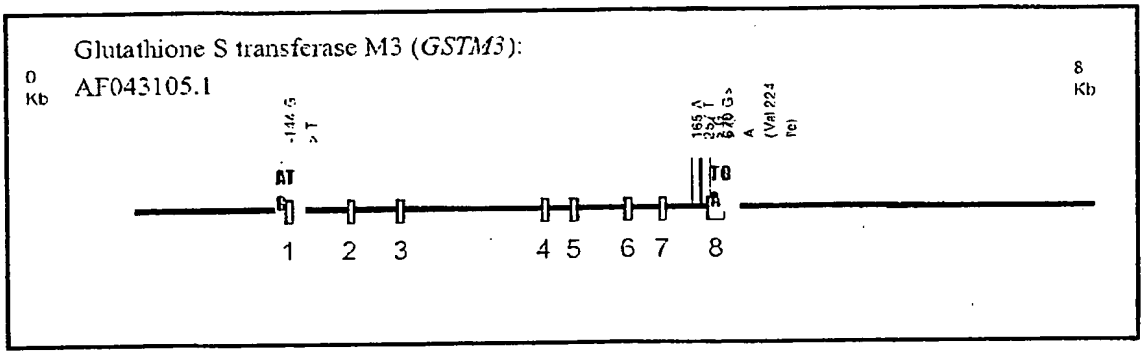
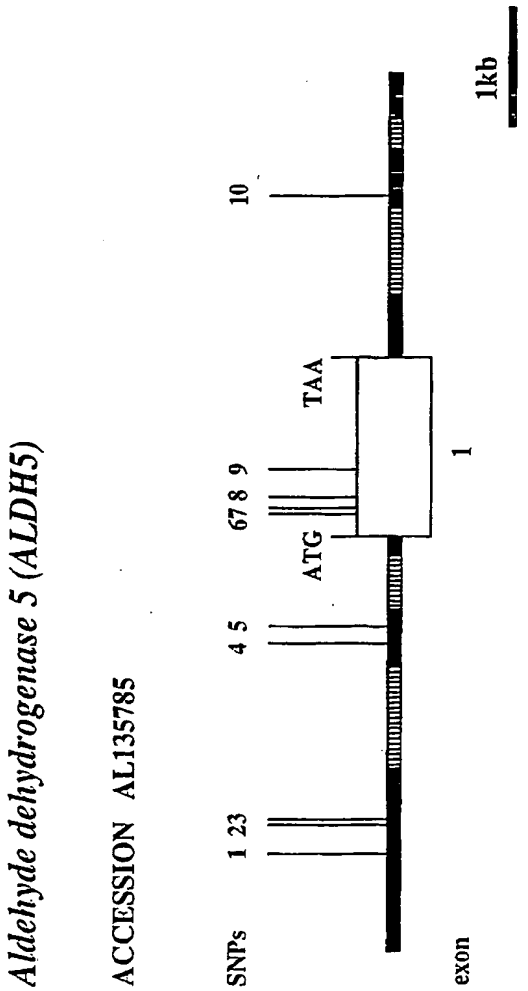

Glutathione S transferase M3 (GSTM3):
0 Kb
AF043105.1
8 Kb
1 2 3 4 5 6 7 8

Fig. 18


Aldehyde dehydrogenase 5 (ALDH5)
ACCESSION AL135785
SNPs
1 2 3
4 5
6 7 8 9
10
ATG
TAA
1
exon
1kb

Transglutaminase 1 (TGM1)

ACCESSION M98447

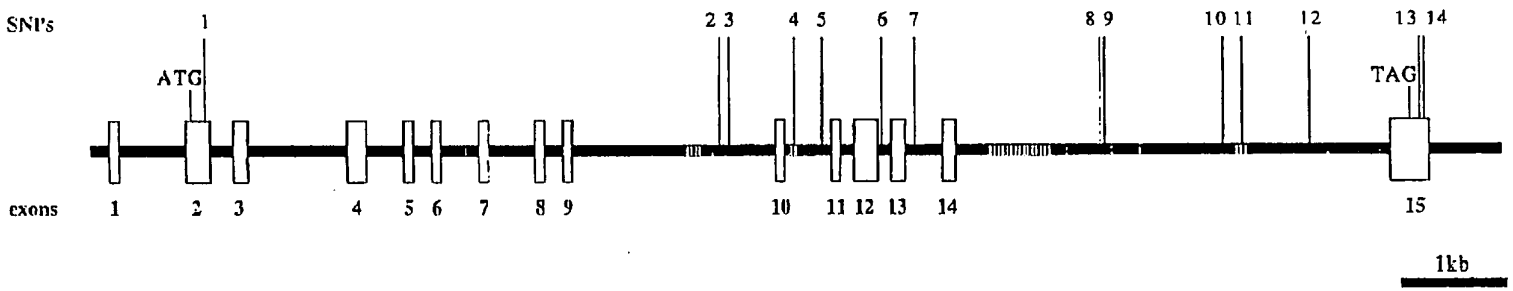


Fig. 19

Fig. 20

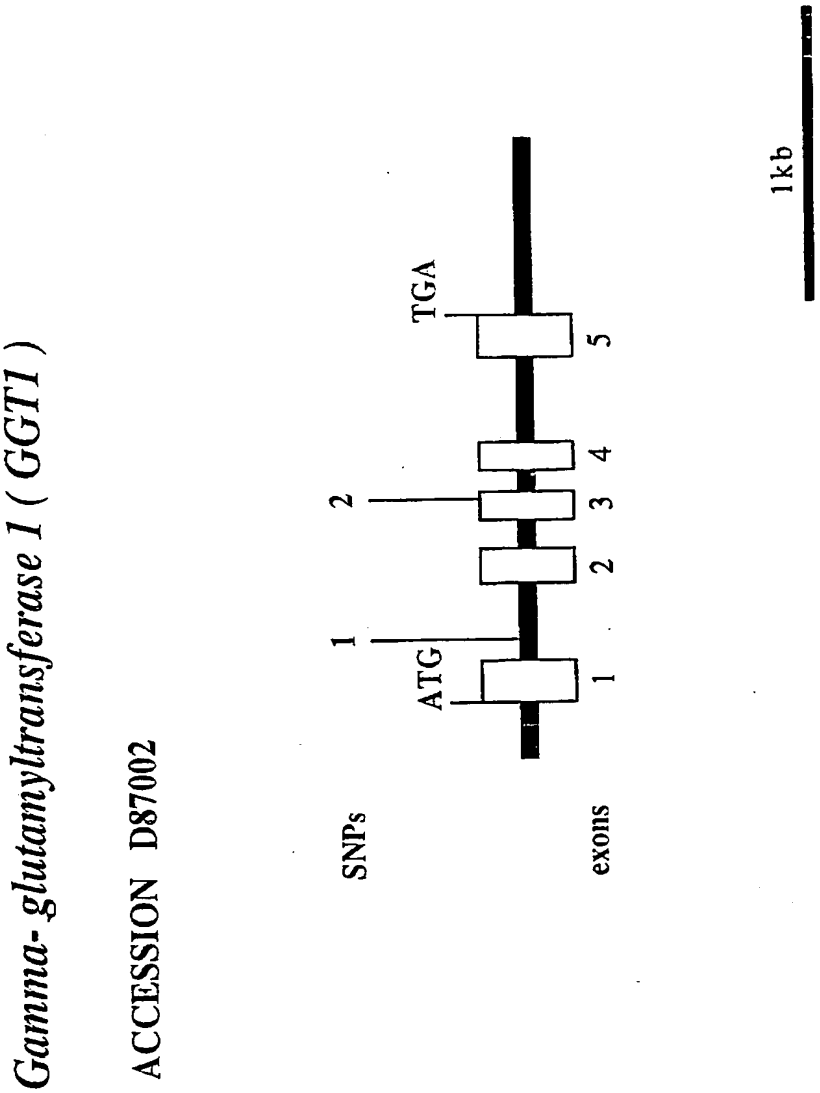

Gamma- glutamyltransferase 1 (GGT1)
ACCESSION D87002
SNPs
exons
ATG
TGA
1
2
1
2
3
4
5
1kb

Fig. 21

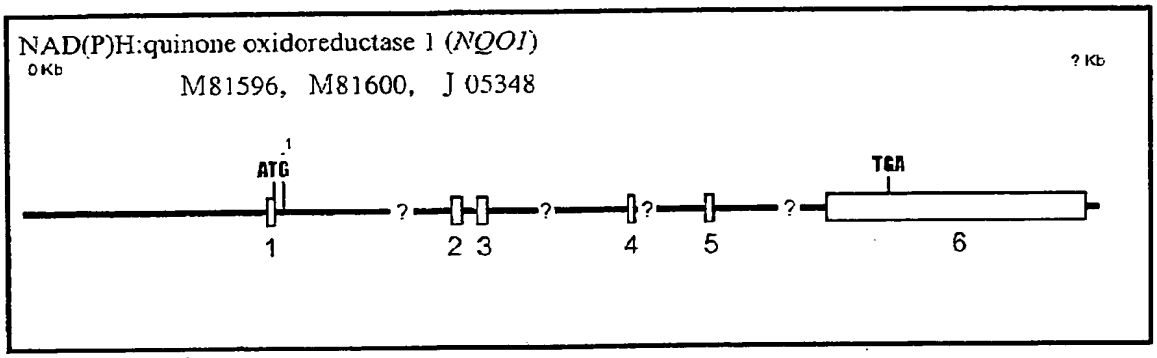

NAD(P)H:quinone oxidoreductase 1 (NQO1)
0 Kb
M81596, M81600, J 05348
? Kb
ATG
TGA
1
2 3
4
5
6

Fig. 22

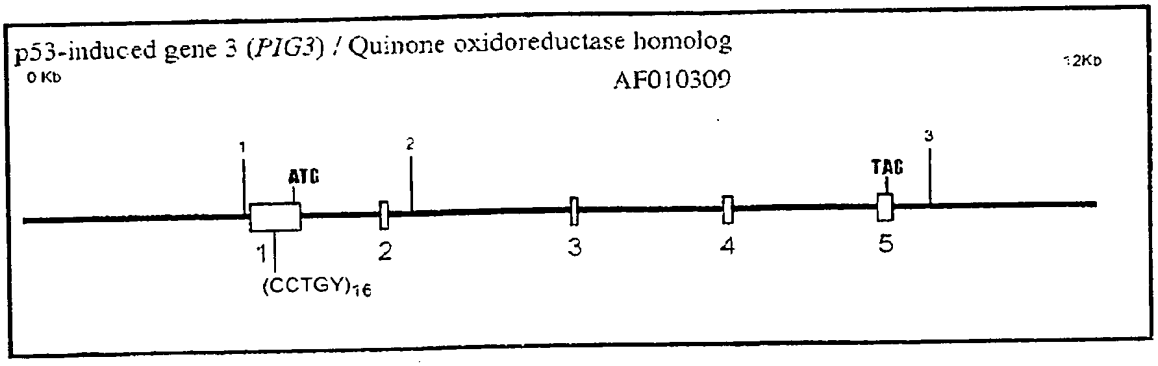


Fig. 23

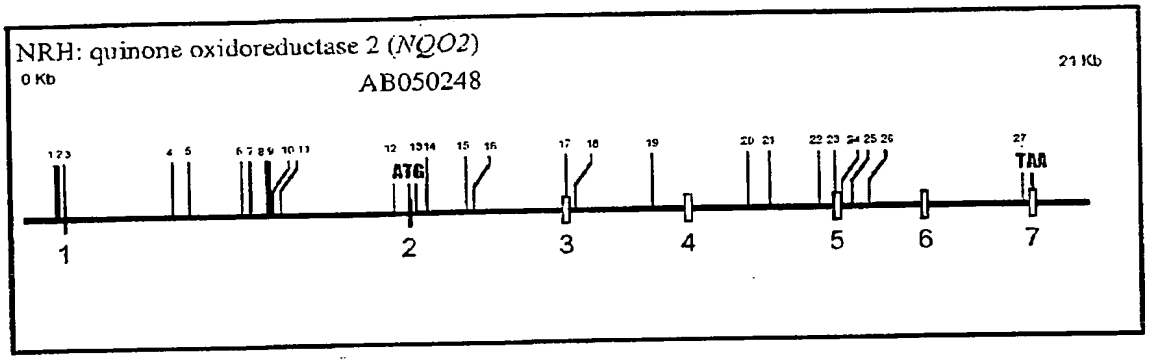


Fig. 24

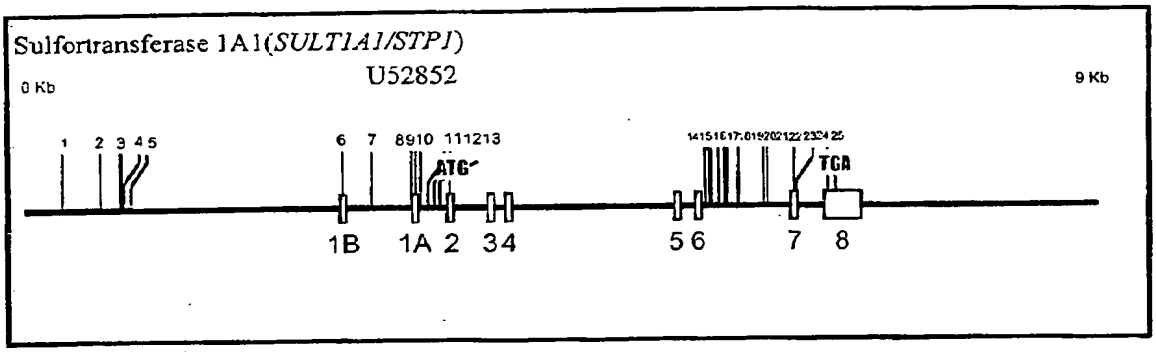


Fig. 25

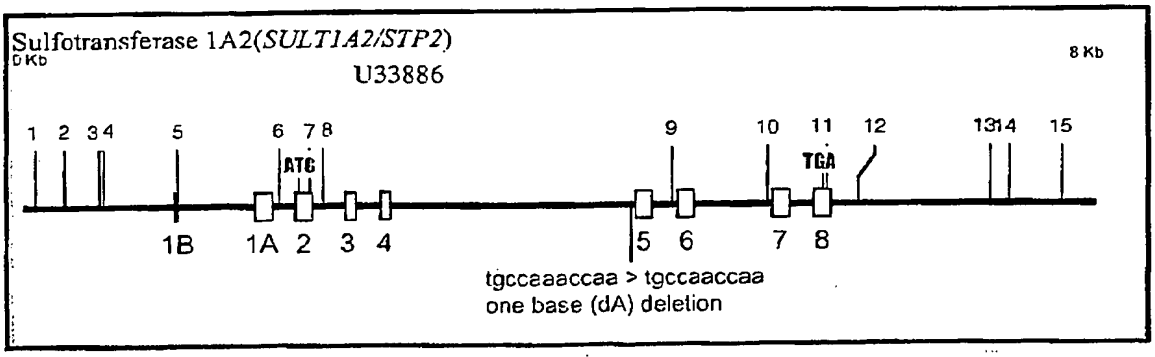


Fig. 26

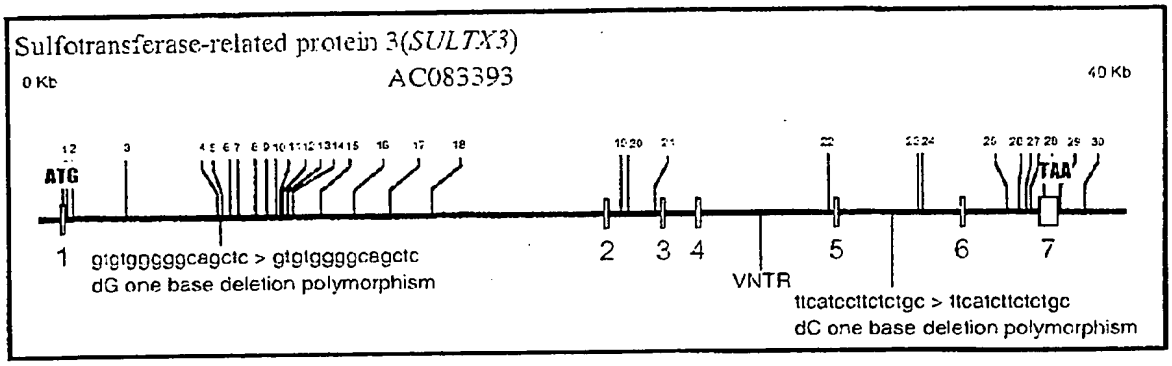


Fig. 27

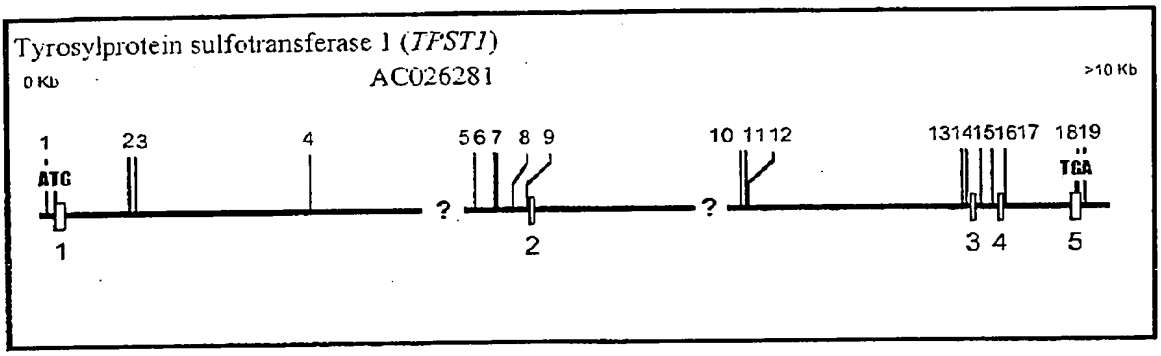


Fig. 28

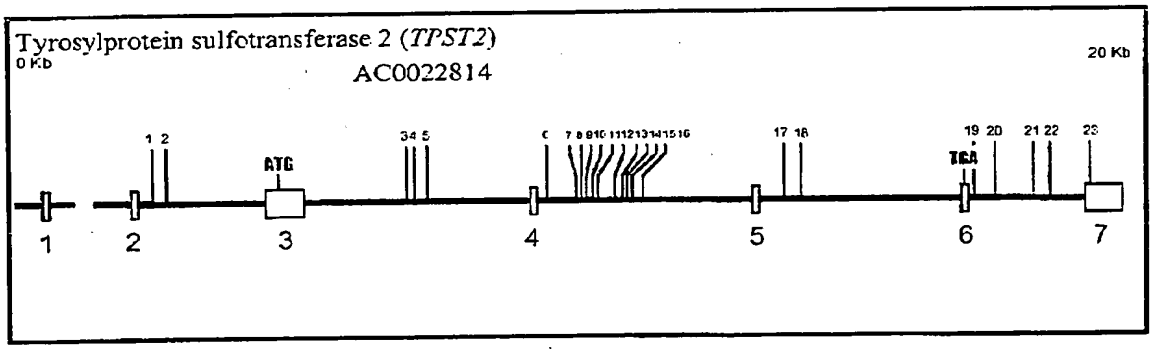


Fig. 29

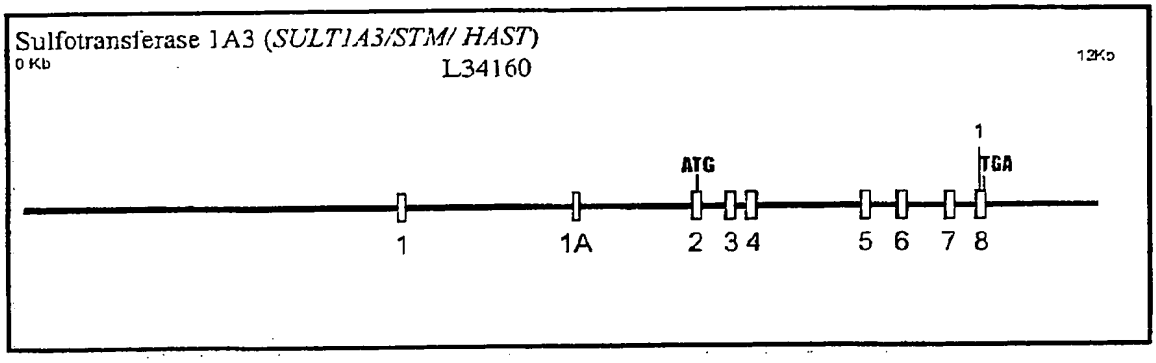


Fig. 30

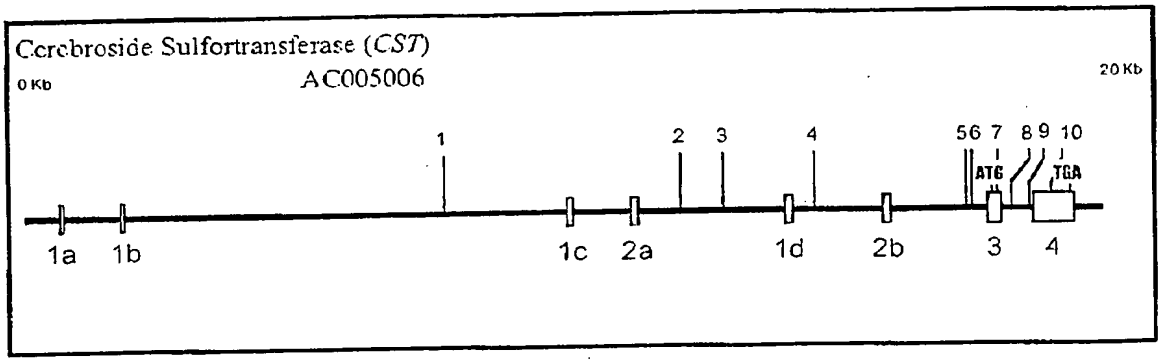


Fig. 31

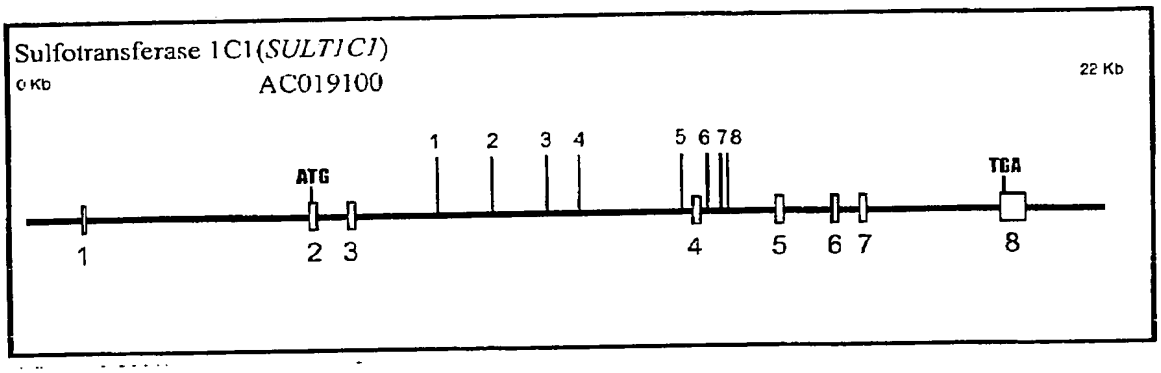


Fig. 32

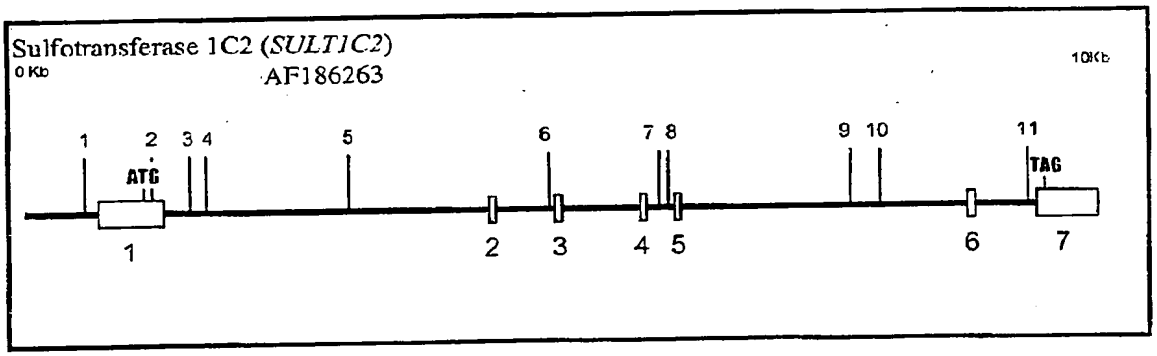


Fig. 33

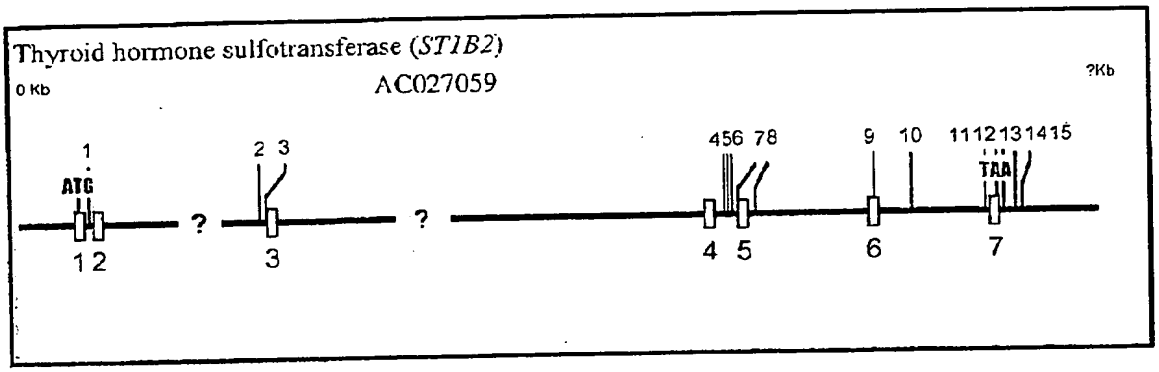


Fig. 34

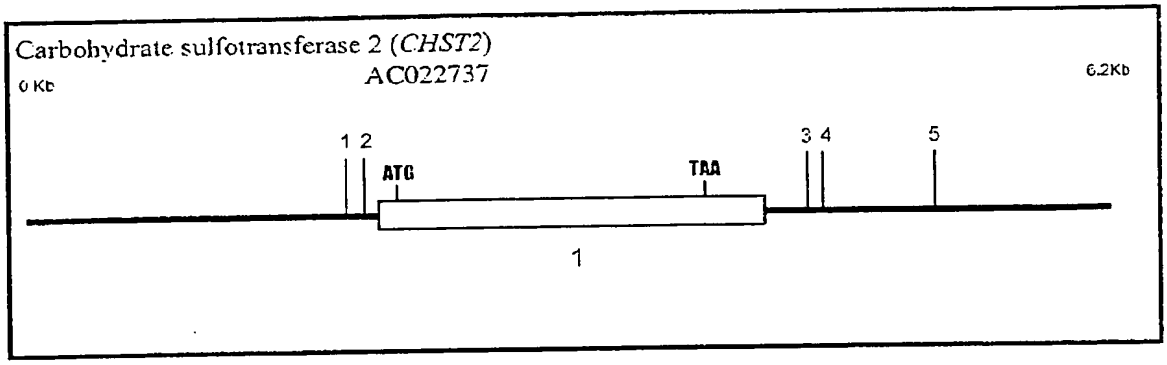


Fig. 35

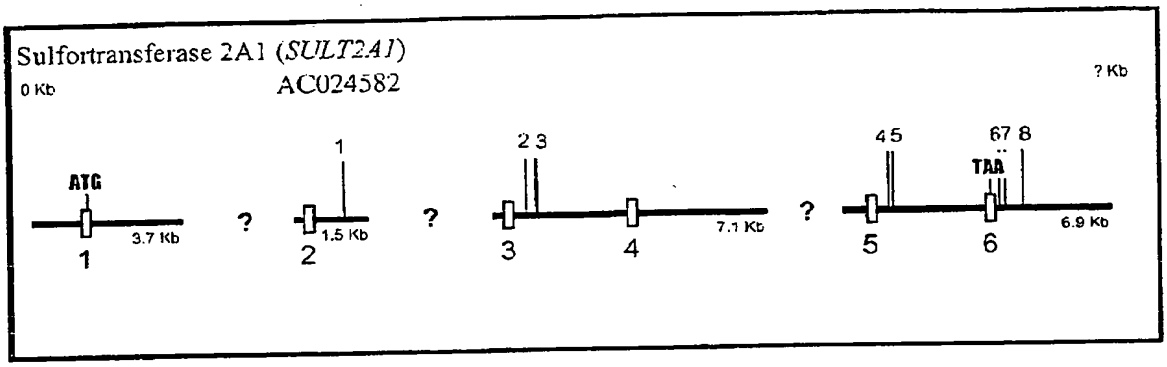


Fig. 36

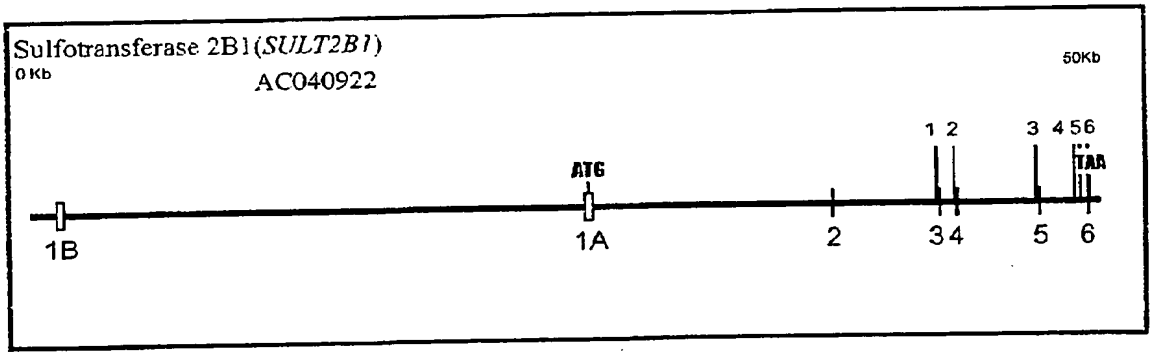


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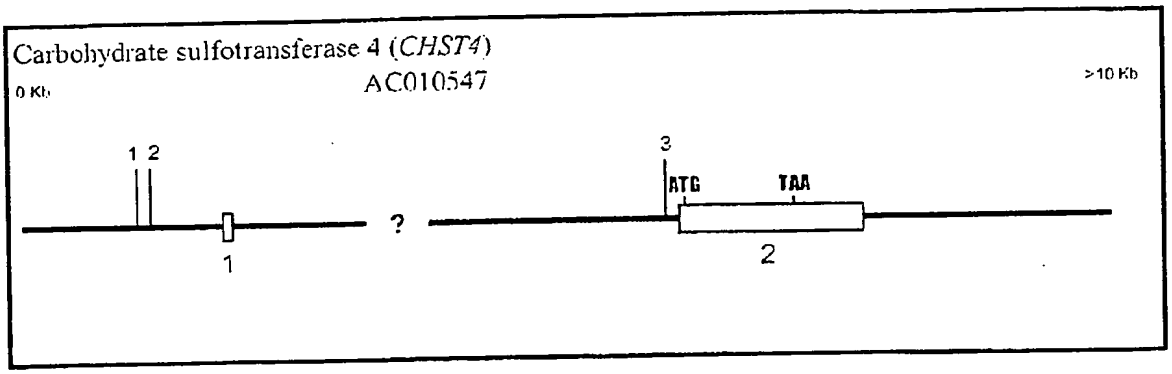


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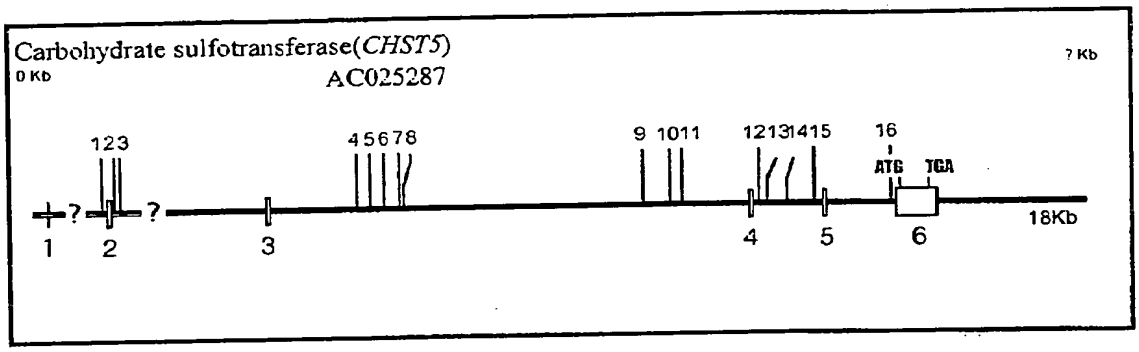


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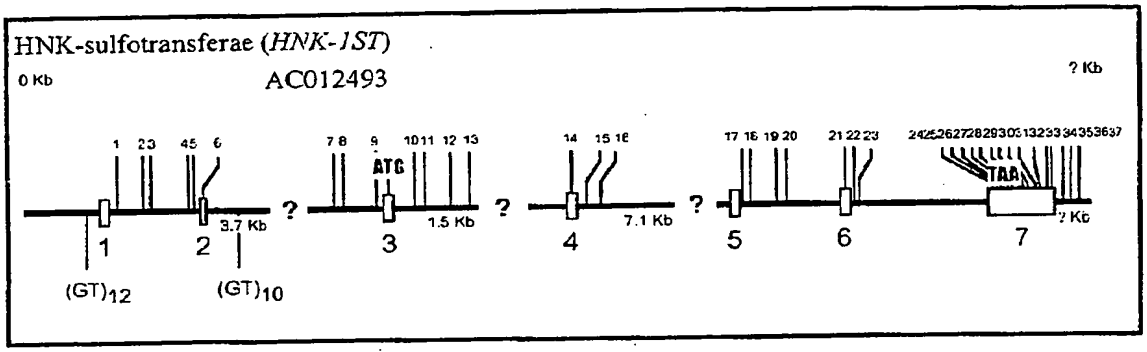


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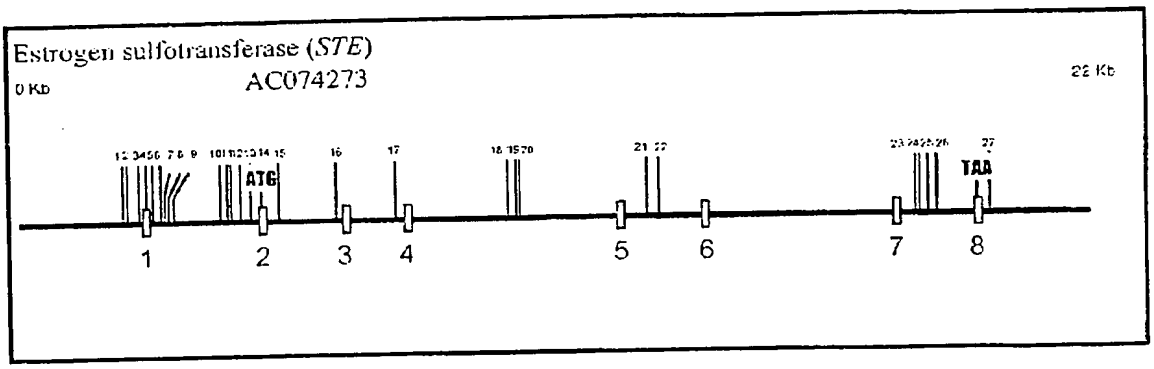


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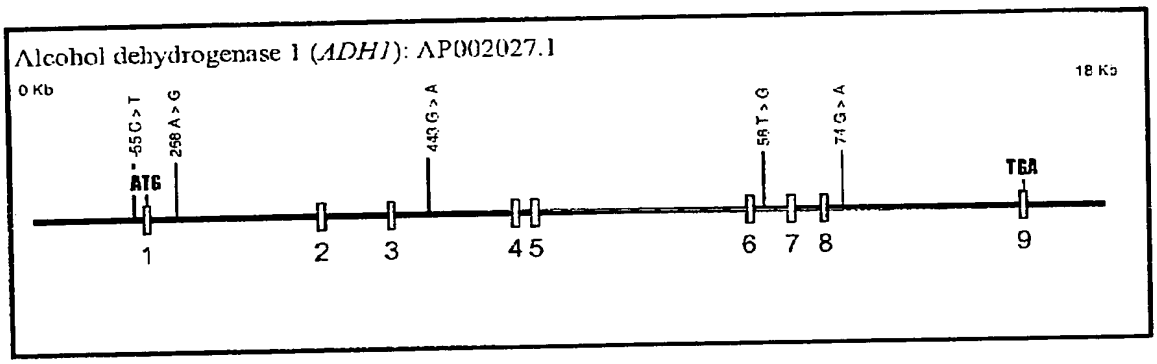


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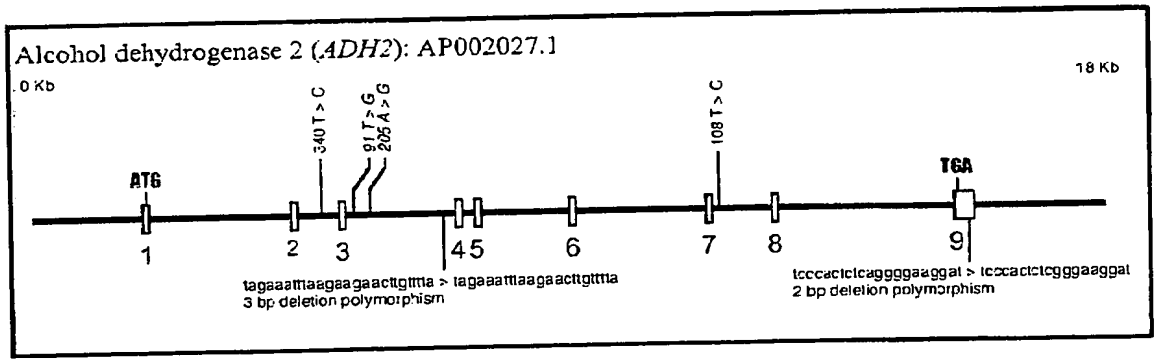


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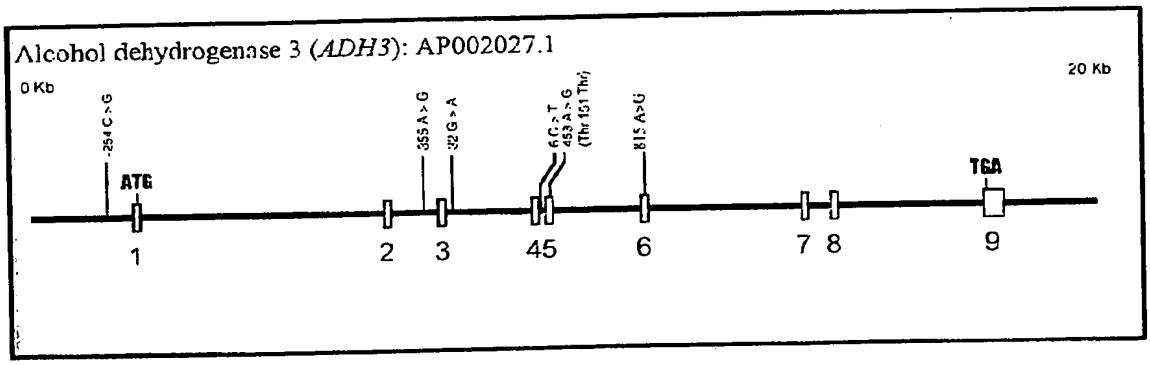


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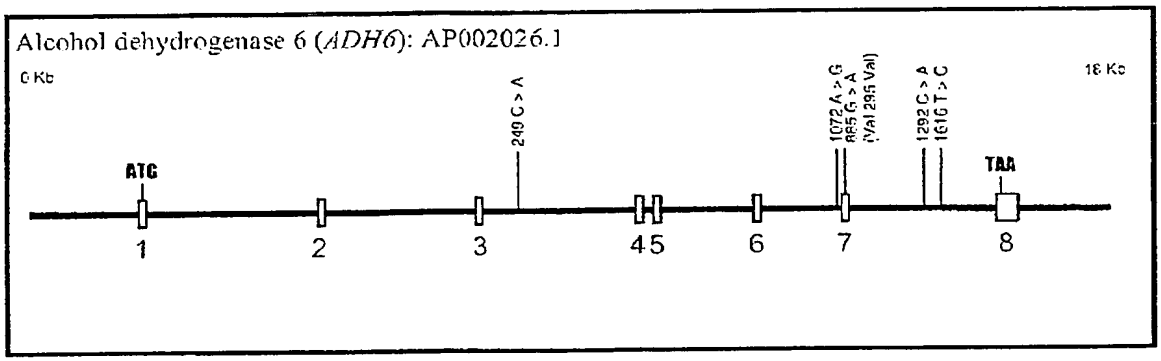


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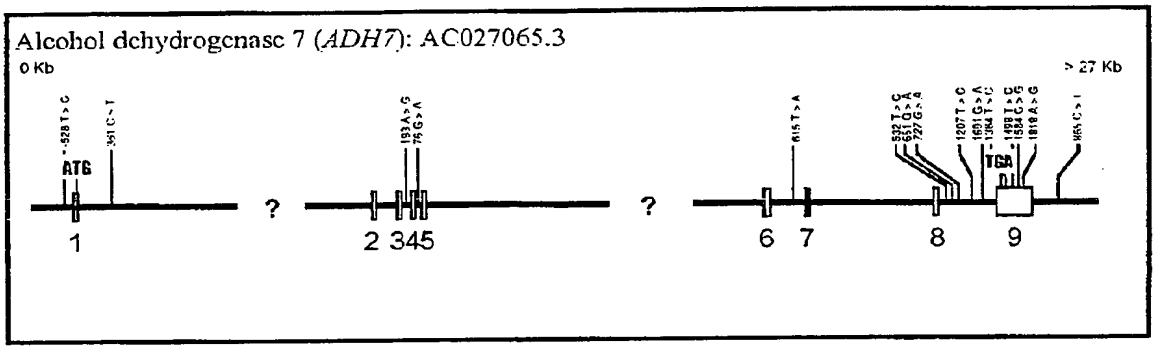
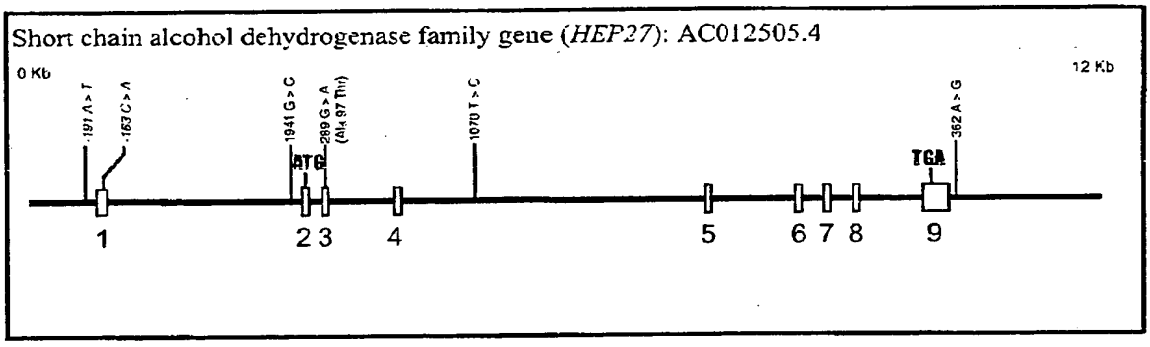


Fig. 46



L1 cell adhesion molecule (L1CAM)

Accession No. U52112

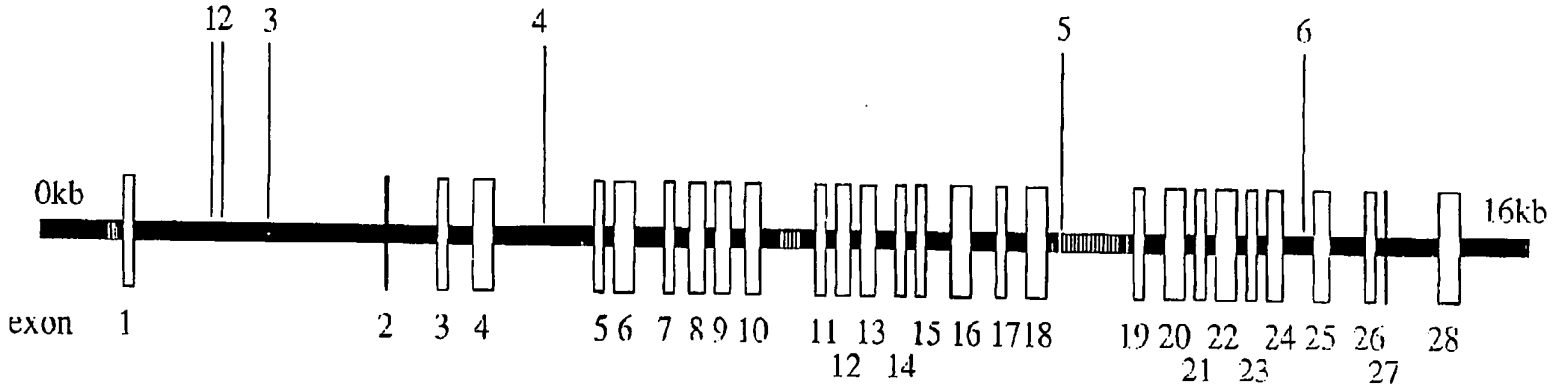


Fig. 47

arylalkylamine N-acetyltransferase(AANAT)

Accession No. U40391

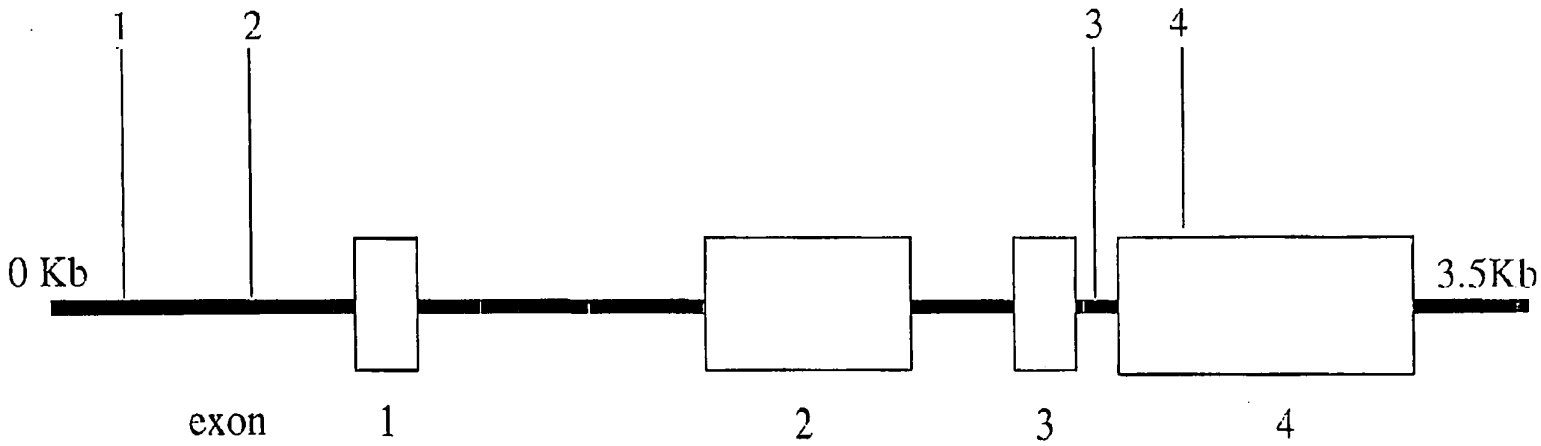


Fig. 48

N-acetyltransferase, homolog of S. cerevisiae (ARD1)

Accession No. U52112

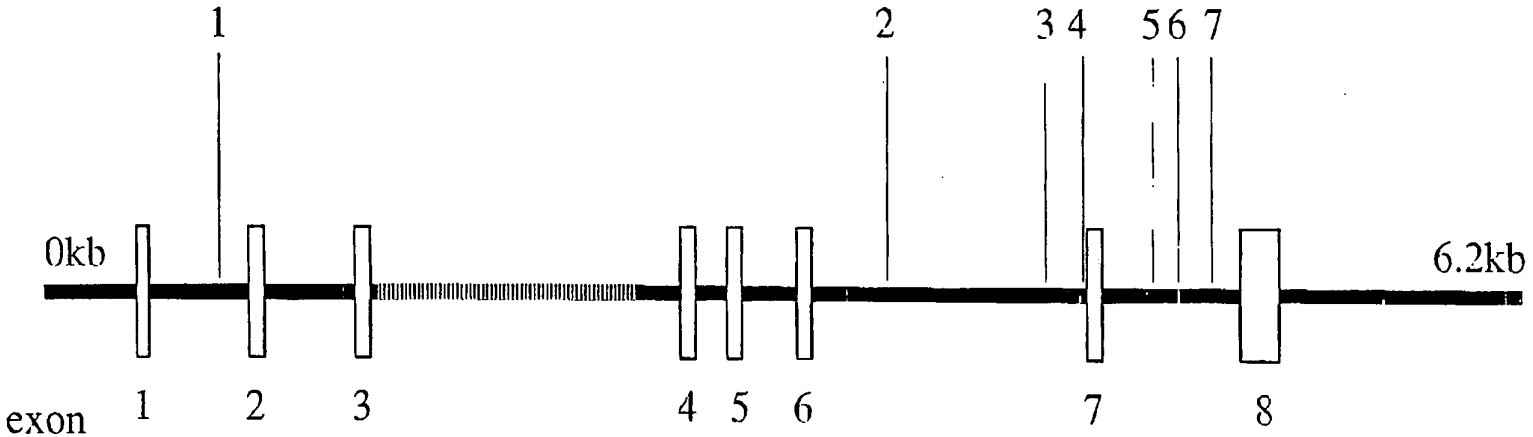
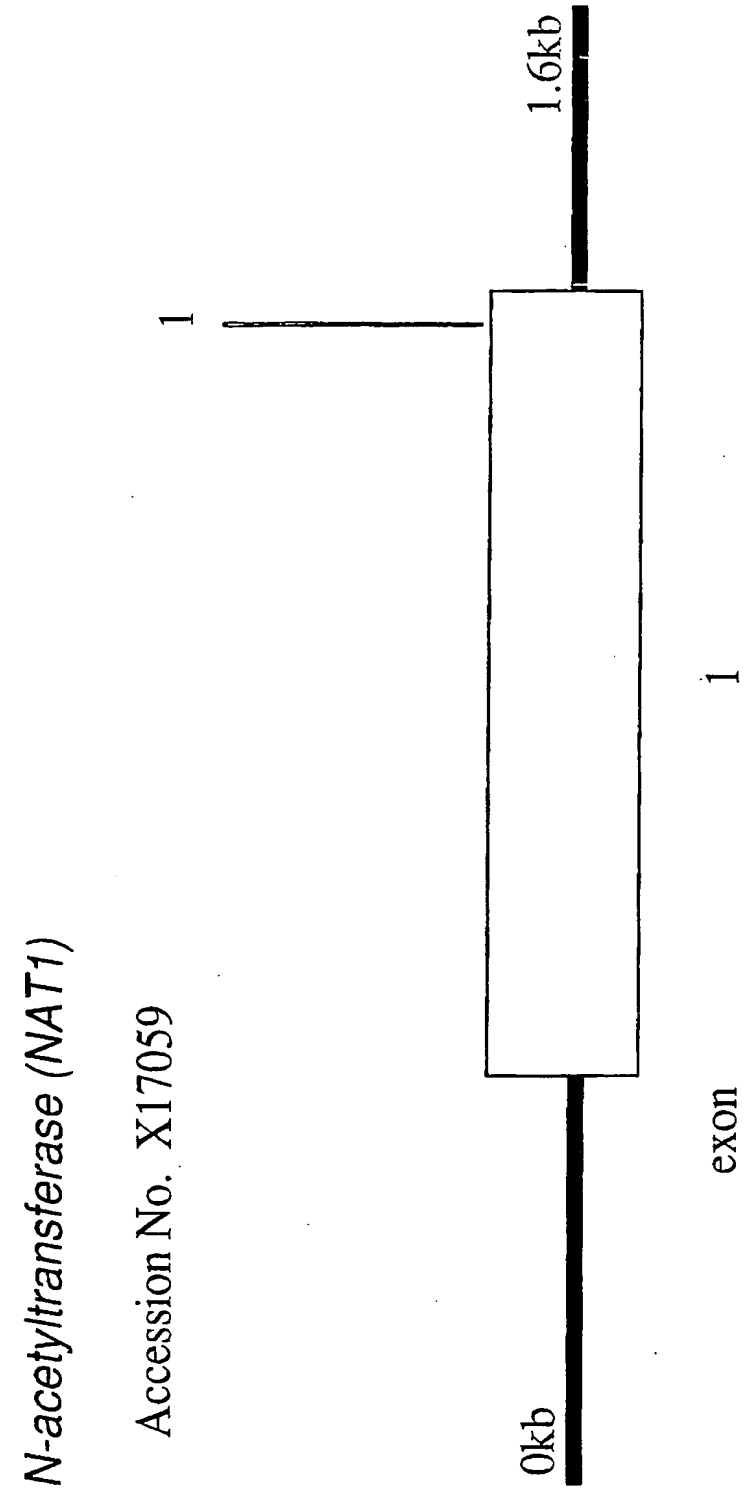


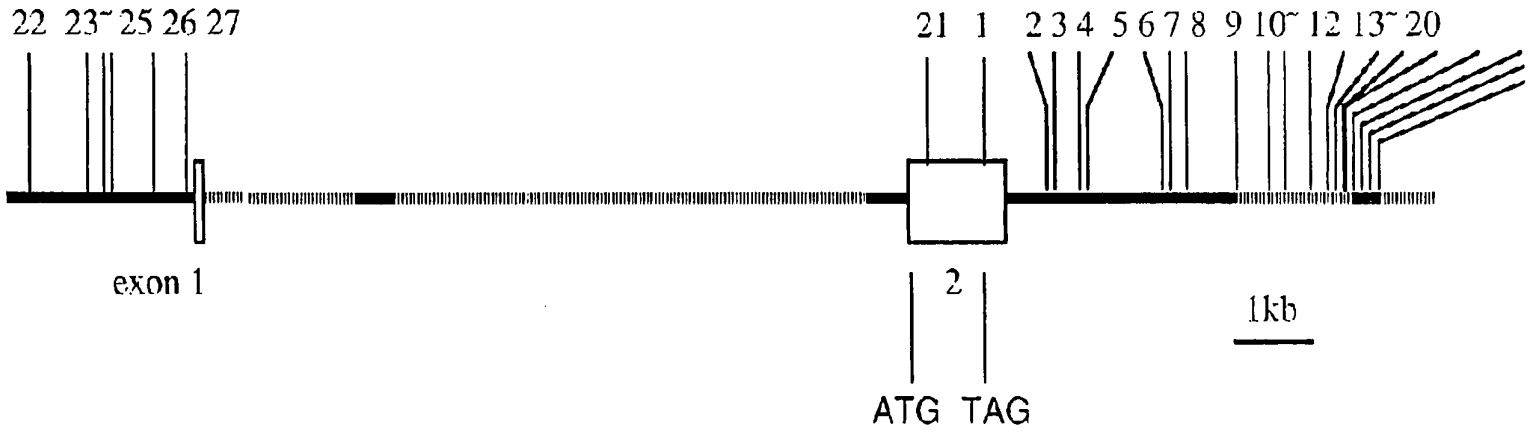
Fig. 49

Fig. 50


N-acetyltransferase (NAT1)
Accession No. X17059
1
1.6kb
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exon

arylamine N-acetyltransferase (NAT2) Accession No.: I22255, AC025062, AC025648, D10870

Fig. 51



Granzyme A(GZMA)

Accession No. AC025790

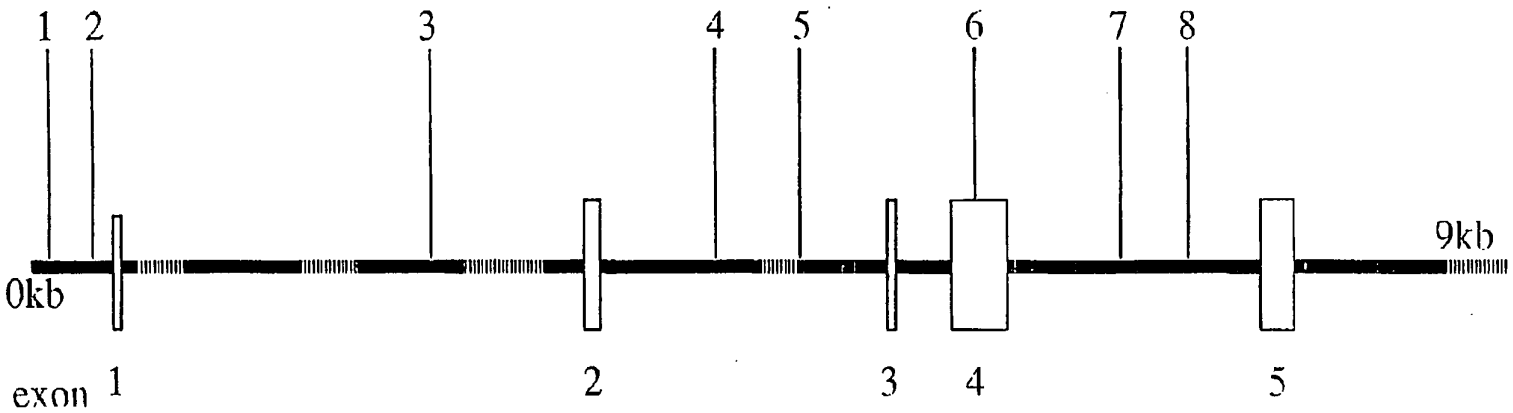


Fig. 52

Granzyme B (GZMB)

Accession No. M72150

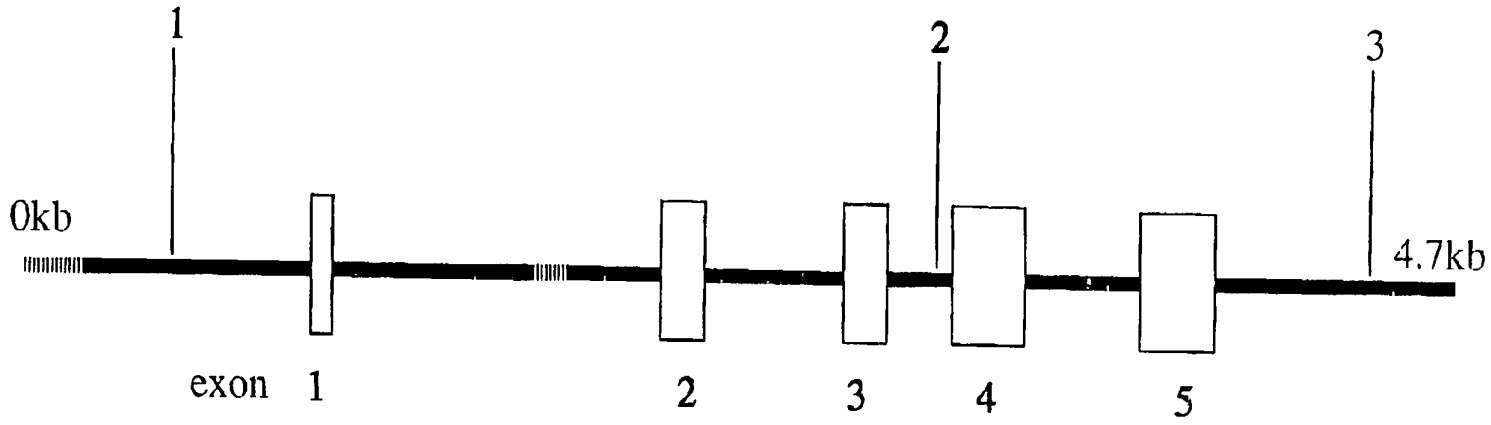


Fig. 53

esterase D/formylglutathione hydrolase (ESD)

Accession No. AC136958

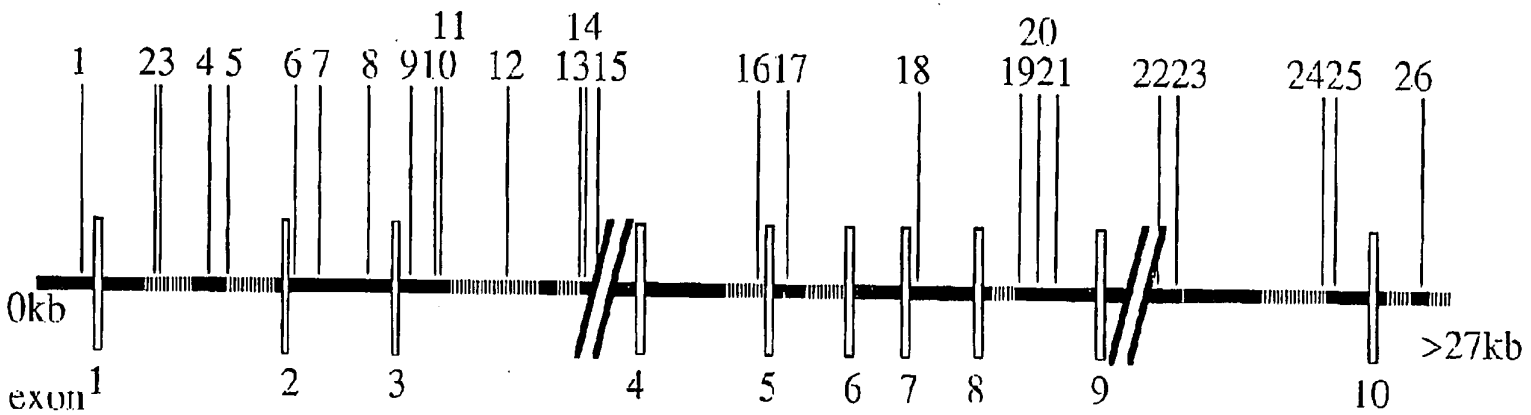


Fig. 54

dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST)

Accession No. D89060

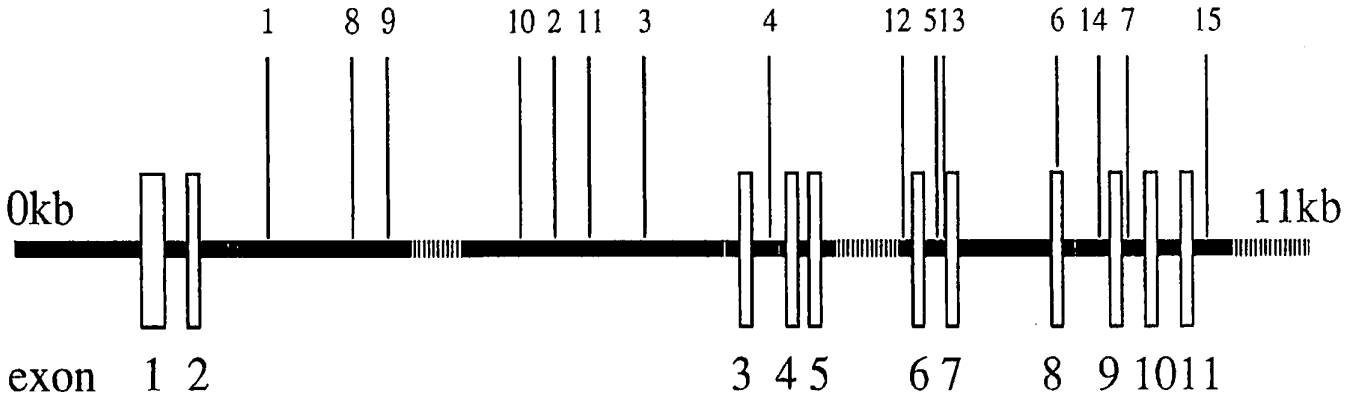


Fig. 55

Fig. 56

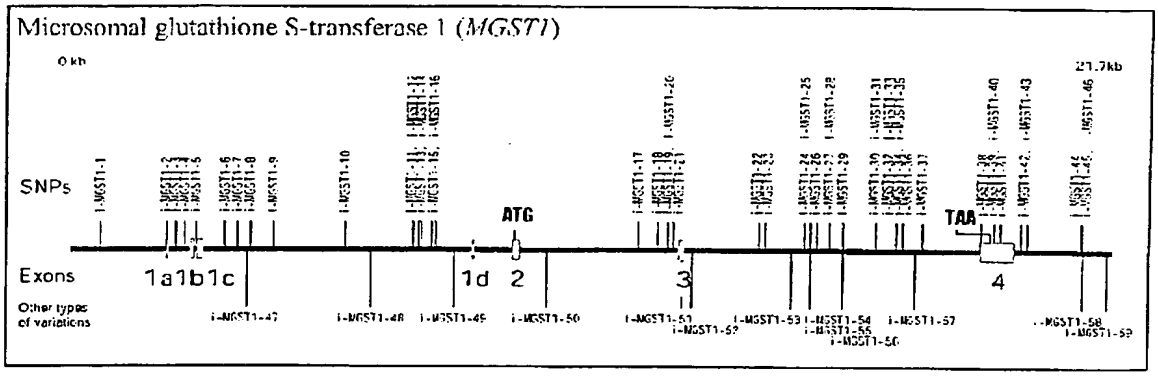


Fig. 57

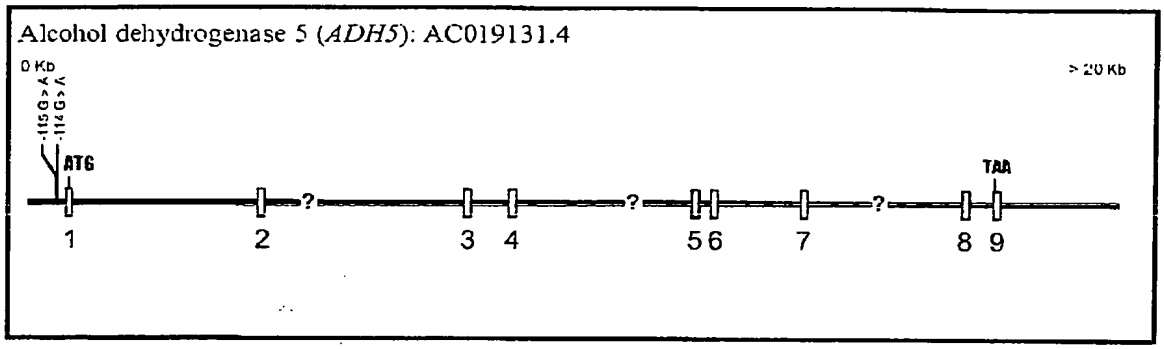


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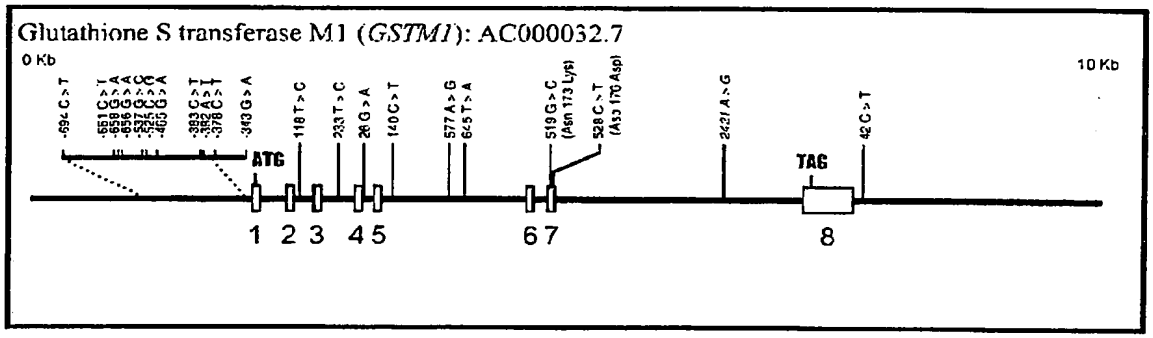


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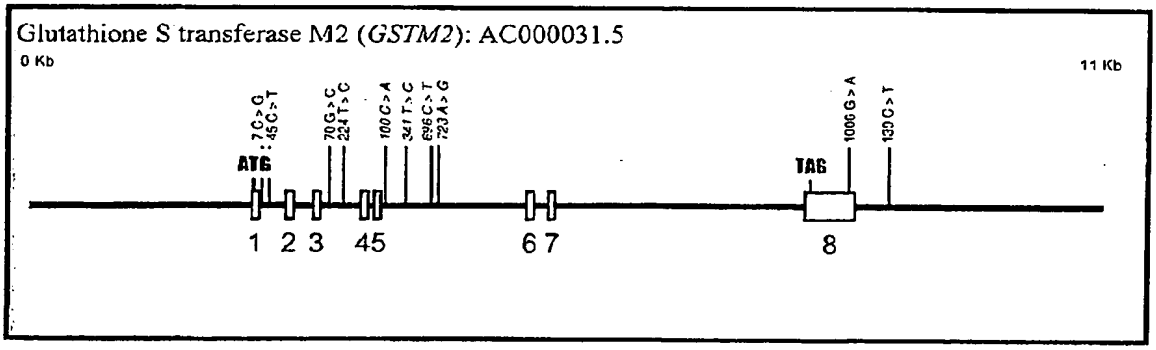


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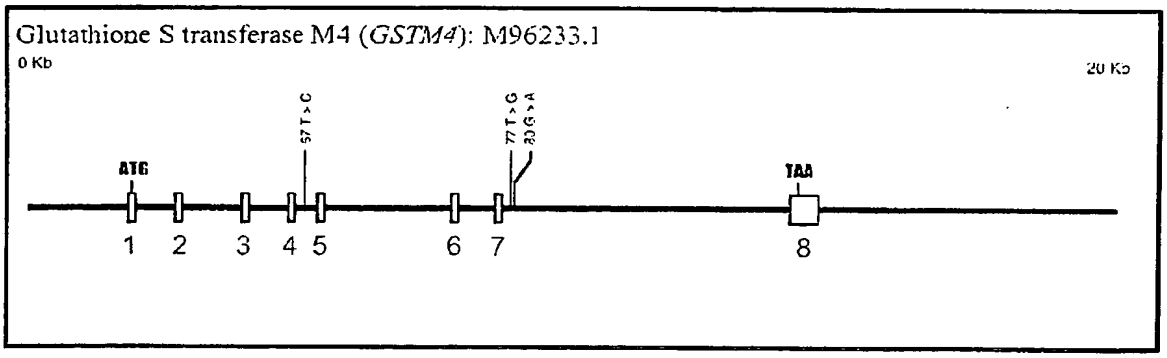


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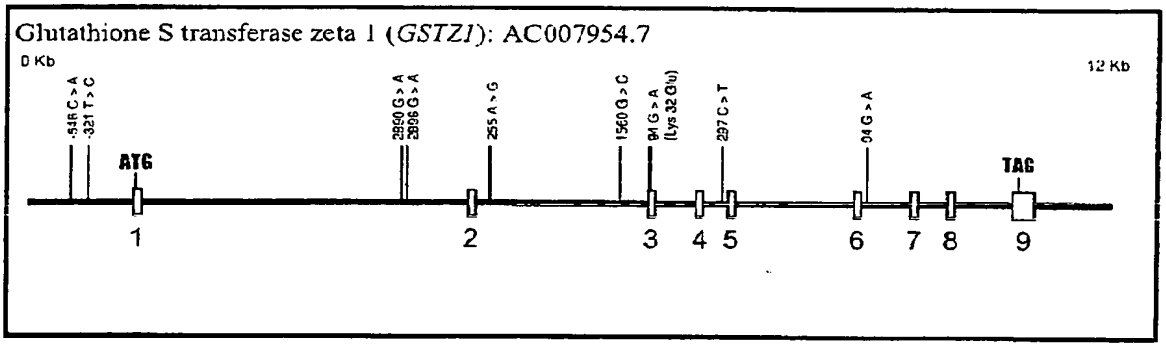


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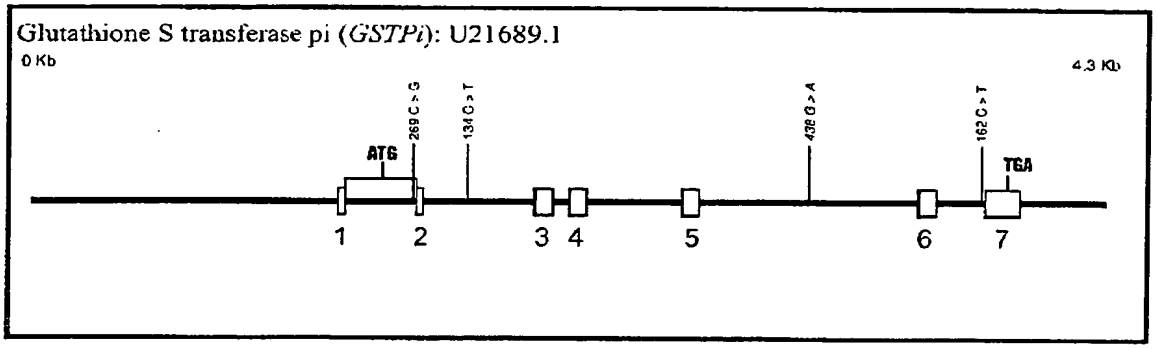


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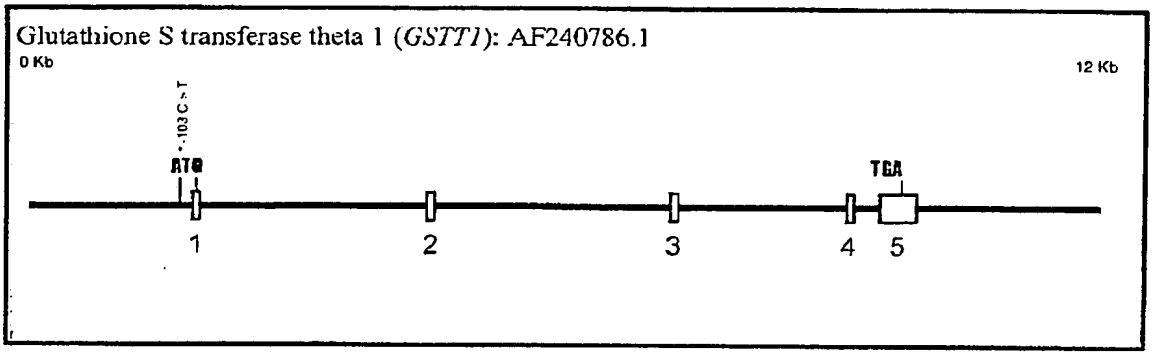


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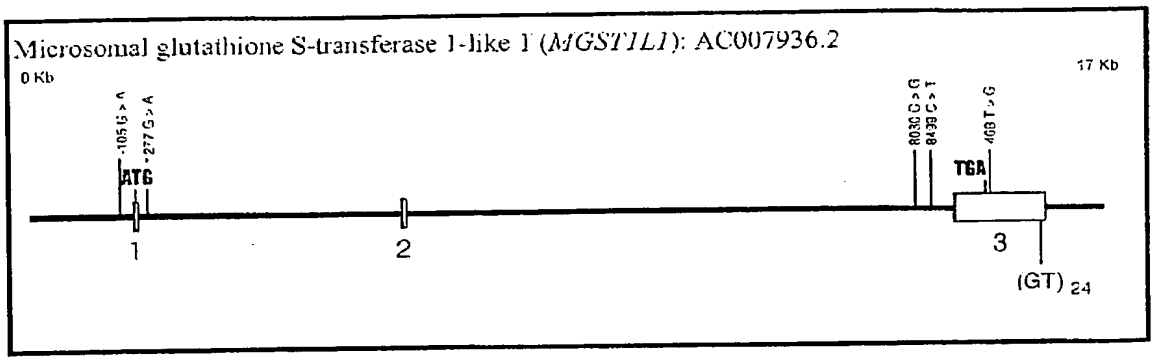


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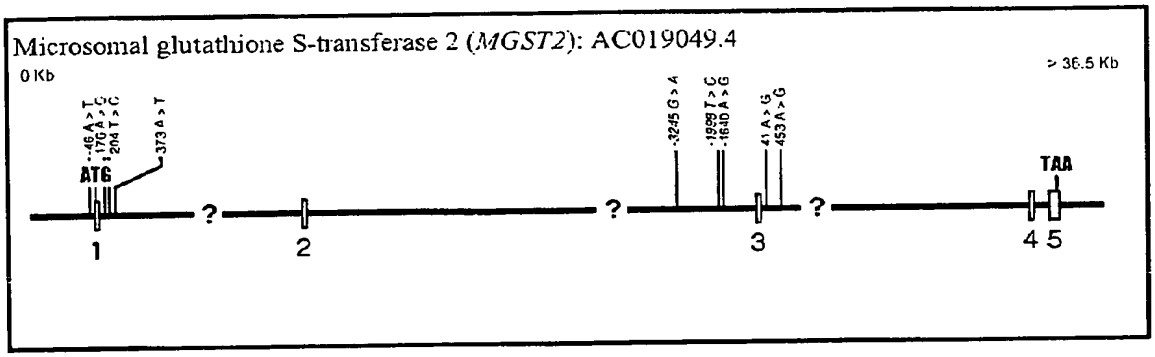


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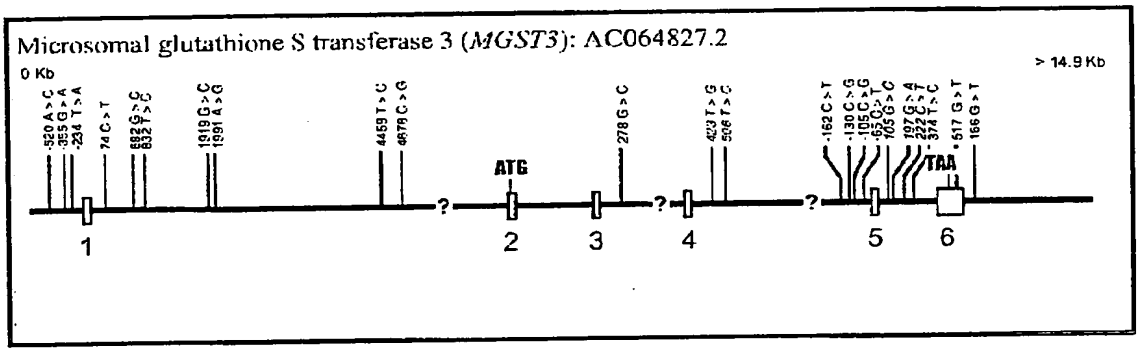


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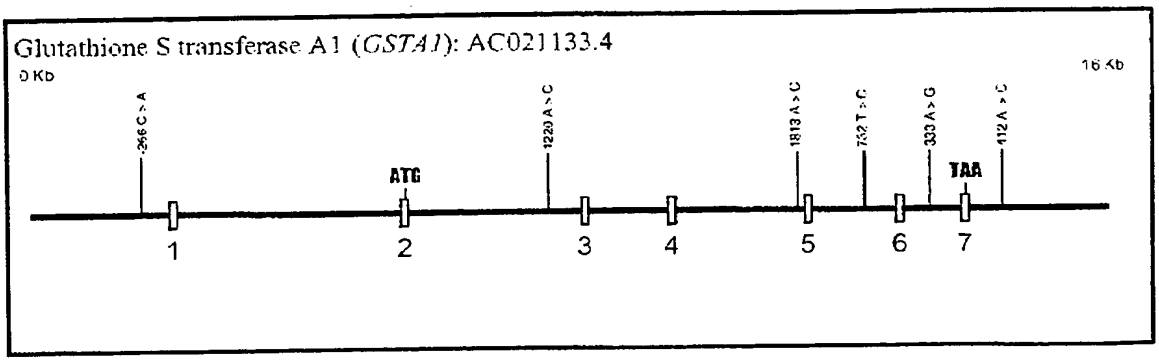


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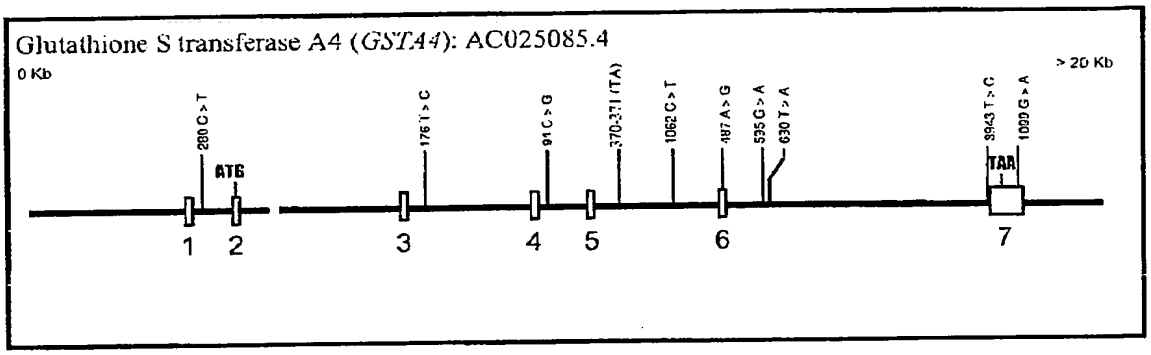


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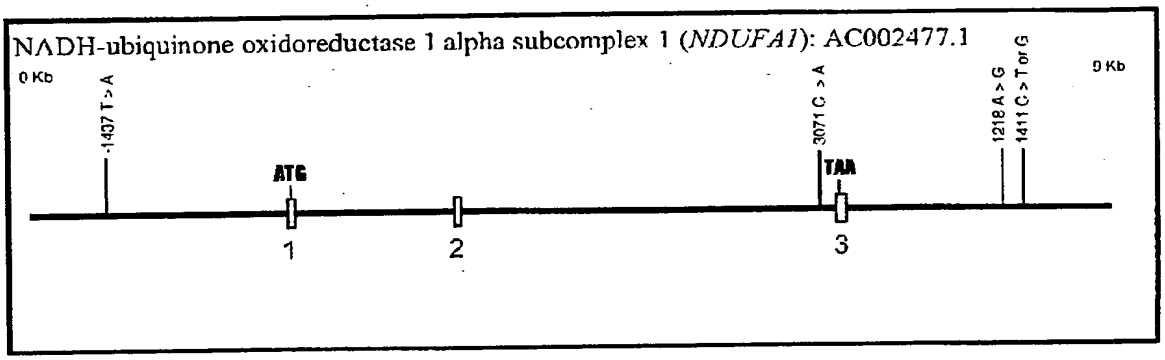


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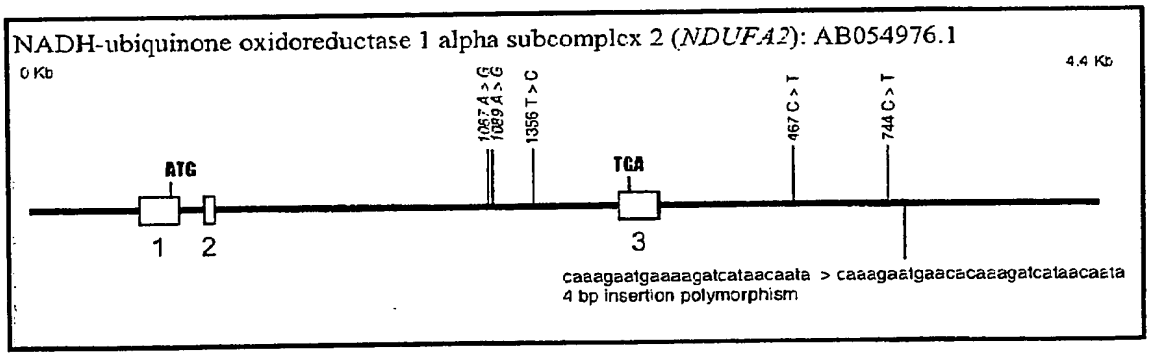


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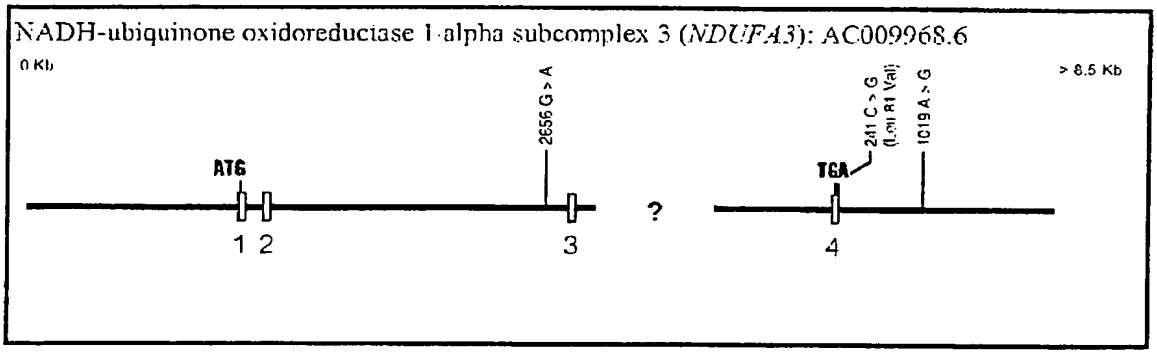


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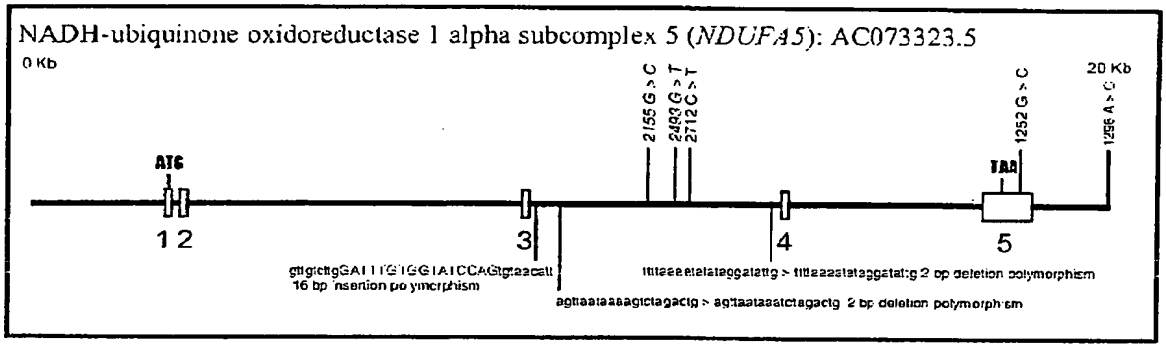


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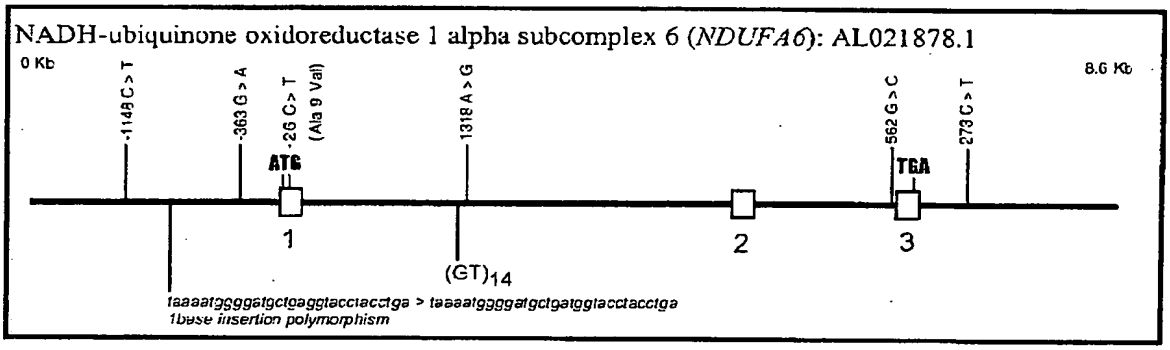


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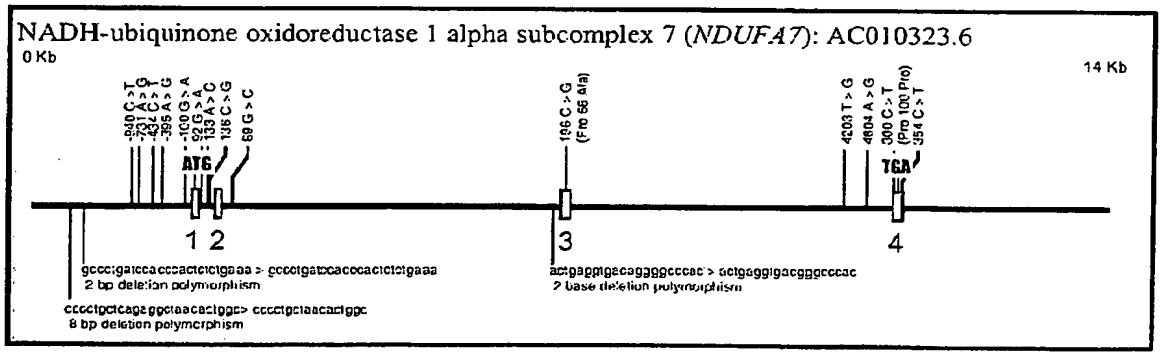


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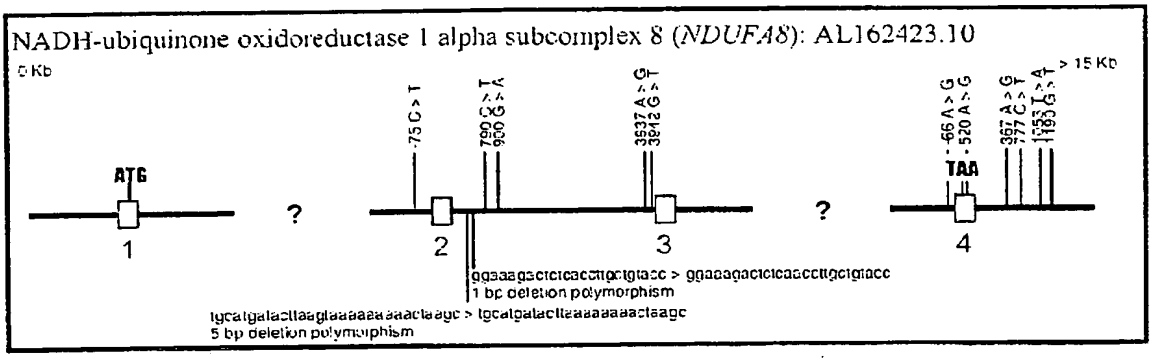


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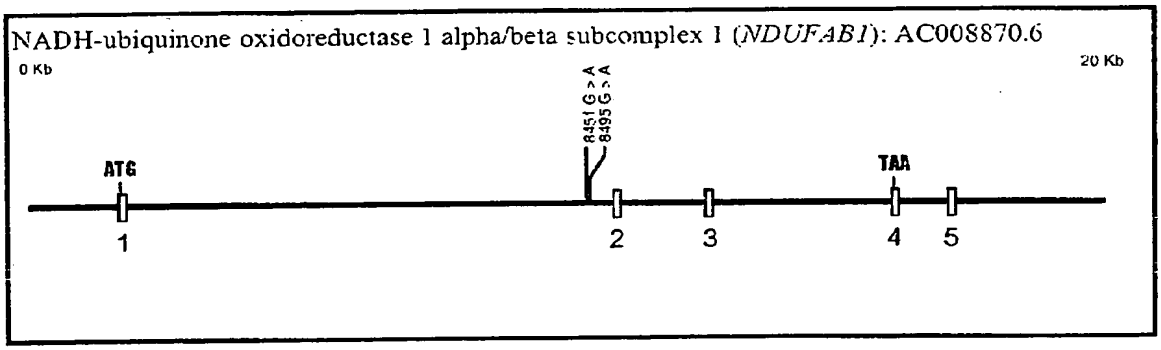


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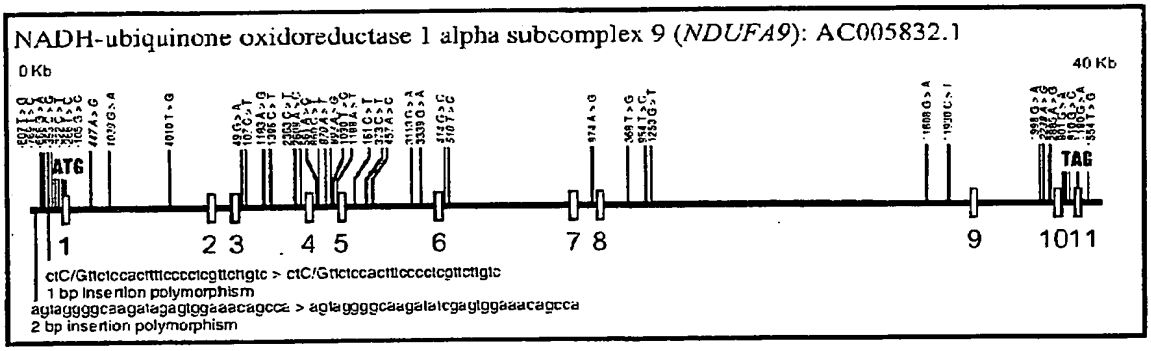


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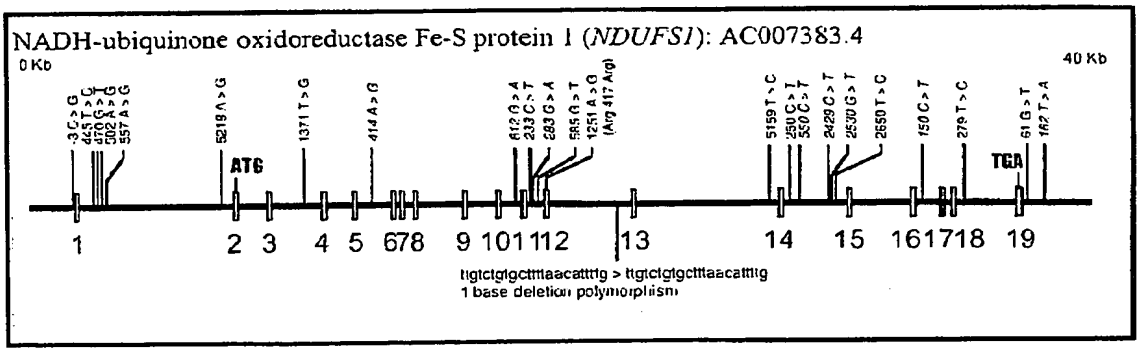


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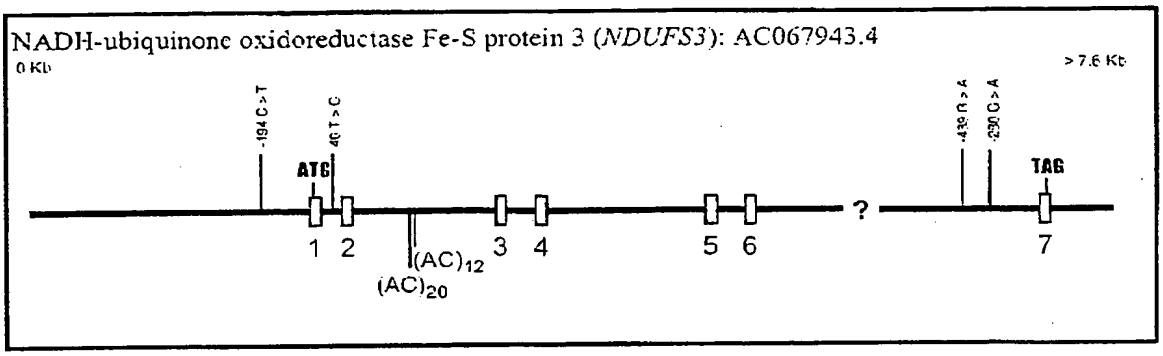


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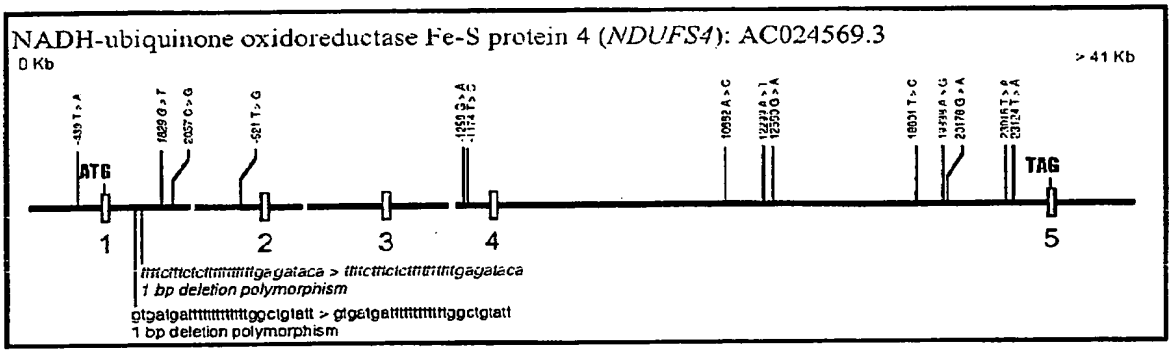


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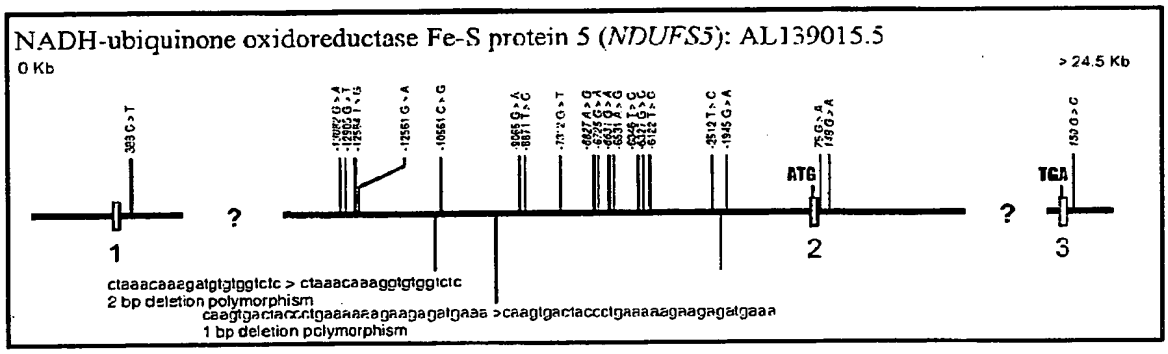


Fig. 82

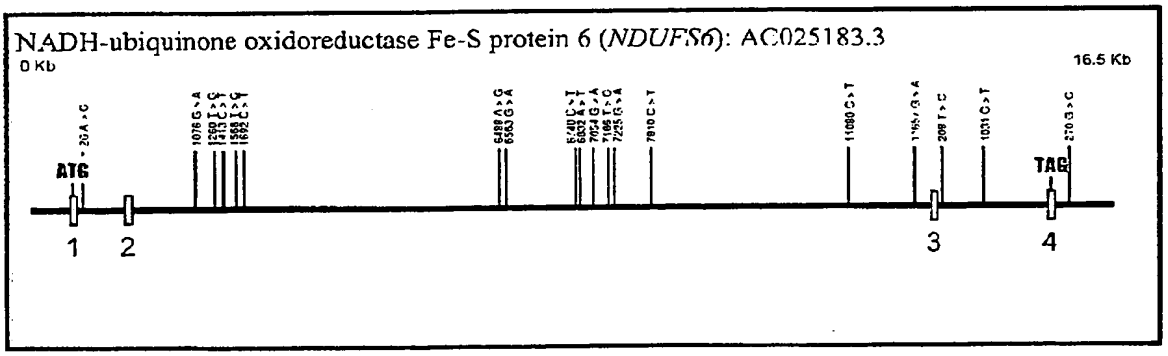


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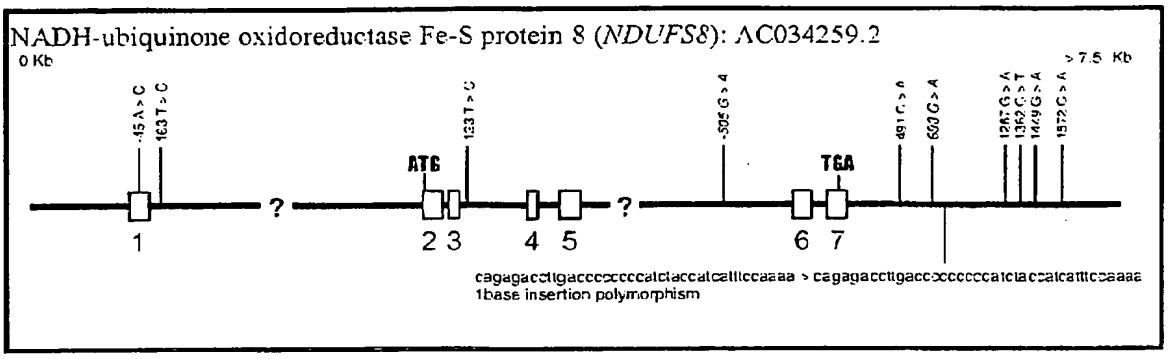


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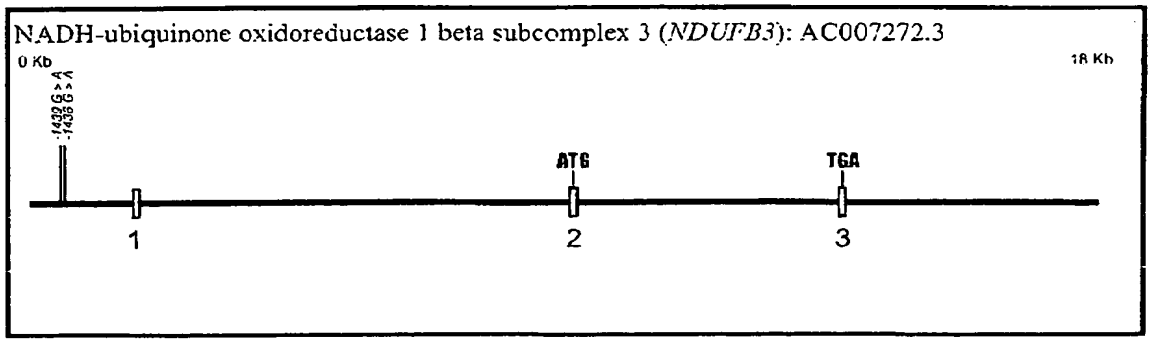


Fig. 85

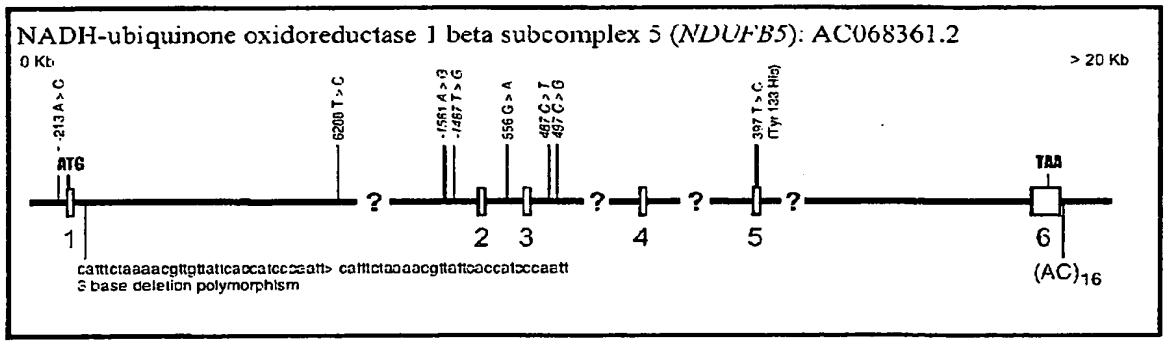
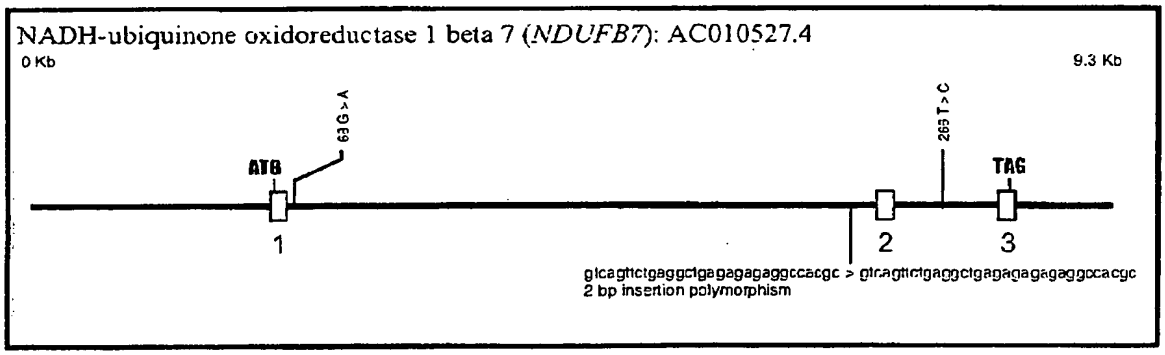


Fig. 86



SNPs

ABCA1 ACCESSION AF275948.1

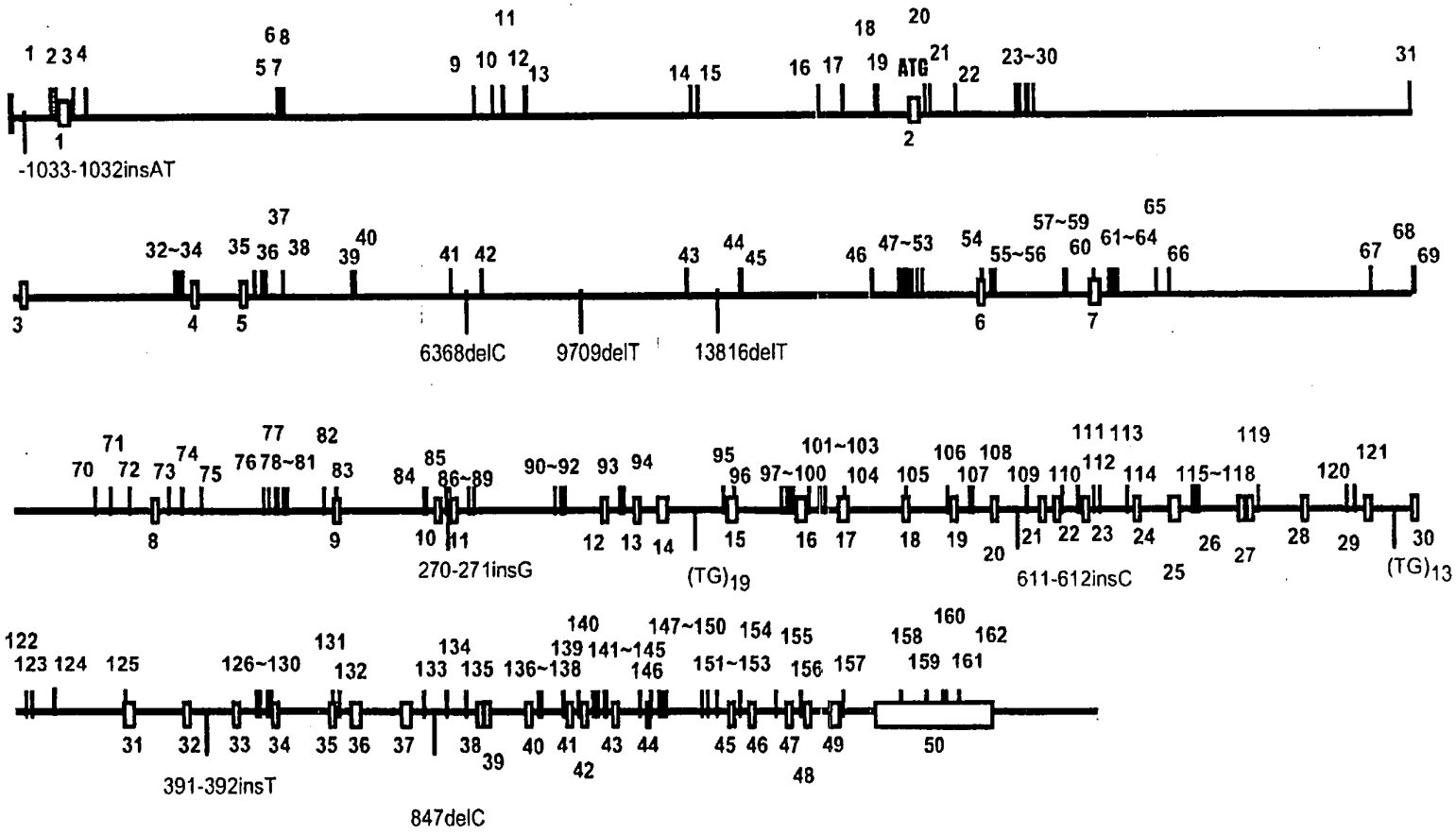


Fig. 87

Catechol-O-methyltransferase (COMT)

ACCESSION AC000080

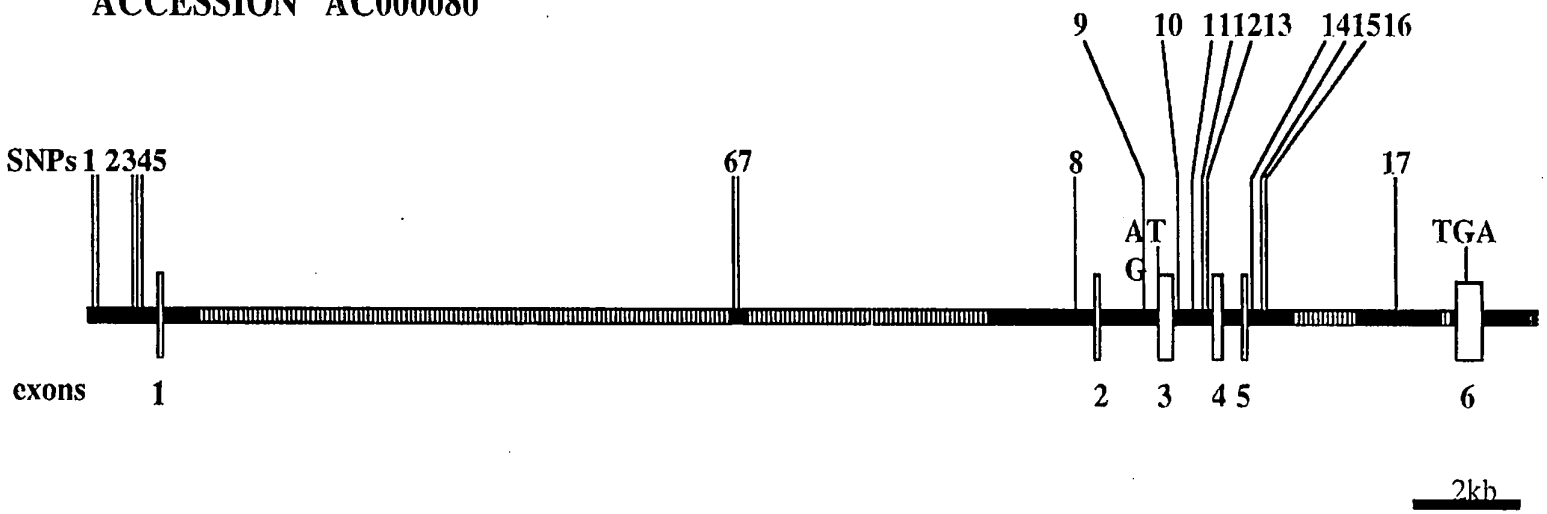


Fig. 88

Fig. 89

Histamine N-methyltransferase (HNMT)

ACCESSION AC019304

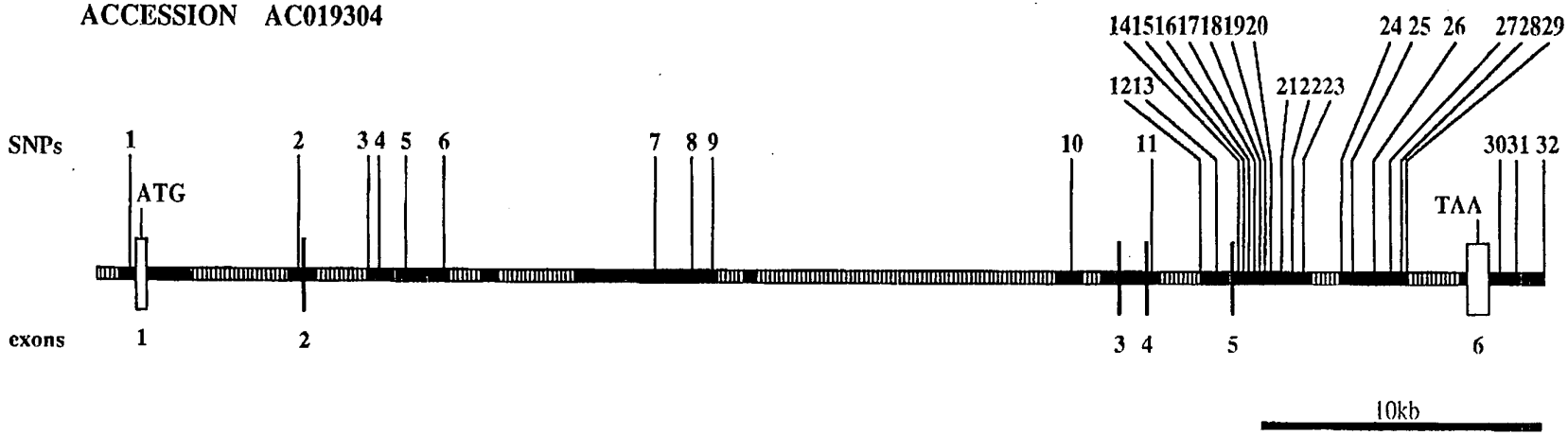
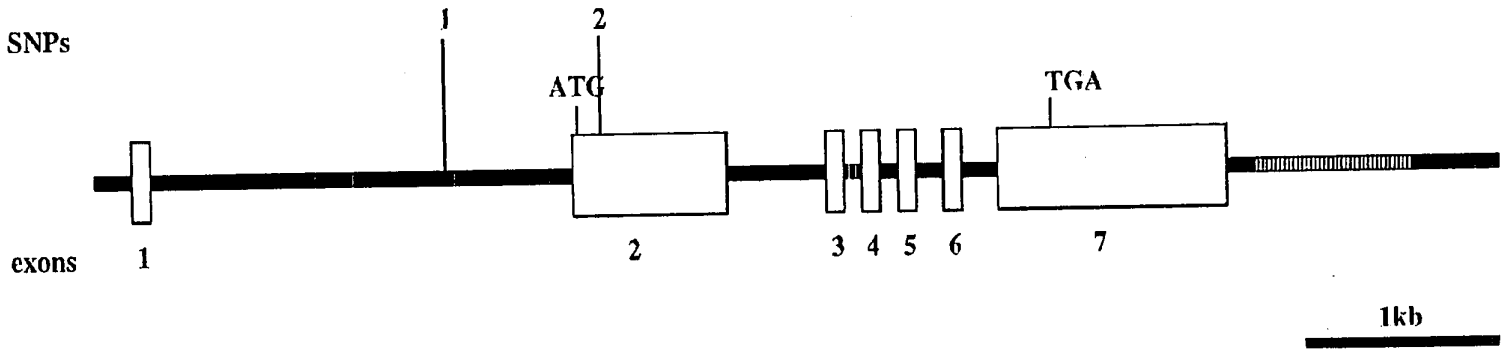


Fig. 90

Cytochrome P450, subfamily I, polypeptide 1 (CYP1A1)

ACCESSION X04300



Cytochrome P450, subfamily 1, polypeptide 2 (CYP1A2)

ACCESSION AC020705

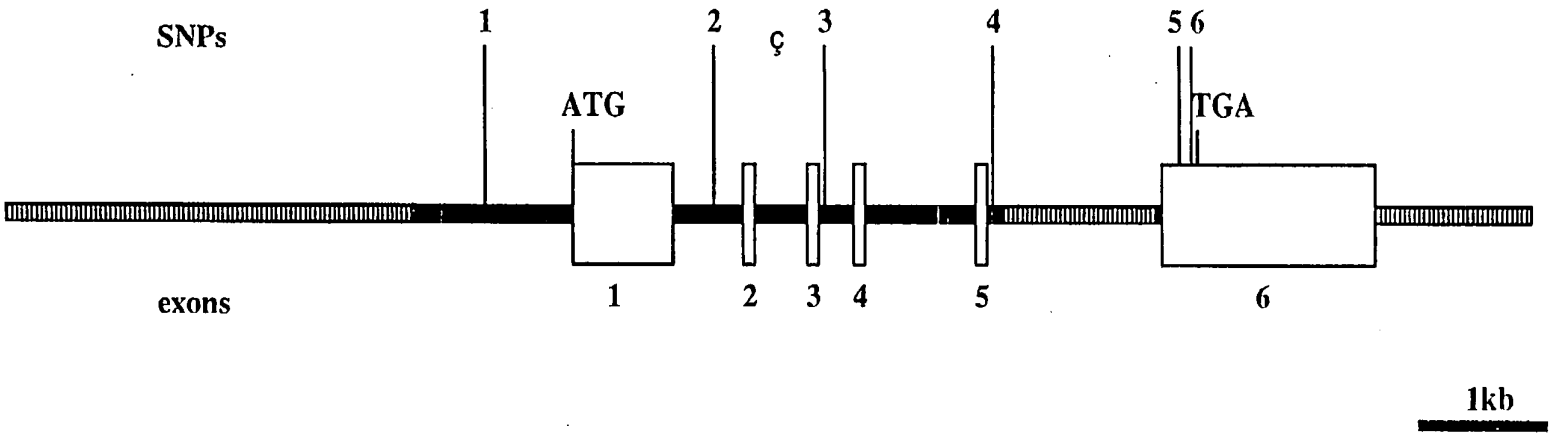


Fig. 91

Fig. 92

Cytochrome P450, subfamily I, polypeptide 1 (CYP1B1)

ACCESSION AC009229

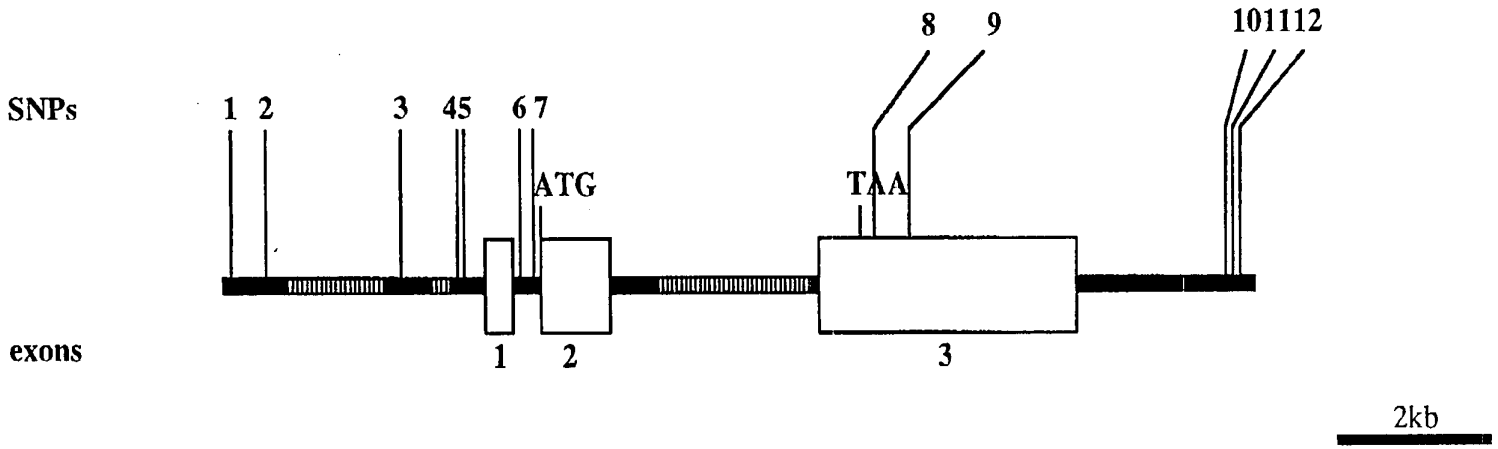
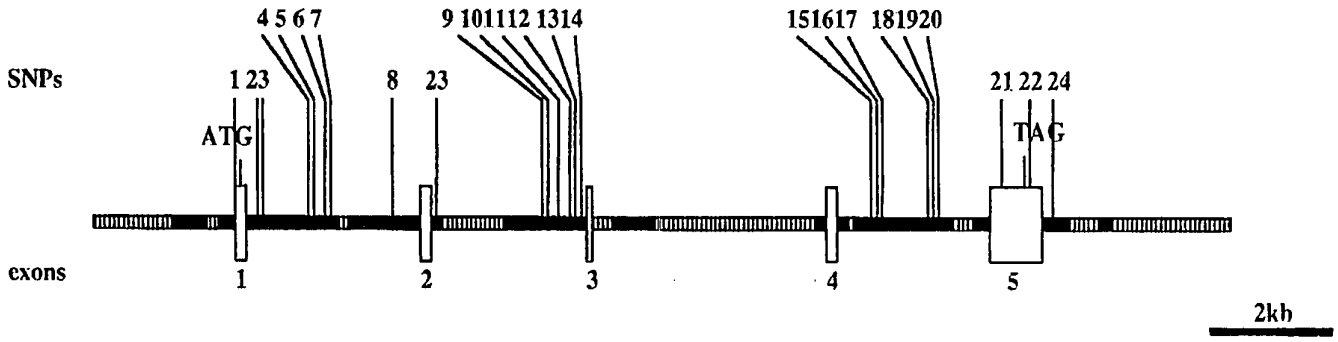


Fig. 93

Arylacetamide deacetylase (AADAC)

ACCESSION AC068647



neuropathy target esterase (NTE)

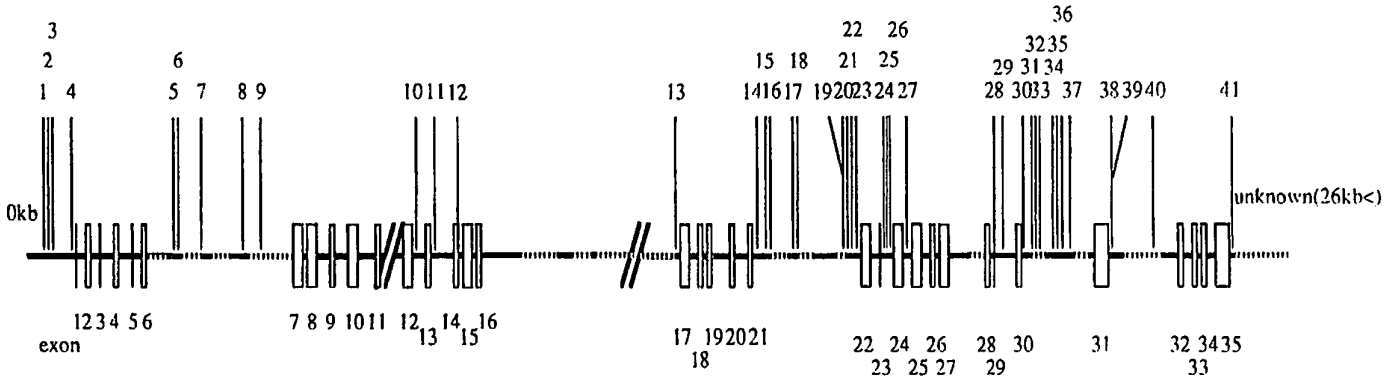


Fig. 94

ATP-binding cassette, sub-family C (CFTR/MRP), member2 (MRP2)

ACCESSION AL392107

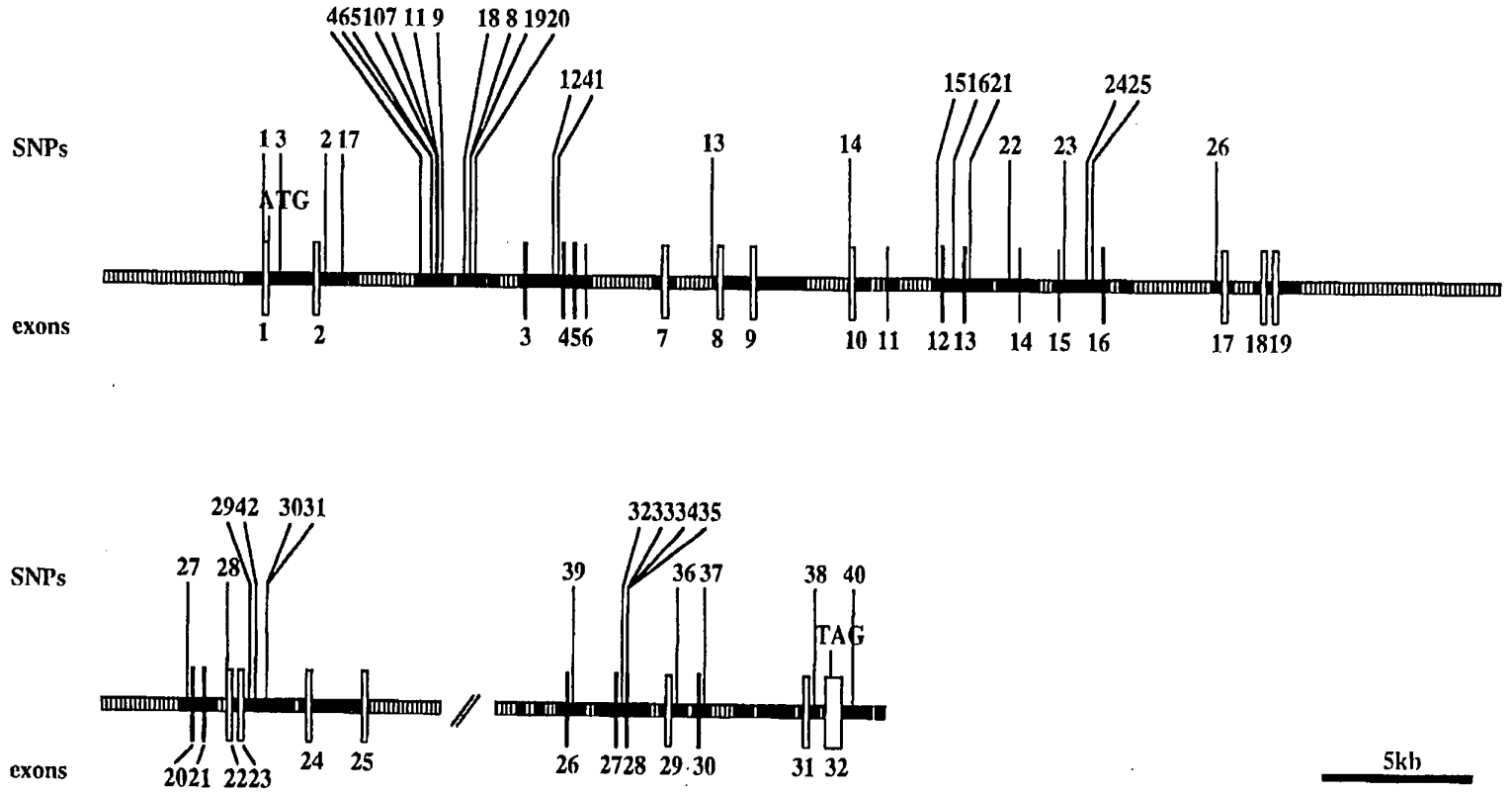


Fig. 95

Fig. 96

ATP-binding cassette, sub-family B, member1 (ABCB1)

ACCESSION AC002457
AC005068

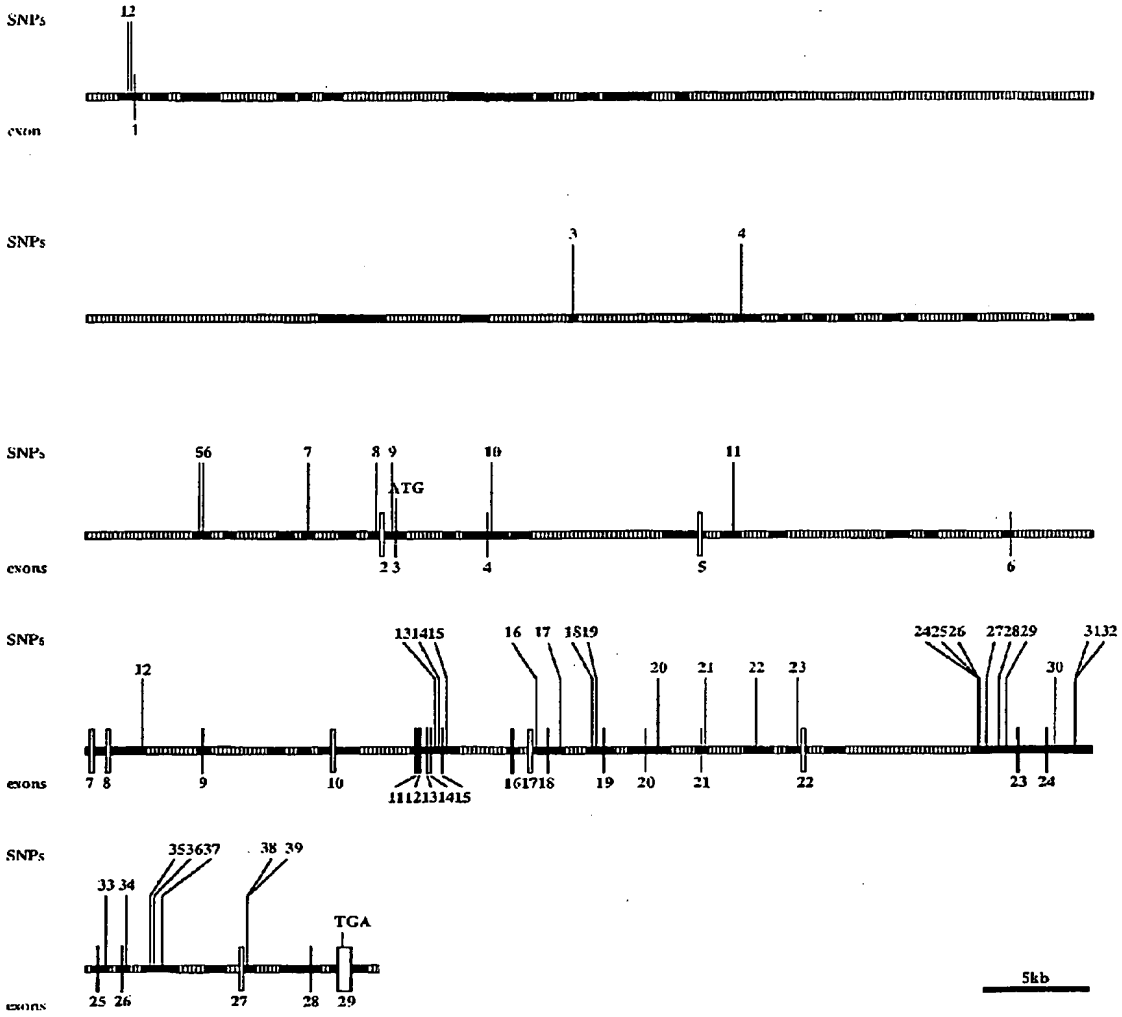


Fig. 97

ATP-binding cassette, sub-family B, member 3 (ABCB3)
ACCESSION X66401

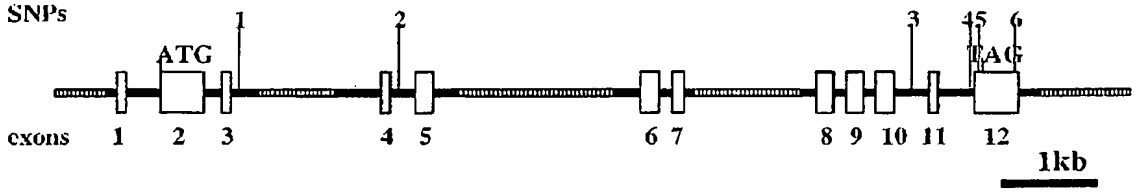


Fig. 98

ATP-binding cassette, sub-family B, member 7 (ABCB7)
ACCESSION
AL360179

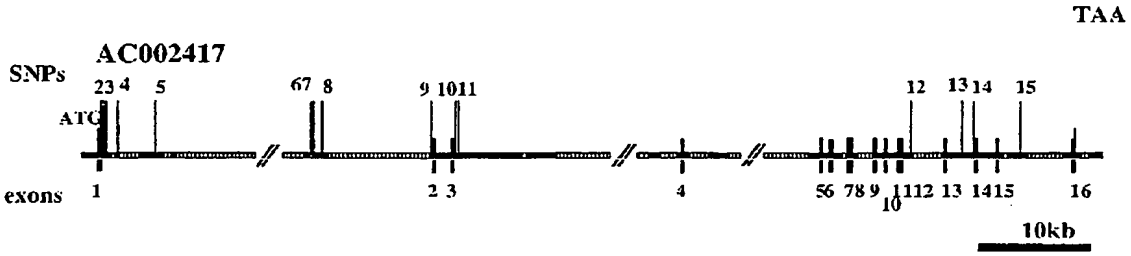


Fig. 99

ATP-binding cassette, sub-family B, member 8 (ABCB8)
ACCESSION AC010973

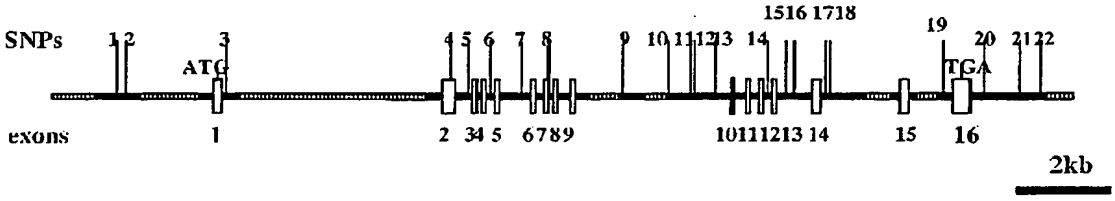


Fig. 100

ATP binding cassette, sub-family B, member 9 (ABCB9)

ACCESSION AC026362

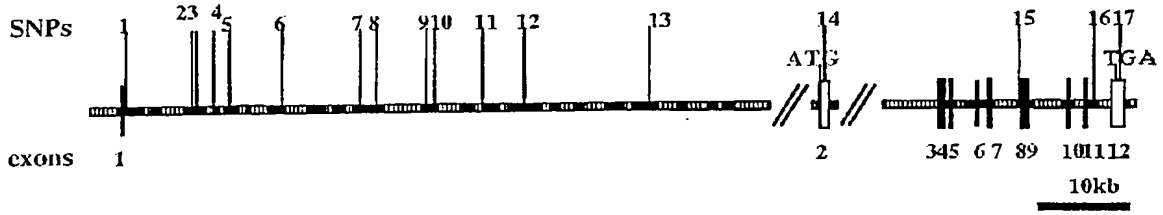


Fig. 101

ATP binding cassette, sub-family B, member 10 (ABCB10)

ACCESSION AL121990

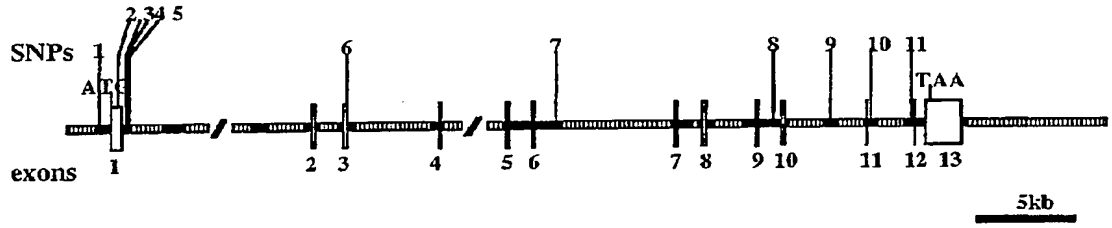


Fig. 102

ATP-binding cassette, sub-family B, member 11 (ABCB11)

ACCESSION AC008177
AC069137

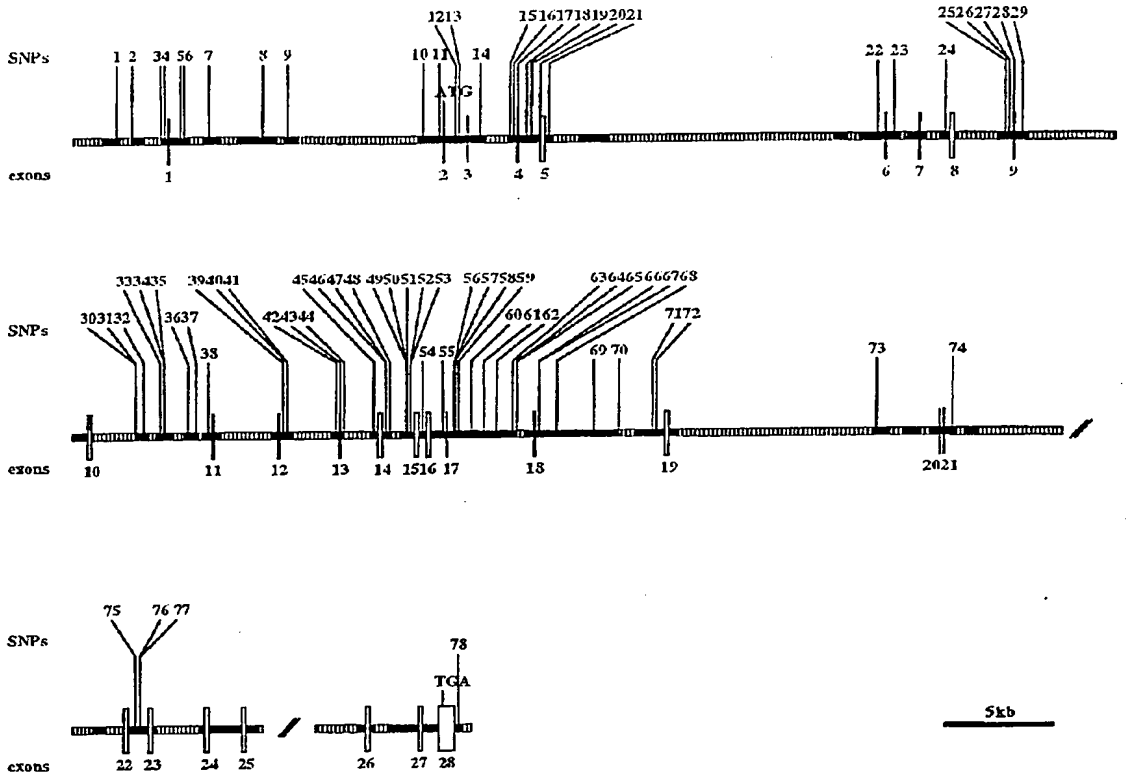


Fig. 103

Cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1)

ACCESSION AL356793

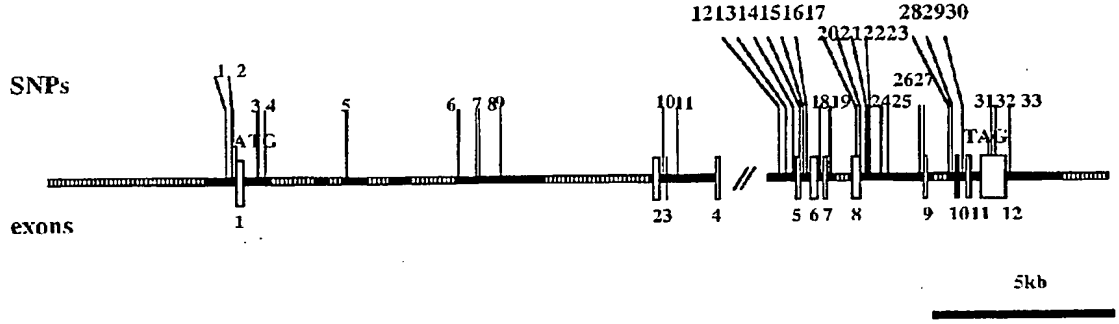


Fig. 104

Cytochrome P450, subfamily XXVIIA, polypeptide 1 (CYP27A1)

ACCESSION AC009974

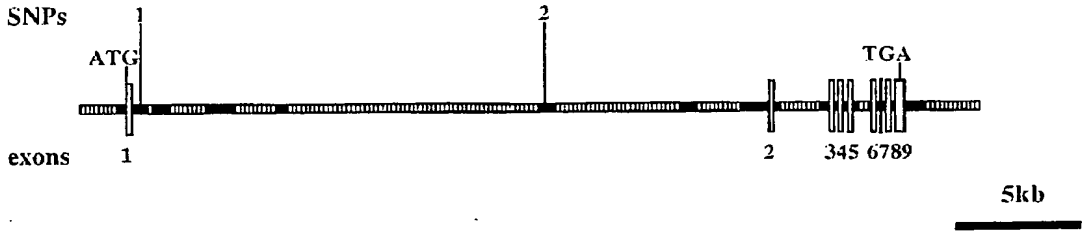


Fig. 105

Cytochrome P450, subfamily IVF, polypeptide 2 (CYP4F2)

ACCESSION AC005336

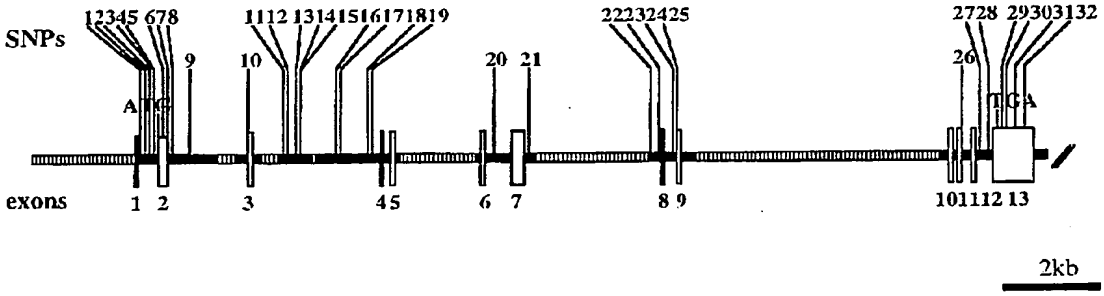


Fig. 106

Cytochrome P450, subfamily 4F, polypeptide 3 (CYP4F3)

ACCESSION AD000685

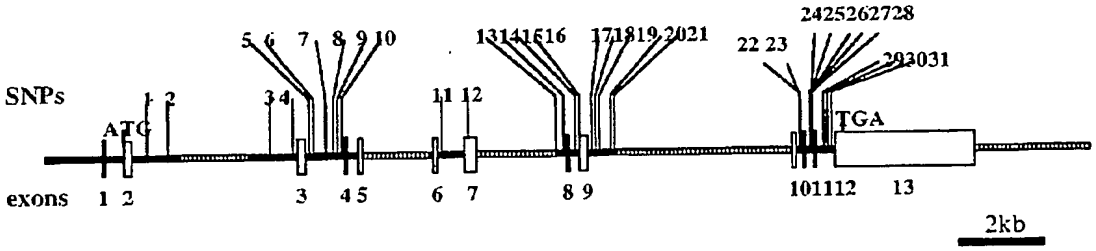


Fig. 107

Cytochrome P450, subfamily 4F, polypeptide 8 (CYP4F8)

ACCESSION AC068845

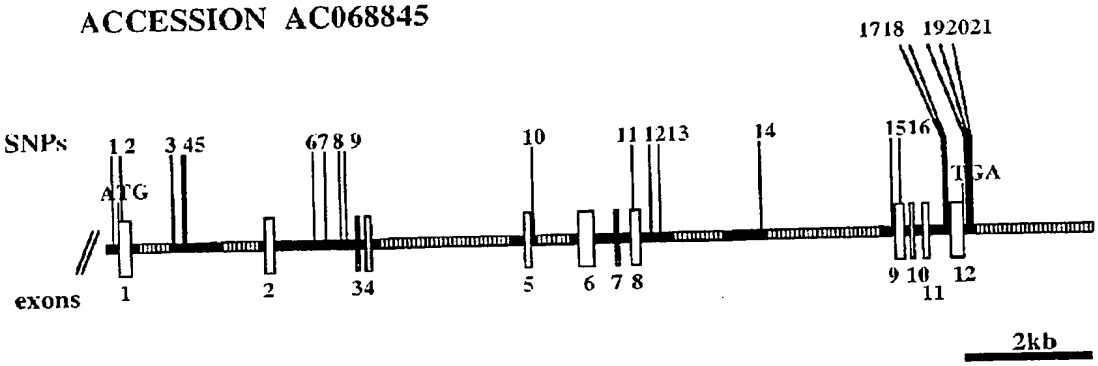


Fig. 108

Aldehyde dehydrogenase 1 (ALDH1)

ACCESSION
AC009284

AL162416

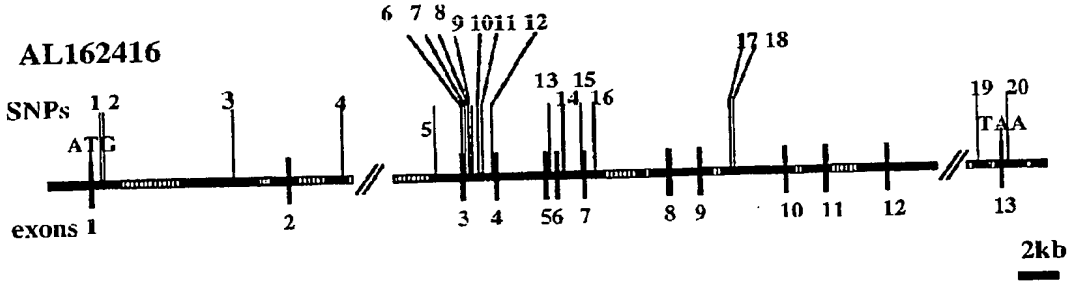


Fig. 109

Aldehyde dehydrogenase 2 (ALDH2)

ACCESSION AC002996
AC003029

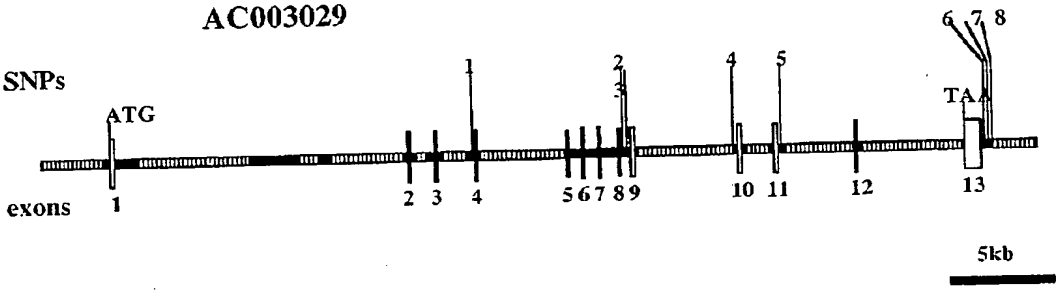


Fig. 110

Aldehyde dehydrogenase 7 (ALDH7)

ACCESSION AC004923

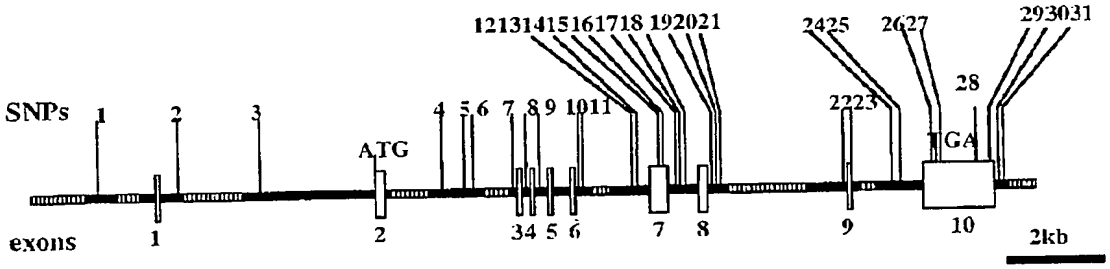


Fig. 111

Aldehyde dehydrogenase 8 (ALDH8)

ACCESSION AC021987

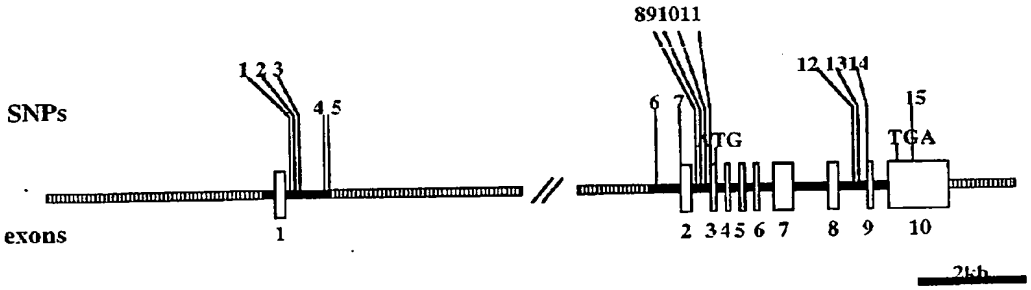


Fig. 112

Aldehyde dehydrogenase 9 (ALDH9)

ACCESSION AL451074

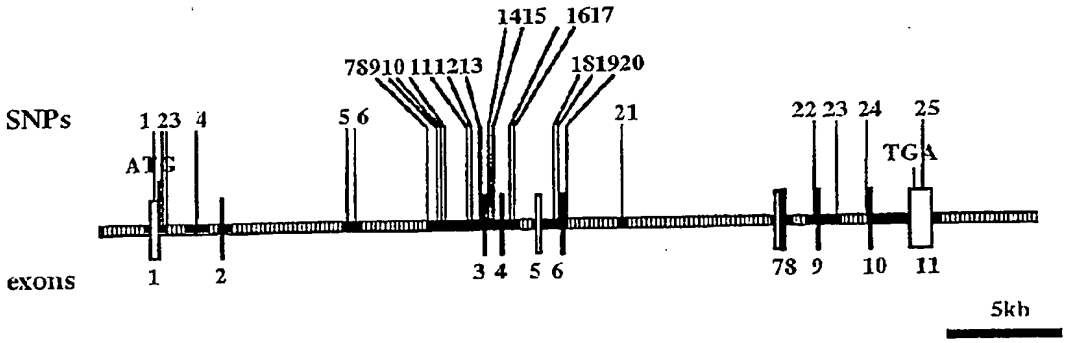


Fig. 113

Aldehyde dehydrogenase 10 (ALDH10)

ACCESSION AC005722

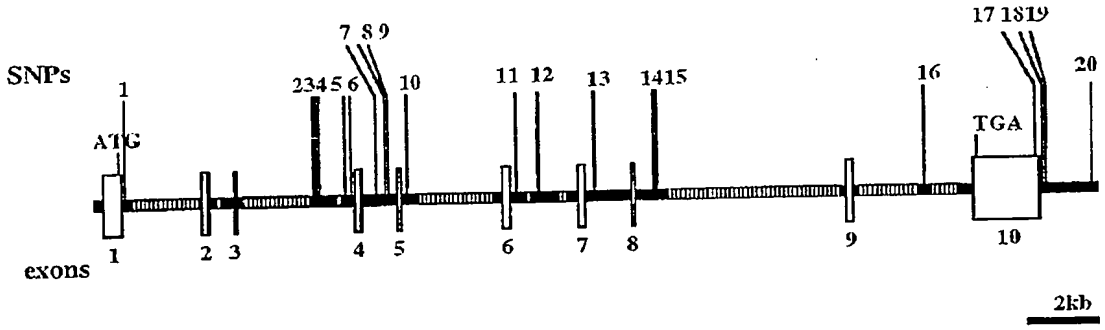
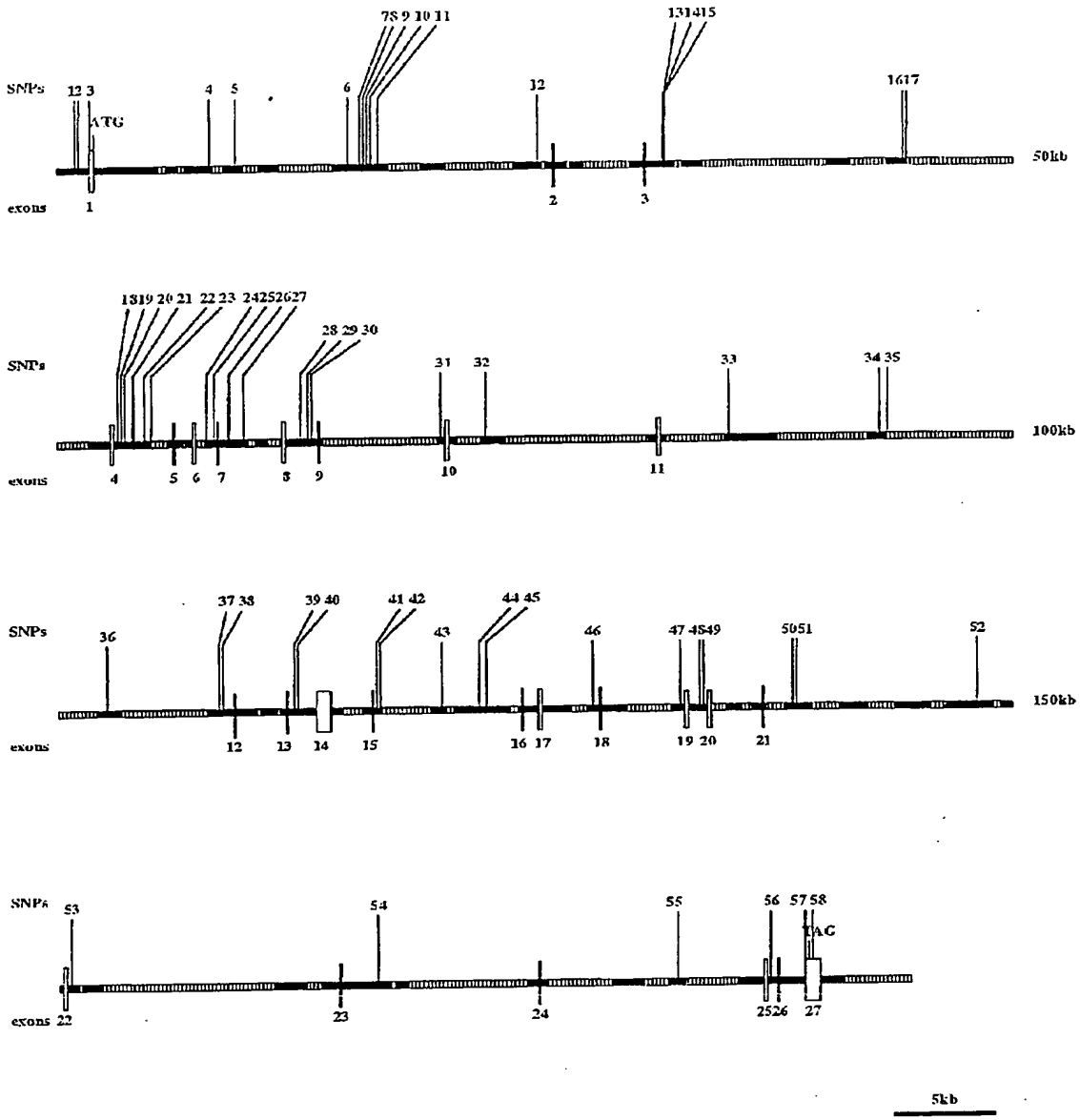


Fig. 114

ATP binding cassette, sub-family C, member 7 (ABCC7)

ACCESSION AC000111
AC000061



ATP binding cassette, sub-family C, member 8 (ABCC8)

ACCESSION AC000406

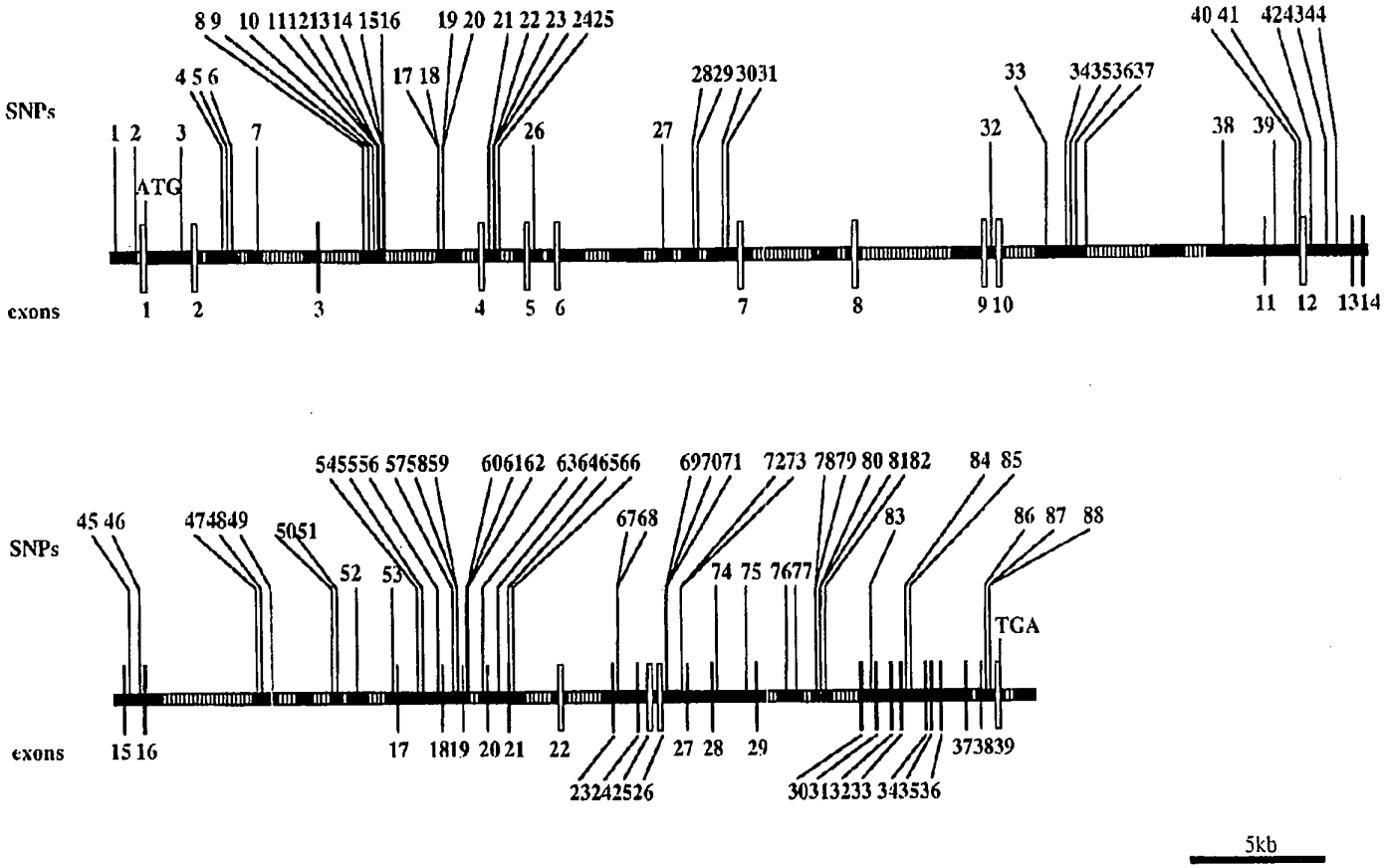


Fig. 115

Fig. 116

ATP binding cassette, sub-family C, member 9 (ABCC9)

ACCESSION AC084806
AC008250

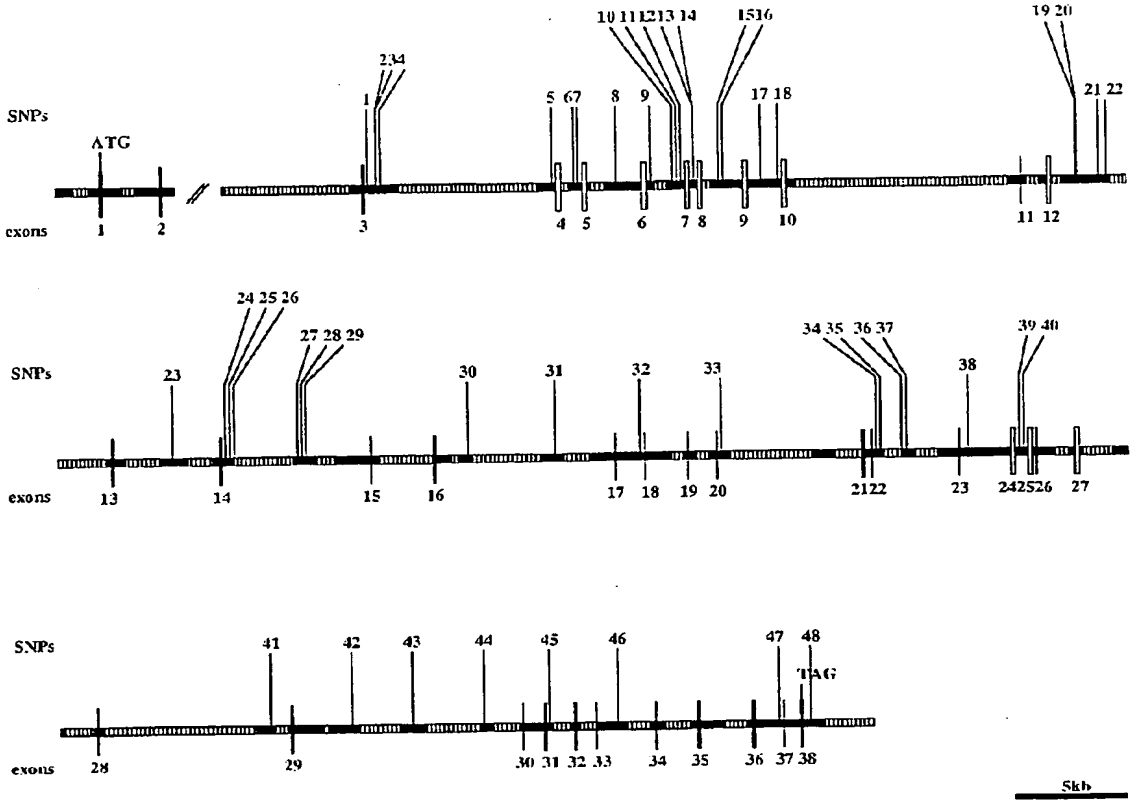


Fig. 117

Carboxylesterase 1 (CES1)

ACCESSION AC007602

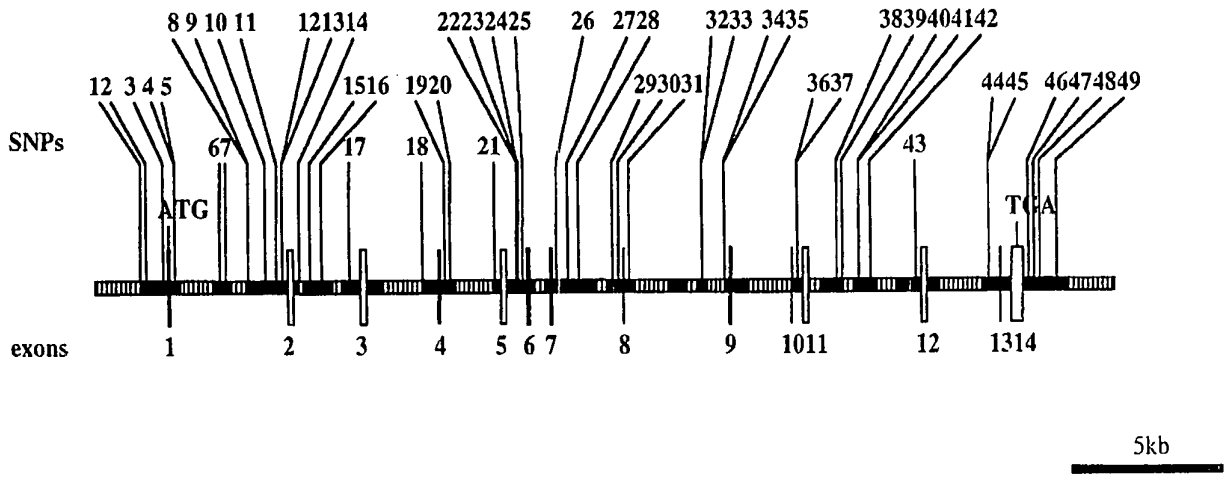


Fig. 118

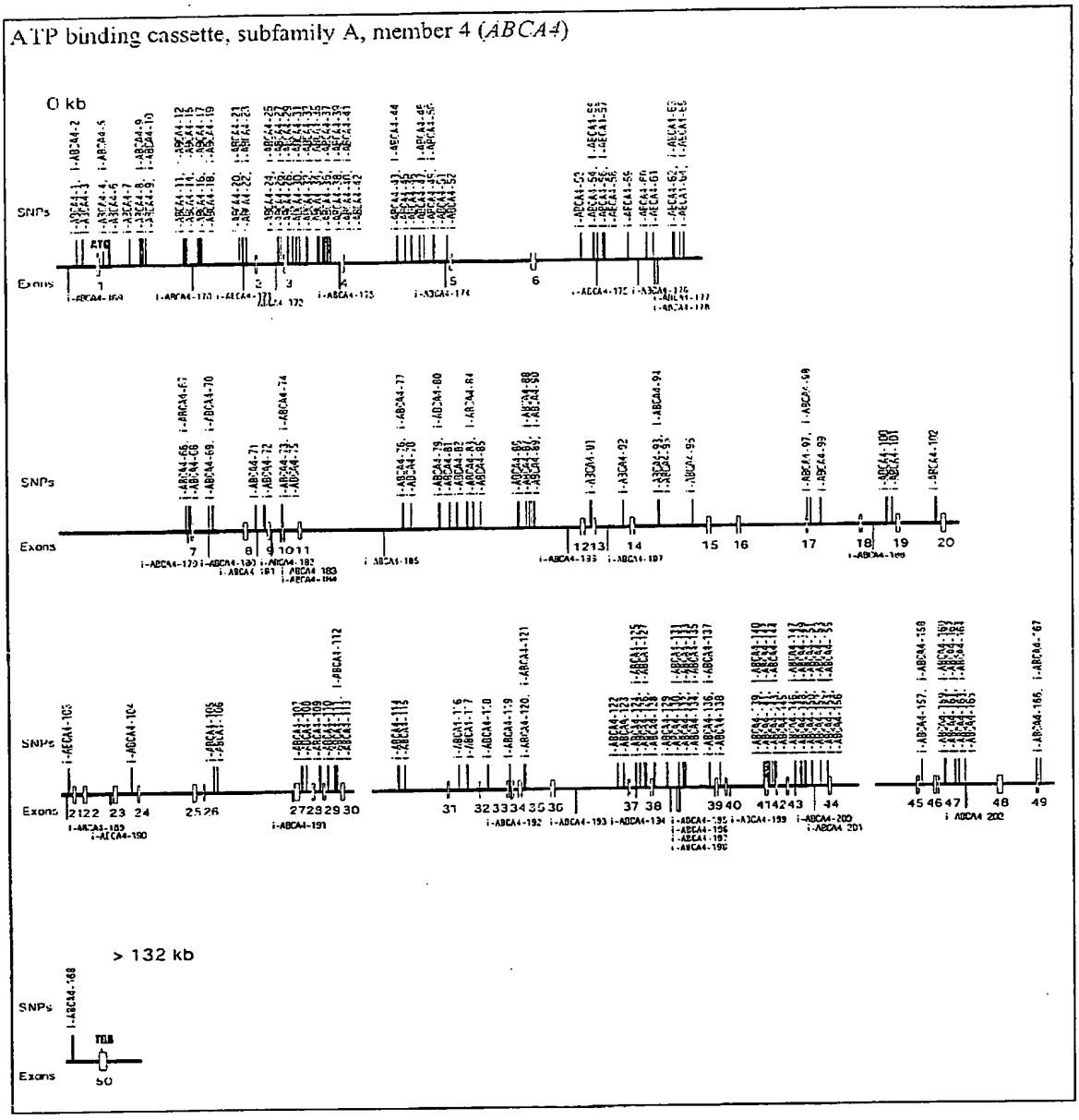

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ATG
Exons
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> 132 kb
TGA

Fig. 119

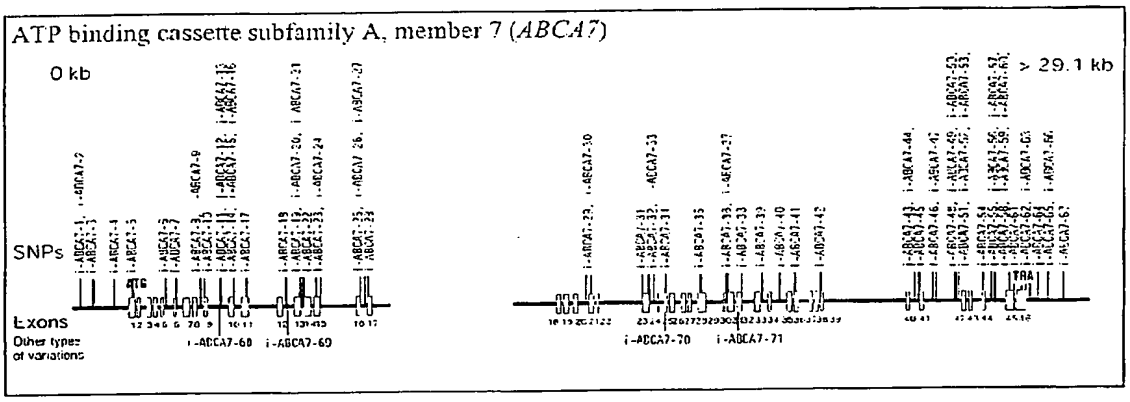


Fig. 120

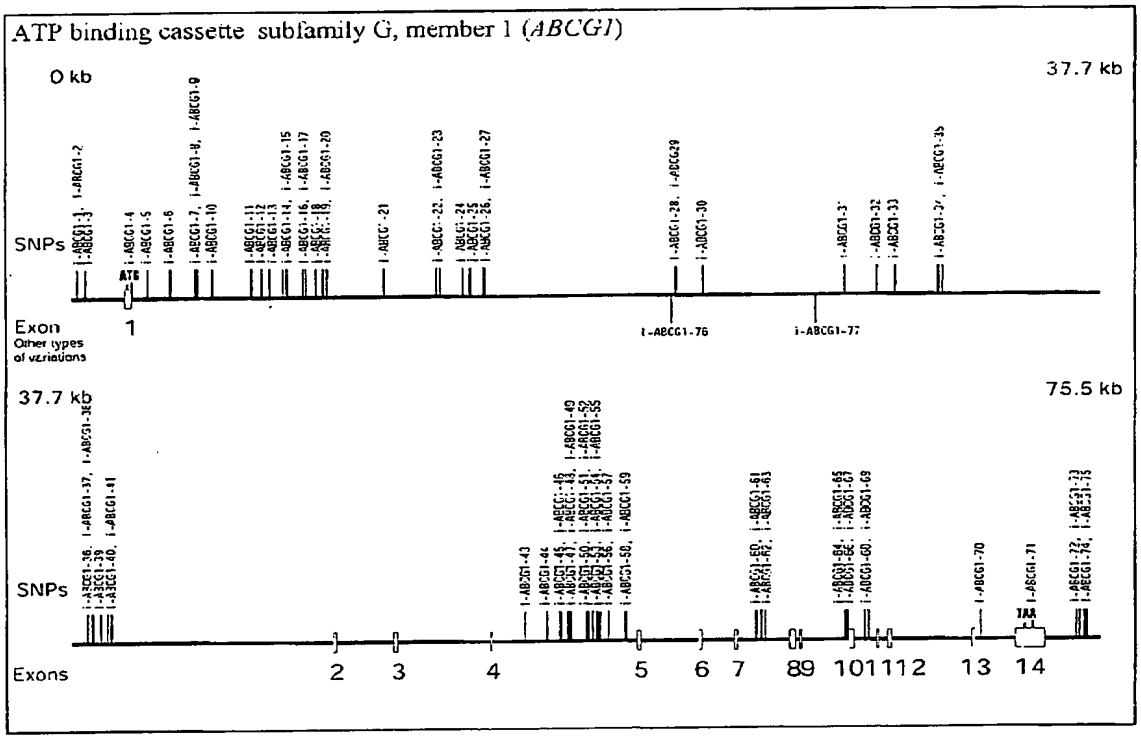


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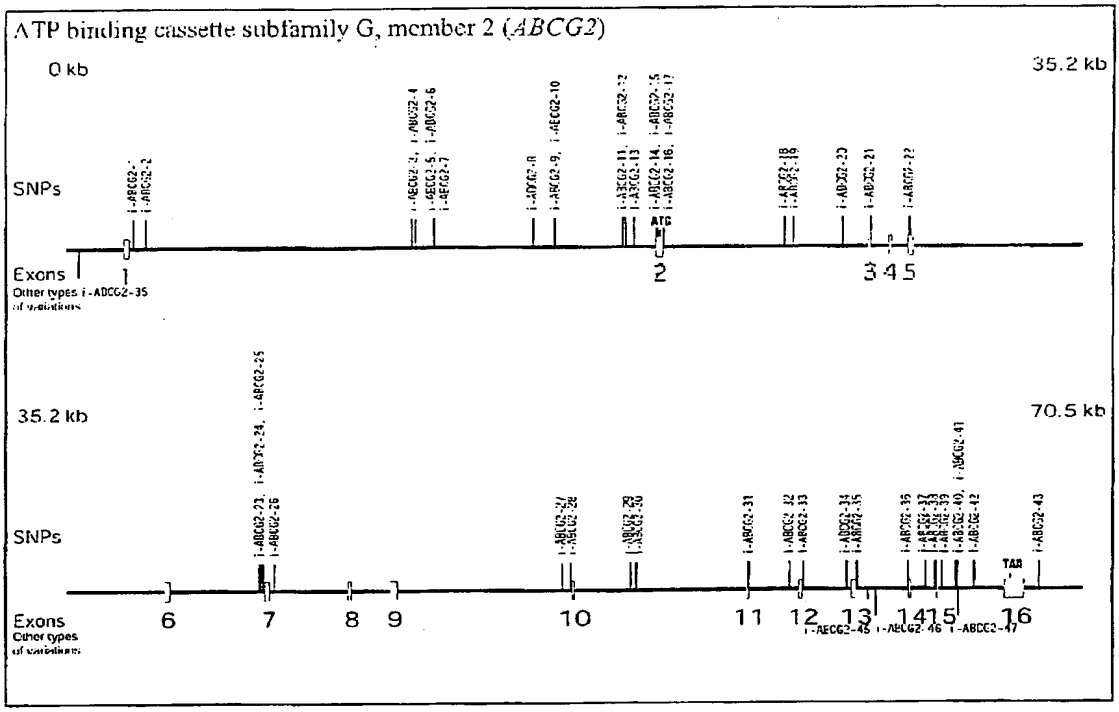


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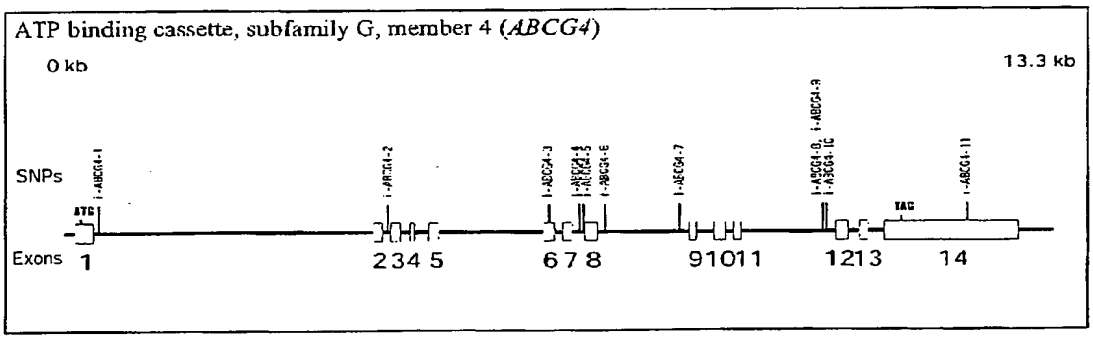


Fig. 123

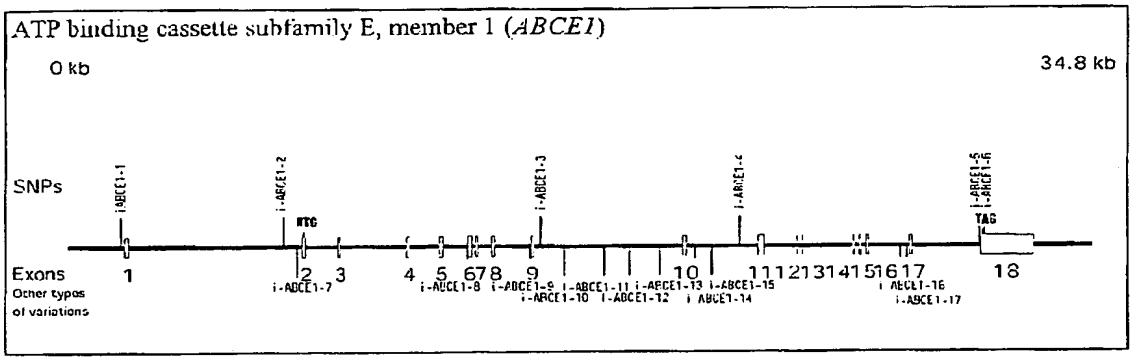


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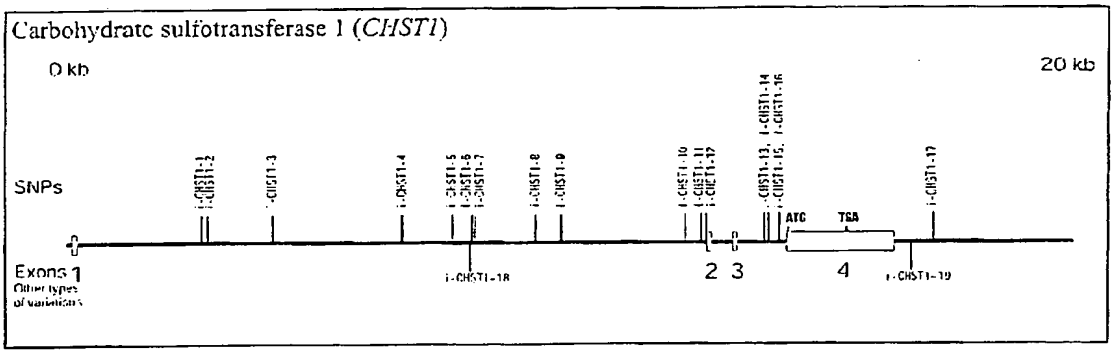


Fig. 125

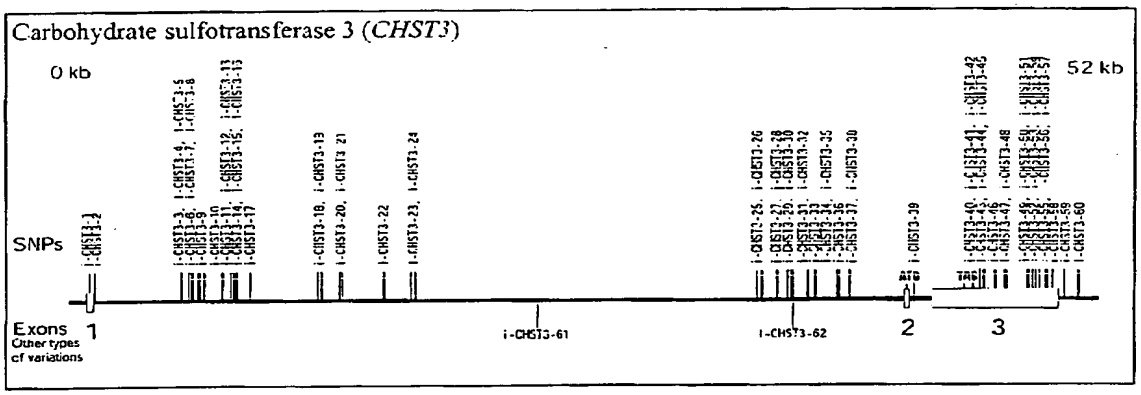


Fig. 126

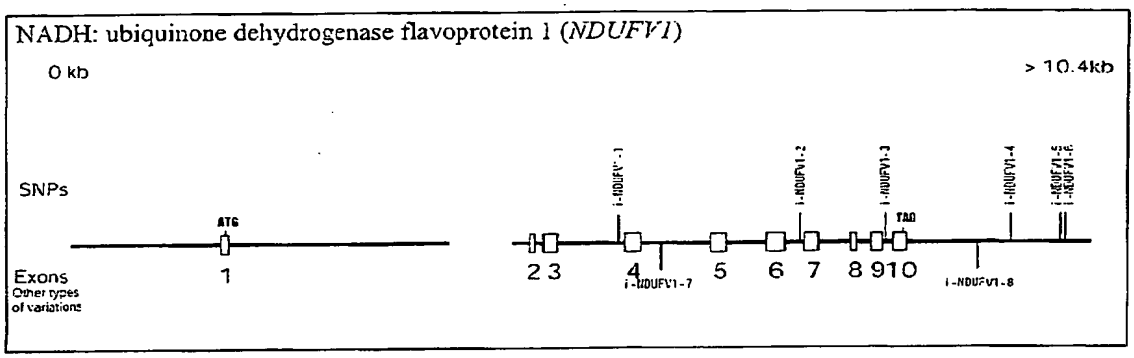


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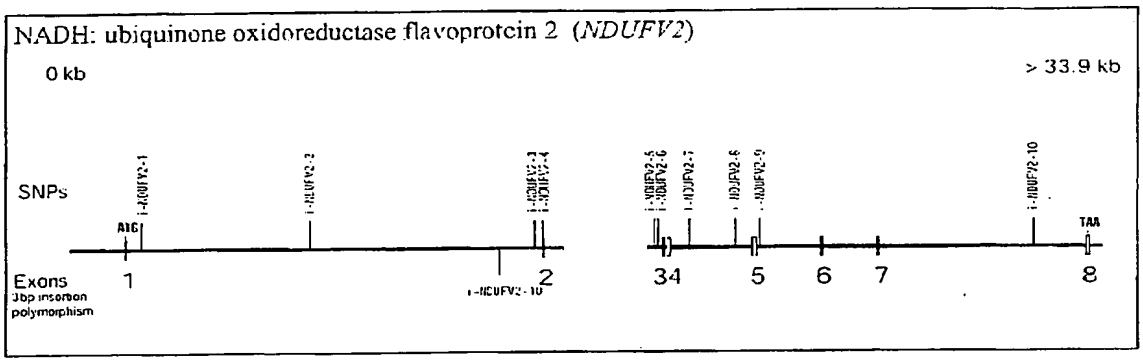


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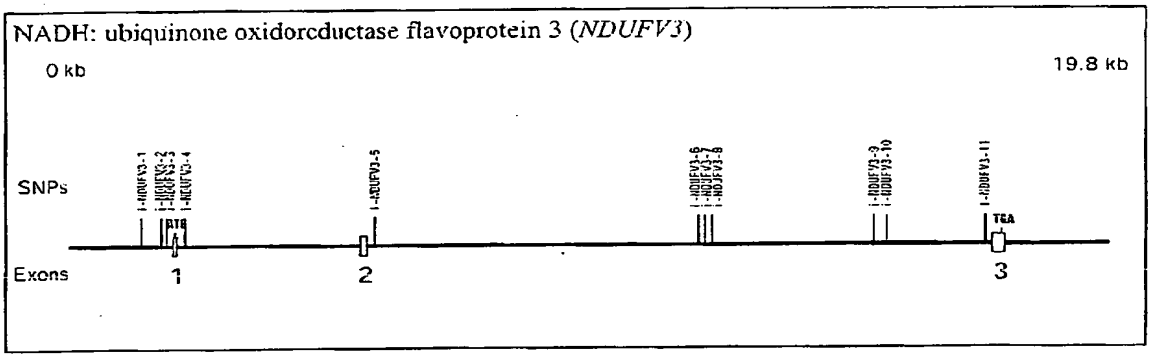


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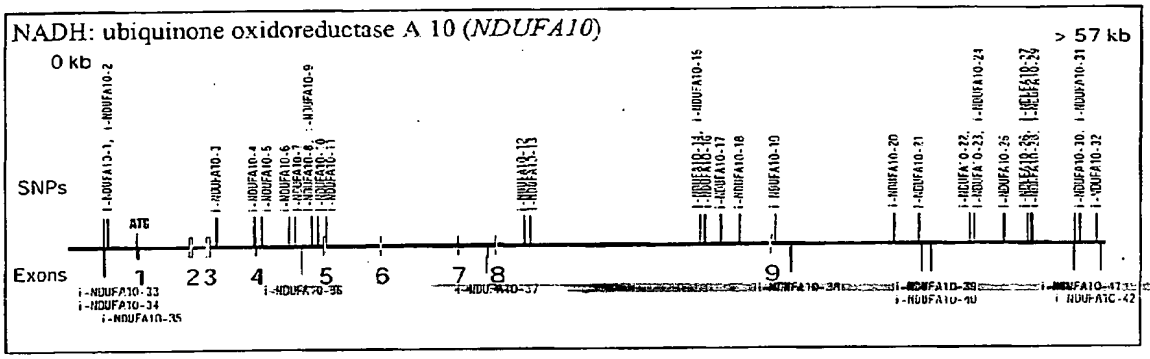


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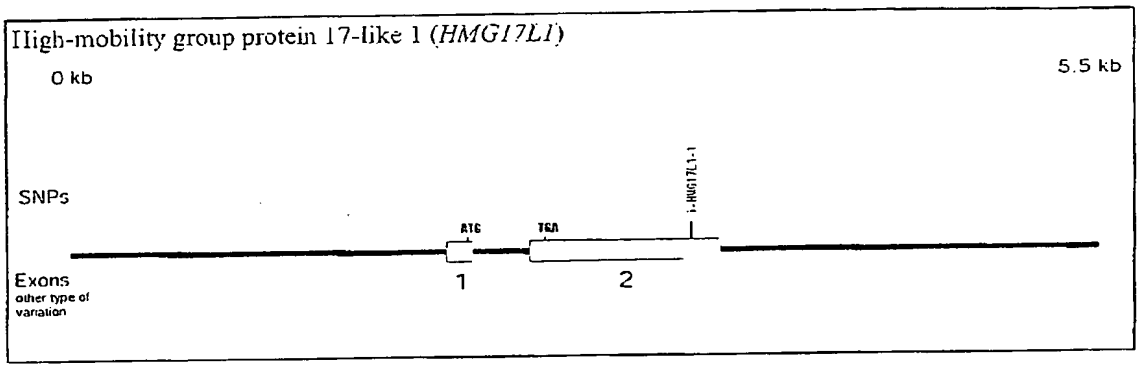


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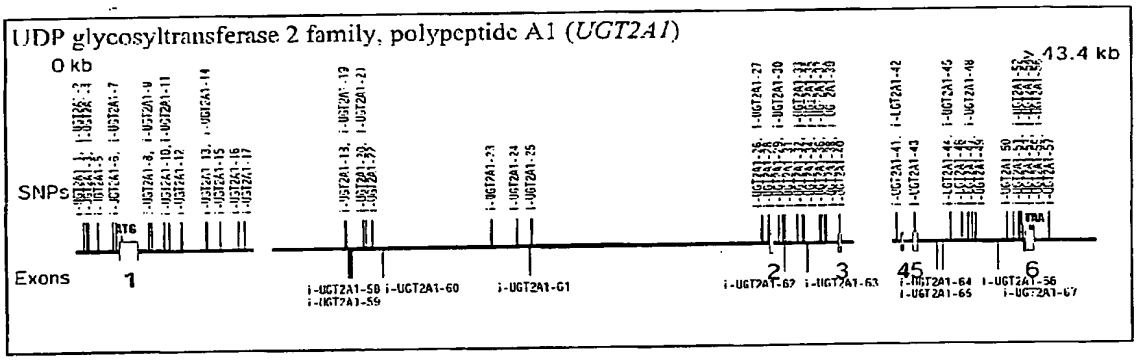


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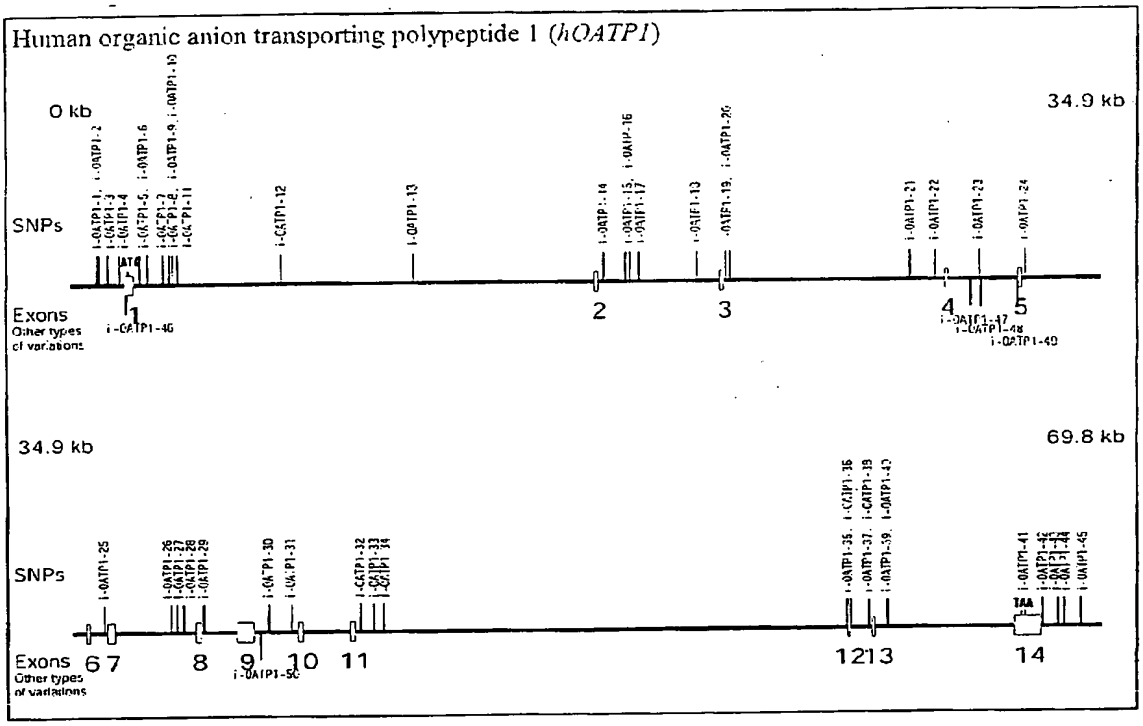

Human organic anion transporting polypeptide 1 (hOATP1)
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SNPs
Exons
Other types of variations
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2
3
4
5
34.9 kb
69.8 kb
SNPs
Exons
Other types of variations
6 7
8
9
10
11
12 13
14
TAA

Fig. 133

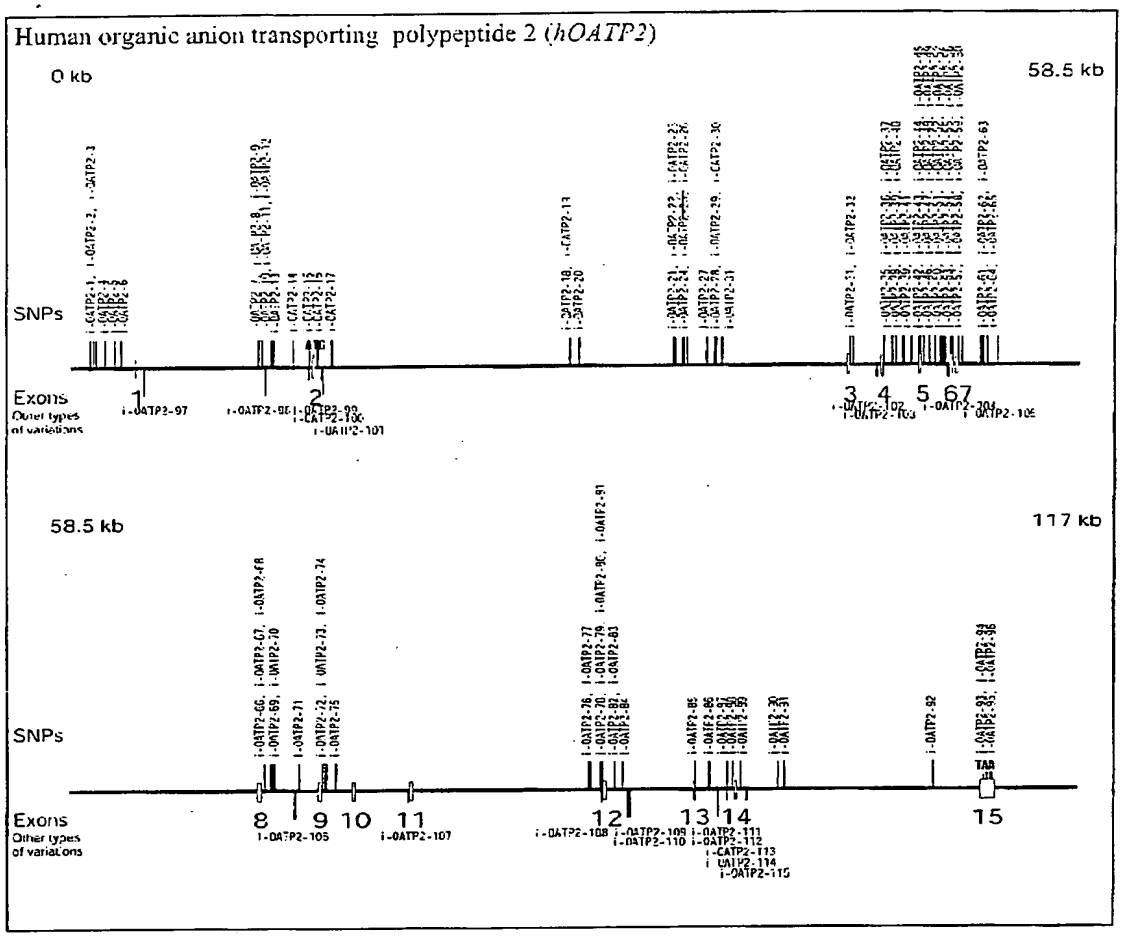

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Other types of variations
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Exons
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Fig. 134

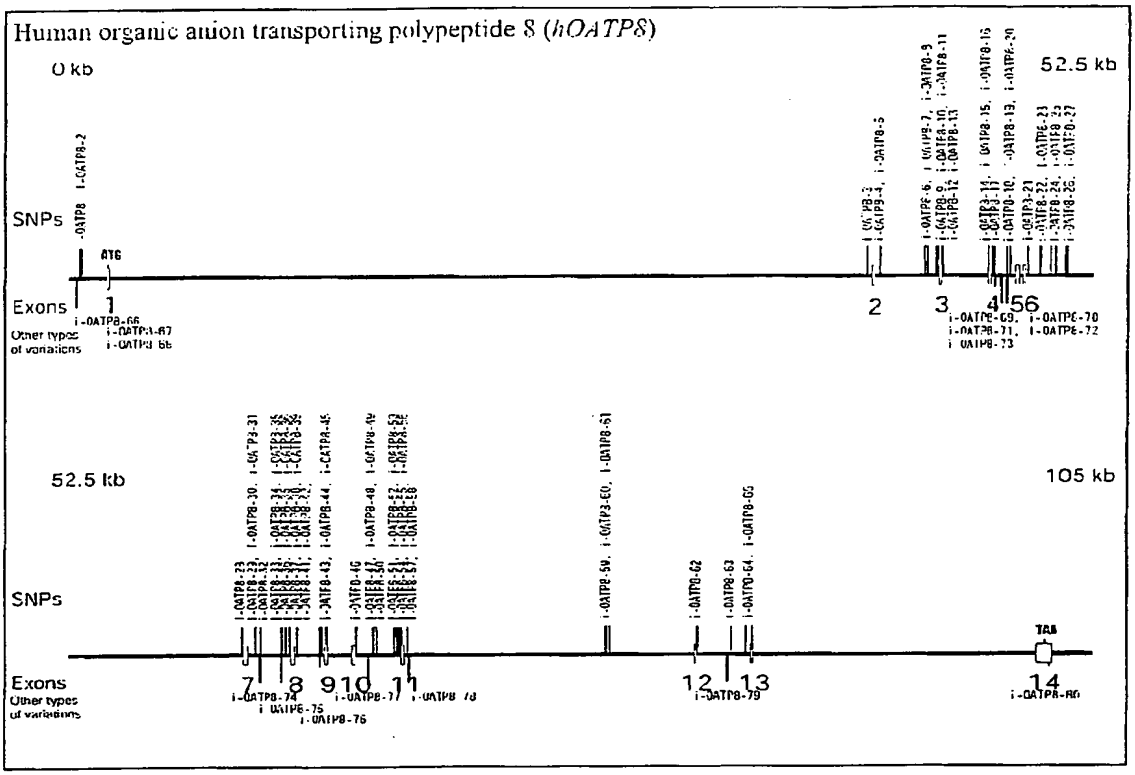


Fig. 135

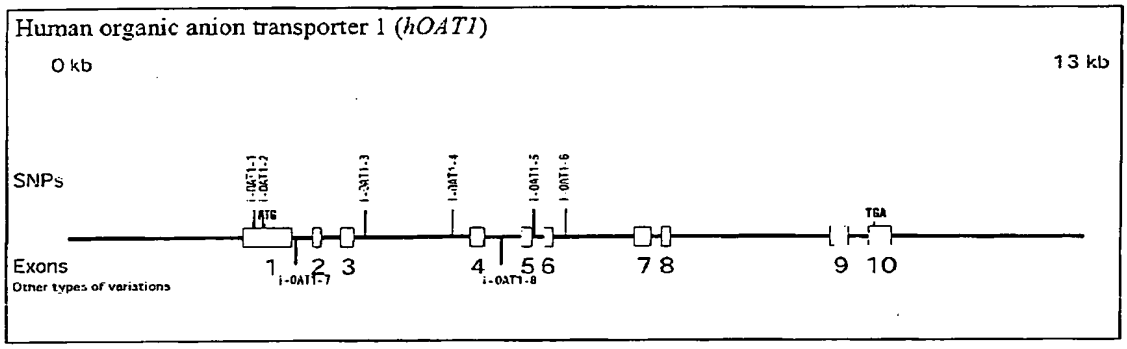


Fig. 136

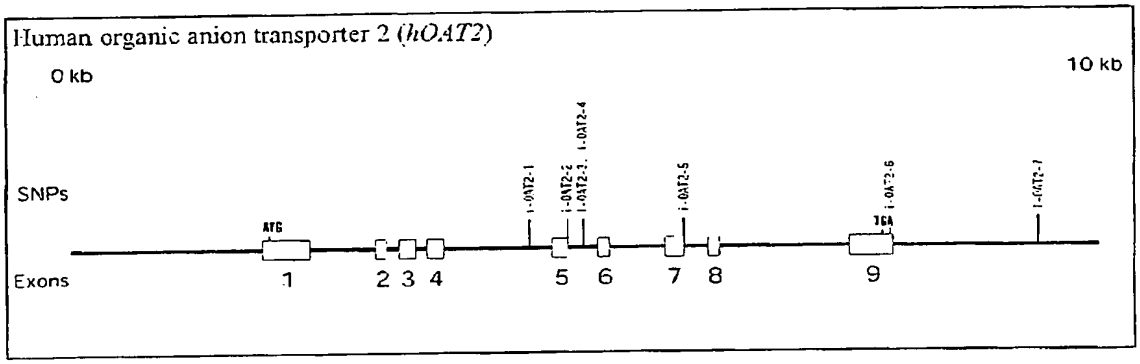
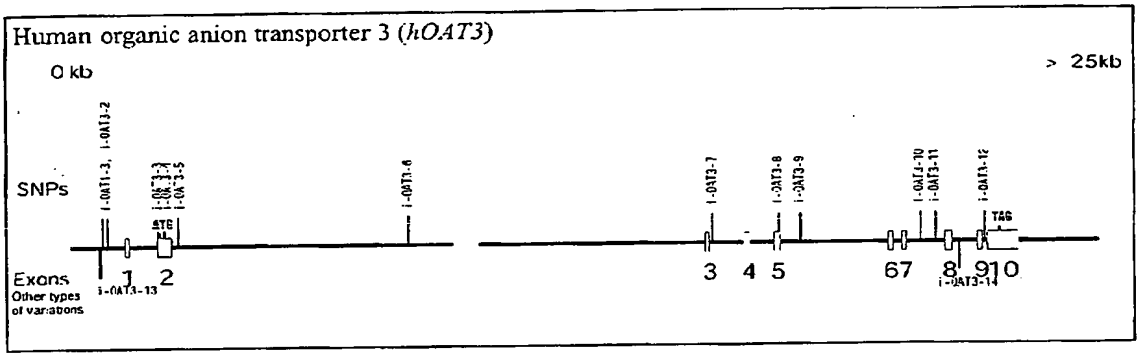


Fig. 137



Aldehyde dehydrogenase 1 family, member A2 (ALDH1A2)

ACCESSION AC025431
AC012653

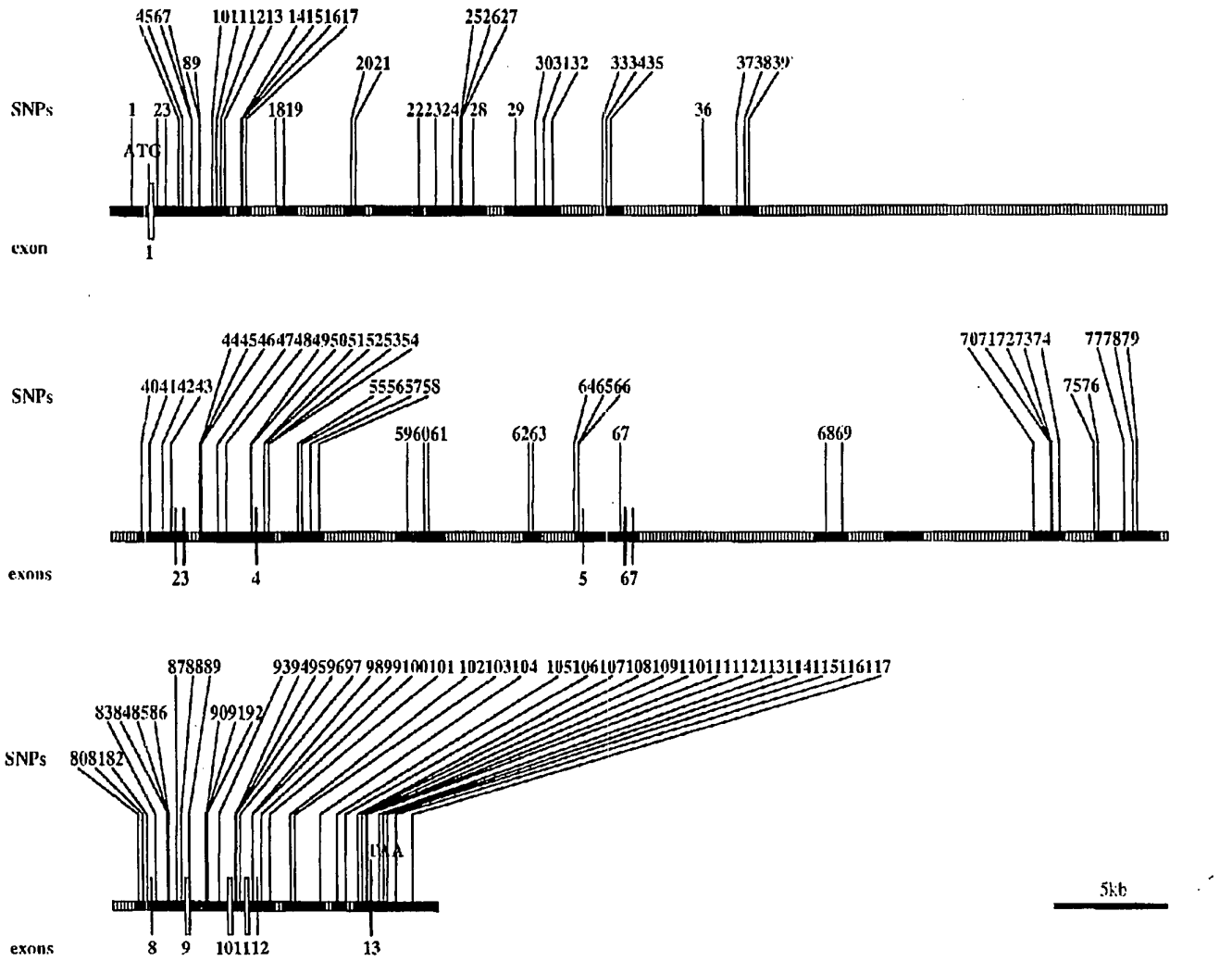


Fig. 138

Aldehyde dehydrogenase 1 family, member A3 (ALDH1A3)

ACCESSION AC015712

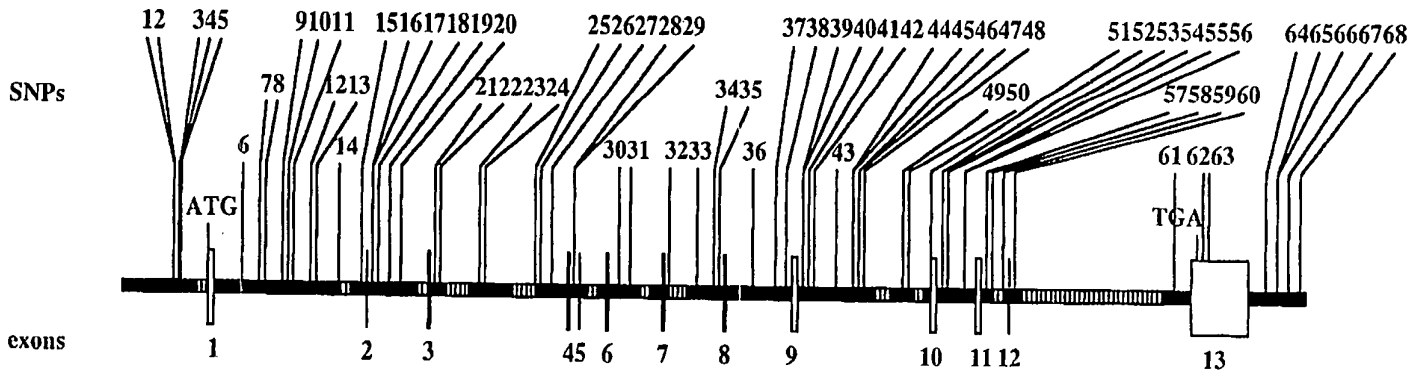


Fig. 139

Formyltetrahydrofolate dehydrogenase (FTHFD /ALDH1L1)

ACCESSION AC079848

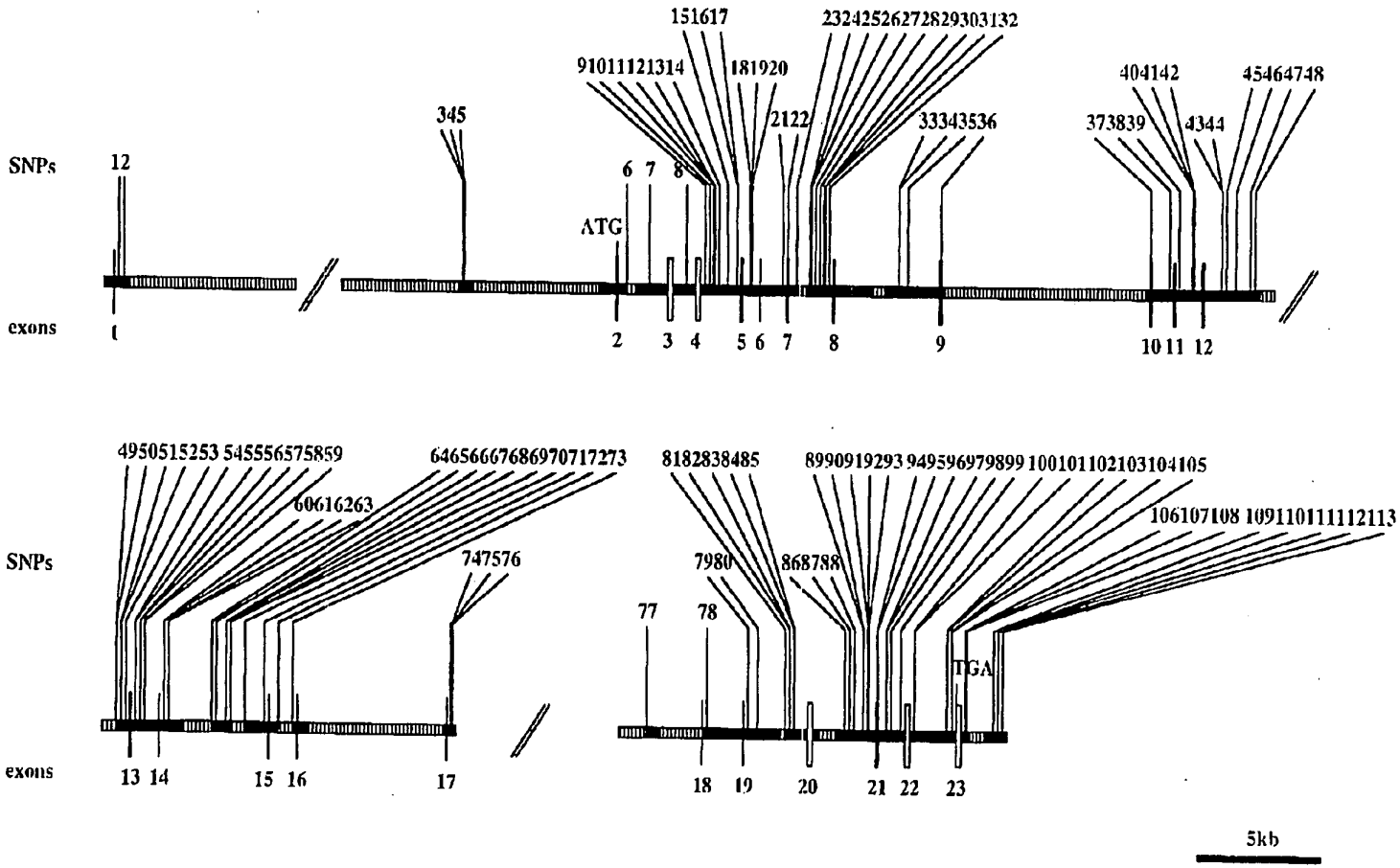


Fig. 140

Cytochrome P450, subfamily IIIA, polypeptide 4 (CYP3A4)

ACCESSION AF280107

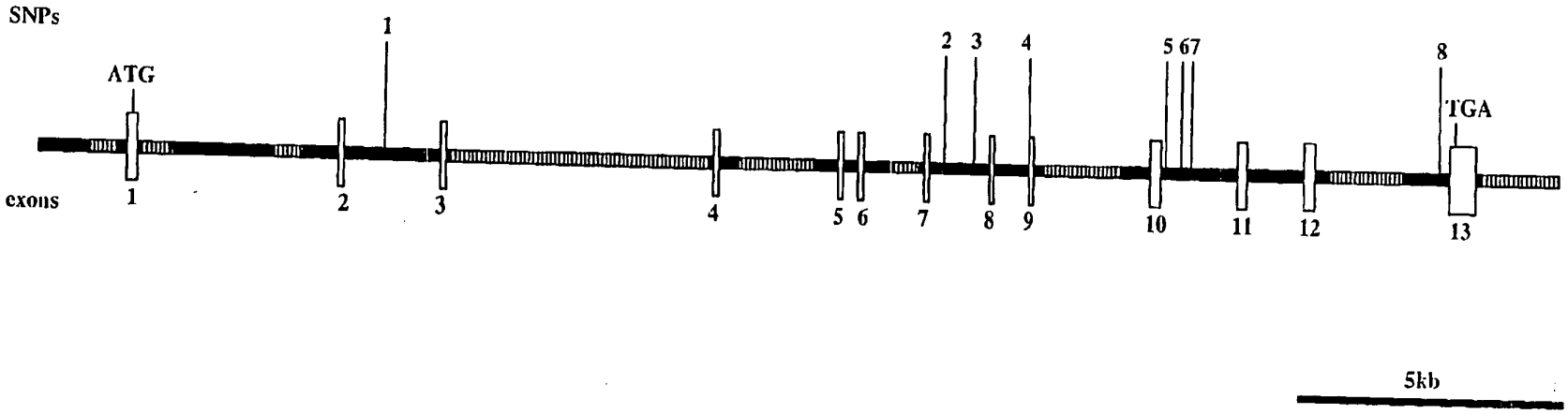
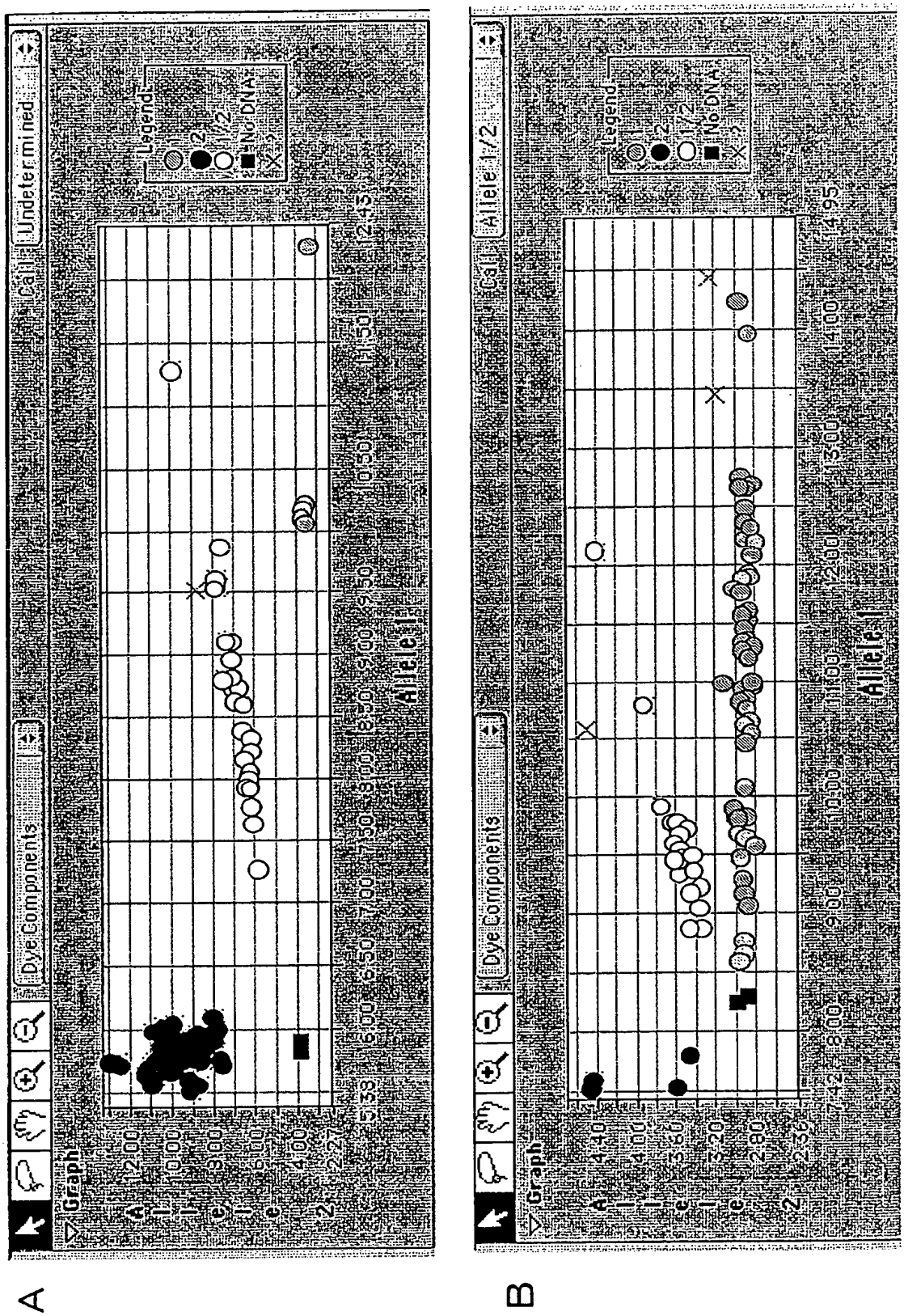


Fig. 141

Fig. 142


A
Graph
Dye Components
Call
Undetermined
Legend
No DNA
Allele 1
B
Graph
Dye Components
Call
Allele 1/2
Legend
No DNA
Allele 1

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【書類名】　明細書

【発明の名称】　遺伝子多型の検出方法

【特許請求の範囲】

【請求項１】　薬物代謝酵素をコードする遺伝子中に存在する遺伝子多型情報から、該遺伝子多型部位を含むように、又は薬物代謝酵素をコードする遺伝子を増幅したときの増幅断片中に前記遺伝子多型部位が含まれるように、オリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーを作製し、得られるオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーを用いて、目的の薬物代謝酵素をコードする遺伝子中の少なくとも１個の遺伝子多型を検出することを特徴とする遺伝子多型の検出方法。

【請求項２】　遺伝子多型部位を含むオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーが、その5'末端若しくは3'末端又は中央の塩基が当該遺伝子多型部位となるように作製されたものである請求項１記載の検出方法。

【請求項３】　遺伝子多型部位を含むオリゴヌクレオチドプローブが、薬物代謝酵素をコードする遺伝子とハイブリダイズし得る断片とハイブリダイズしない断片とが結合したものであって、前記遺伝子多型部位が、当該ハイブリダイズし得る断片の5'末端又は3'末端である請求項１記載の検出方法。

【請求項４】　遺伝子多型部位を含むオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーが、配列番号１～3360に示す塩基配列のうち第21番目の塩基を含む少なくとも13塩基の配列又はこれに相補的な配列を有するものからなる群から選択される少なくとも１つである請求項１～３のいずれかに記載の検出方法。

【請求項５】　遺伝子多型が、一塩基多型、複数個の塩基の欠失、置換若しくは挿入による多型、又はVNTR若しくはマイクロサテライトによる多型である請求項１～４のいずれかに記載の検出方法。

【請求項６】　請求項１～５のいずれかの方法により得られた検出結果から、当該薬物代謝酵素によって代謝される薬物の有効性及び安全性を評価することを特徴とする薬物の評価方法。

【請求項７】　請求項６記載の評価方法により得られた評価を指標として、使用すべき薬物を選択することを特徴とする薬物のスクリーニング方法。

【請求項８】　薬物代謝酵素をコードする遺伝子中に含まれる遺伝子多型情報と、被験者から採取した当該薬物代謝酵素をコードする遺伝子の遺伝子多型情報とを比較して、当該薬物代謝酵素によって代謝される薬物の有効性及び/又は安全性を解析し、得られる解析結果から使用すべき薬物を選択することを特徴とする薬物のスクリーニング方法。

【請求項９】　遺伝子多型情報が表１に示されるものである請求項１～８のいずれかに記載の方法。

【請求項１０】　薬物代謝酵素が、エポキシドハイドロラーゼ、メチルトランスフェラーゼ、N-アセチルトランスフェラーゼ、スルホトランスフェラーゼ、キノンオキシドレダクターゼ、グルタチオン-S-トランスフェラーゼ、UDP-グリコシルトランスフェラーゼ、アルデヒドデヒドロゲナーゼ、アルコールデヒドロゲナーゼ、エステラーゼ、NDUF、チトクロームp450（CYP）及びATP-結合カセットからなる群から選択される少なくとも１つである請求項１～９のいずれかに記載の方法。

【請求項１１】　配列番号１～3360に示される塩基配列又はこれに相補的な塩基配列からなる群から選択されるオリゴヌクレオチド。

【請求項１２】　薬物代謝酵素をコードする遺伝子中に存在する遺伝子多型情報から、該遺伝子多型部位を含むように作製されたオリゴヌクレオチド。

【請求項１３】　オリゴヌクレオチドの5'末端若しくは3'末端又は中央の塩基が、当該遺伝子多型部位となるように作製されたものである請求項12記載のオリゴヌクレオチド。

【請求項１４】　遺伝子多型部位を含むオリゴヌクレオチドが、薬物代謝酵素をコードする遺伝子とハイブリダイズし得る断片とハイブリダイズしない断片とが結合したものであって、前記遺伝子多型部位が、当該ハイブリダイズし得る断片の5'末端又は3'末端である請求項12記載のオリゴヌクレオチド。

【請求項１５】　オリゴヌクレオチドが、配列番号１～3360に示すいずれかの塩基配列のうち第21番目の塩基を含む少なくとも13塩基の配列又はこれに相補

的な配列を有するものである請求項12～14のいずれかに記載のオリゴヌクレオチド。

【請求項１６】　請求項11～15のいずれかに記載のオリゴヌクレオチドを含む遺伝子多型検出用キット。

【発明の詳細な説明】

【０００１】

【発明の属する技術分野】

本発明は、遺伝子多型情報、遺伝子多型情報の検出方法、遺伝子多型を用いた薬物の評価方法、及び薬物のスクリーニング方法に関する。

【０００２】

【従来の技術】

ヒトの姿形が千差万別であるように、30億からなる遺伝暗号も個人間で比較するとかなり多くの部位で異なっている。この遺伝暗号の違いを遺伝子多型（ポリモルフィズム）と呼んでおり、代表的な遺伝子多型として一塩基多型が知られている。

【０００３】

一塩基多型（SNP:single nucleotide polymorphism）とは、個人間における１遺伝暗号の違いを意味する。ヒトの顔貌や体型が千差万別であるように、遺伝暗号である塩基配列も一人ひとりかなり多くの部位で異なっている。SNPは、その存在する位置によってcSNP(coding SNP)とgSNP(genome SNP)に分類され、cSNPには、さらにsSNP(silent SNP)、rSNP(regulatory SNP)及びiSNP(intron SNP)が含まれる。

【０００４】

上記SNPは、多型マーカーとしての疾患の発症や増悪に関連する遺伝子を見つけるために有用であり、最終的に臨床分野において疾患のリスク診断や薬剤の使い分けなどに直接関係する。また、疾患の原因となっている物質を標的分子とした証拠に基づく薬剤開発は、世界的趨勢となっている。ある疾患に対して薬剤を投与した場合、患者の応答性は様々であり、著効を示すもの、有効性の低いもの、全く効果を示さないもののように、薬剤に対する応答性には大きな違いがある

。これは、症状が同じで同じ診断名であっても、その背景となっている疾患を起こしている経路が異なっていたり、あるいは薬剤の代謝速度が大きく異なっている可能性があるからである。従って、SNPなど遺伝子多型を参考にしながら、目的の疾患に応じた薬物の選択、治療法の開発（いわゆるオーダーメイド医療）が望まれる。

【０００５】

薬剤に対する応答性に加えて、時には致死的となるような強い副作用の問題も、医療従事者が対処していかなければならない大きな問題の一つである。これは、処方ミスなどによる過剰投与がなくても、時には思わぬ致死的な副作用に遭遇することがある。従って、薬剤の応答性に対しては、薬剤の代謝、薬剤の輸送、薬剤のレセプターなどによる薬剤応答性や副作用の強さを、SNPなどの遺伝子多型を参考にしながら決定することが望まれる。

【０００６】

【発明が解決しようとする課題】

本発明は、遺伝子多型情報の検出方法とその情報に基づく薬物の有効性並びに安全性を評価するための方法、及び薬物のスクリーニング方法を提供することを目的とする。

【０００７】

【課題を解決するための手段】

本発明者は、上記課題を解決するため鋭意研究を行った結果、薬物代謝酵素をコードする遺伝子中の遺伝子多型を見出し、これを用いて薬物と疾患との因果関係を評価することに成功し、本発明を完成するに至った。

【０００８】

すなわち、本発明は以下の通りである。

(1) 薬物代謝酵素をコードする遺伝子中に存在する遺伝子多型情報から、該遺伝子多型部位を含むように、又は薬物代謝酵素をコードする遺伝子を増幅したときの増幅断片中に前記遺伝子多型部位が含まれるように、オリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーを作製し、得られるオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーを用いて、目的の薬物

代謝酵素をコードする遺伝子中の少なくとも１個の遺伝子多型を検出することを特徴とする遺伝子多型の検出方法。

【０００９】

遺伝子多型部位を含むオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーとしては、その5'末端若しくは3'末端又は中央の塩基が当該遺伝子多型部位となるように作製されたものが挙げられる。また、薬物代謝酵素をコードする遺伝子とハイブリダイズし得る断片とハイブリダイズしない断片とが結合したものであって、前記遺伝子多型部位が、当該ハイブリダイズし得る断片の5'末端又は3'末端であるものも、遺伝子多型部位を含むオリゴヌクレオチドプローブに含まれる。さらに、配列番号１～3360に示す塩基配列のうち第21番目の塩基を含む少なくとも13塩基の配列又はこれに相補的な配列を有するものからなる群から選択される少なくとも１つのヌクレオチドも、遺伝子多型部位を含むオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーに含まれる。上記遺伝子多型としては、一塩基多型、複数個の塩基の欠失、置換若しくは挿入による多型、又はVNTR若しくはマイクロサテライトによる多型が挙げられる。

【００１０】

(2) 前記検出方法により得られた検出結果から、当該薬物代謝酵素によって代謝される薬物の有効性及び安全性を評価することを特徴とする薬物の評価方法。

(3) 前記評価方法により得られた評価を指標として、使用すべき薬物を選択することを特徴とする薬物のスクリーニング方法。

(4) 薬物代謝酵素をコードする遺伝子中に含まれる遺伝子多型情報と、被験者から採取した当該薬物代謝酵素をコードする遺伝子の遺伝子多型情報とを比較して、当該薬物代謝酵素によって代謝される薬物の有効性及び/又は安全性を解析し、得られる解析結果から使用すべき薬物を選択することを特徴とする薬物のスクリーニング方法。

【００１１】

上記検出方法、評価方法又はスクリーニング方法において、遺伝子多型情報としては、表１に示されるものを、また、薬物代謝酵素としては、エポキシドハイドロラーゼ、メチルトランスフェラーゼ、N-アセチルトランスフェラーゼ、スル

ホトランスフェラーゼ、キノンオキシドレダクターゼ、グルタチオン-S-トランスフェラーゼ、UDP-グリコシルトランスフェラーゼ、アルデヒドデヒドロゲナーゼ、アルコールデヒドロゲナーゼ、エステラーゼ、NDUF、チトクロームp450（CYP）及びATP-結合カセットからなる群から選択される少なくとも１つを例示することができる。

(5) 配列番号１～3360に示される塩基配列又はこれに相補的な塩基配列からなる群から選択されるオリゴヌクレオチド。

(6) 薬物代謝酵素をコードする遺伝子中に存在する遺伝子多型情報から、該遺伝子多型部位を含むように作製されたオリゴヌクレオチド。

【００１２】

上記オリゴヌクレオチドとしては、その5'末端若しくは3'末端又は中央の塩基が、当該遺伝子多型部位となるように作製されたものが挙げられる。また、薬物代謝酵素をコードする遺伝子とハイブリダイズし得る断片とハイブリダイズしない断片とが結合したオリゴヌクレオチドであって、前記遺伝子多型部位が、当該ハイブリダイズし得る断片の5'末端又は3'末端となるように作製されたオリゴヌクレオチドも、本発明のオリゴヌクレオチドに含まれる。さらに、配列番号１～3360に示すいずれかの塩基配列のうち第21番目の塩基を含む少なくとも13塩基の配列又はこれに相補的な配列を有するものも、本発明のオリゴヌクレオチドに含まれる。

(7) 前記オリゴヌクレオチドを含む遺伝子多型検出用キット。

以下、本発明を詳細に説明する。

【００１３】

【発明の実施の形態】

本発明は、薬物代謝酵素に関する遺伝子多型情報を用いて、被検対象の遺伝子多型を検出する方法に関する。また、本発明は、薬物代謝酵素によって代謝される薬物の有効性及び安全性の有無又は強弱を解析することを特徴とし、この解析結果により、疾患と薬物との関係を評価するものである。複数人が同じ疾患に罹患している場合であっても、薬物代謝酵素遺伝子の遺伝子多型情報は個々の患者ごとに異なることが多い。従って、その異なる遺伝子多型情報から薬物代謝との

関係を導き、どのような遺伝子多型情報を有する場合に特定の薬物の有効性が認められるのか認められないのか、また、どのような遺伝子多型情報を有する場合に副作用が出やすいのか出にくいのか、その薬物の有効性及び/又は安全性を評価する。その結果、ある疾患に対してどのような薬物を使用すべきなのか、遺伝子多型情報からそれぞれの患者ごとに適した投薬（オーダーメイド医療）が可能となる。

【００１４】

１．遺伝子多型

遺伝子多型には、一塩基多型、インサーション/デリーション型多型、及び塩基配列の繰り返し数が異なっていることにより生じる多型が含まれる。一塩基多型（SNP）とは、一般にはある遺伝子領域の特定の1個の塩基が他の塩基に置換することによる多型を意味するが、本発明においては、上記置換による多型のほか、当該1個の塩基が欠失したことによる多型、当該1個の塩基にさらに1個の塩基が挿入したことによる多型も含めることとする。また、インサーション/デリーション型多型とは、複数の塩基（例えば2個～数十塩基）が欠失や挿入をしていることによる多型をいい、数百塩基～数千塩基が欠失や挿入されているものも存在する。さらに、塩基配列の繰り返し数が異なっていることにより生じる多型は、２～数十塩基の配列が繰り返されており、その繰り返し回数が個人間で異なっているものをいう。繰り返しの単位が数塩基から数十塩基のものをVNTR(variable number of tandem repeat)といい、２～４塩基単位程度のものをマイクロサテライト多型という。VNTRやマイクロサテライト多型においては、この繰り返し回数の違いが個々人のアレル（対立遺伝子）で異なることにより、バリエーションを獲得している。

【００１５】

２．薬物代謝酵素

「薬物代謝酵素」とは、医薬品を含む外来性異物の生体内における構造変換を触媒する酵素群の総称である。また、一部の内在性物質であっても、治療目的で投与される場合にはその代謝に関わる酵素群のことを指す。薬物代謝酵素は、薬物の吸収、代謝、排泄に関わるものであるため、その酵素の多型はその酵素の発

現量（転写や翻訳）や活性を変化させ、結果として未変化体や代謝物の血中濃度などに違いが生じる。

本発明において、遺伝子多型解析の対象となる遺伝子により発現される薬物代謝酵素としては、以下のものが挙げられる。

【００１６】

エポキシドハイドロラーゼ(epoxide hydrolase)

メチルトランスフェラーゼ(methyltransferase)

N-アセチルトランスフェラーゼ(N-acetyltransferase)

スルホトランスフェラーゼ(sulfotransferase)

キノンオキシドレダクターゼ(quinone oxidereductase)

グルタチオン-S-トランスフェラーゼ(glutathione S-transferase)

UDP-グリコシルトランスフェラーゼ(UDP-glycosyltransferase)

アルデヒドデヒドロゲナーゼ(aldehyde dehydrogenase)

アルコールデヒドロゲナーゼ(alcohol dehydrogenase)

エステラーゼ (esterase)

ユビキノンデヒドロゲナーゼ(ubiquinone dehydrogenase：NDUF)

チトクローム P450 (CYP)

ATP-結合カセット(ATP-binding cassette)

【００１７】

その他の酵素

(1) エポキシドハイドロラーゼは、エポキシドをトランス開裂機構で加水分解し、1,2-グリコールを生成させる酵素であり、例えばミクロソームエポキシドハイドロラーゼ1、細胞質エポキシドハイドロラーゼ2などが含まれる。

【００１８】

(2) メチルトランスフェラーゼは、アミノ基、水酸基、チオール基などにメチル基転移を触媒する酵素であり、例えば以下のものが挙げられる。

カテコール-O-メチルトランスフェラーゼ

ヒスタミン N-メチルトランスフェラーゼ

フェニルエタノールアミンN-メチルトランスフェラーゼ

ホスファチジルエタノールアミンN-メチルトランスフェラーゼ

ニコチンアミドN-メチルトランスフェラーゼ

グアニジノアセテートN-メチルトランスフェラーゼ

アセチルセロトニン-O-メチルトランスフェラーゼ

【００１９】

(3) N-アセチルトランスフェラーゼは、アミノ基、スルホンアミド基、ヒドラジン基にアセチル基転移を触媒する酵素であり、例えば以下のものが挙げられる。

アリールアミンN-アセチルトランスフェラーゼ1、2

アリールアルキルアミン N-アセチルトランスフェラーゼ

サッカロミセス・セレビシエ(Saccharomyces cerevisiae)のN-アセチルトランスフェラーゼ相同体

L1 細胞接着分子

【００２０】

(4) スルホトランスフェラーゼは、硫酸抱合に関与し、フェノール類、ステロイド類、アリールアミン、胆汁酸などに硫酸基転移を触媒する酵素であり、例えば以下のものが挙げられる。

スルホトランスフェラーゼ1A1、1A2、1A3、1C1、1C2、2A1、2B1

甲状腺ホルモンスルホトランスフェラーゼ

チロシルタンパク質スルホトランスフェラーゼ1、2

スルホトランスフェラーゼ-関連タンパク質3

エストロゲンスルホトランスフェラーゼ

セレブロシドスルホトランスフェラーゼ

HNK-スルホトランスフェラーゼ-1

炭水化物スルホトランスフェラーゼ２、４、５

【００２１】

(5) キノンオキシドレダクターゼは、 キノン類のo-キノンやp-キノンの還元を触媒する酵素であり、例えば以下のものが挙げられる。

NAD(P)H: キノンオキシドレダクターゼ1

NRH: キノンオキシドレダクターゼ2

キノンオキシドレダクターゼ相同体

【００２２】

(6) グルタチオン-S-トランスフェラーゼは、グルタチオンとの抱合を触媒する酵素であり、例えば以下のものが挙げられる。

グルタチオン-S-トランスフェラーゼMu1、Mu2、Mu3、Mu4、Mu5

グルタチオン-S-トランスフェラーゼZ(zeta)

グルタチオン-S-トランスフェラーゼII(pi)

グルタチオン-S-トランスフェラーゼ シータ1(theta 1)、シータ2

ミクロソームグルタチオン-S-トランスフェラーゼ1

ミクロソームグルタチオン-S-トランスフェラーゼ1-様1

ミクロソームグルタチオン-S-トランスフェラーゼ2、3

グルタチオン-S-トランスフェラーゼHaサブユニット1、2

グルタチオン-S-トランスフェラーゼA3、A4

【００２３】

(7) UDP-グリコシルトランスフェラーゼは、第I相薬物代謝経路である水酸基、カルボキシル基、アミノ基、チオール基などの官能基導入後にその官能基にグルクロン酸供与を触媒する酵素であり、例えば以下のものが挙げられる。

UDP-グリコシルトランスフェラーゼ1

UDP-グリコシルトランスフェラーゼ2ファミリーポリペプチドA1, B7, B10, B4, B11, B15, B17

UDP-グリコシルトランスフェラーゼ8

ドリシル-ジホスホオリゴサッカライド-タンパク質グリコシルトランスフェラーゼ

【００２４】

(8) アルデヒドデヒドロゲナーゼは、アルデヒドをカルボン酸に変換する酵素であり、例えばアルデヒドデヒドロゲナーゼ1～10などが含まれる。

【００２５】

(9) アルコールデヒドロゲナーゼは、アルコールをアルデヒド又はケトンに変

換する酵素であり、例えば以下のものが挙げられる。

アルコールデヒドロゲナーゼ1～7

ヒドロキシ-CoAデヒドロゲナーゼ

短鎖アルコールデヒドロゲナーゼファミリー遺伝子

【００２６】

(10) エステラーゼは、エステル部分を加水分解する酵素であり、例えば以下のものが挙げられる。

アリールアセトアミドデアセチラーゼ

グランザイムA (granzyme A)

グランザイムB

インターロイキン17

ユビキチンカルボキシルーターミナルエステラーゼL1, 3

カルボキシルエステラーゼ1

リパーゼA

エステラーゼD/ホルミルグルタチオンハイドロラーゼ

カルボキシルエステルリパーゼ

【００２７】

(11) NDUF (ubiquinone dehydrogenase) は、ミトコンドリアの呼吸鎖、すなわちエネルギー代謝を担う酵素であり、例えばNADHユビキノンデヒドロゲナーゼ1α サブユニット1～10などが含まれる。

【００２８】

(12) CYP(チトクローム P450) は、第I相薬物代謝を司り、薬物に酸素原子を導入する酵素であり、例えばチトクロームp450(CYP)1A1, CYP1A2, CYP2A6, CYP2B6, CYP2C8, CYP2C18, CYP2C9, CYP2C19, CYP2E1, CYP2D6, CYP2E1, CYP2F1, CYP3A3, CYP3A4, CYP3A7, CYP3A43, CYP4A11, CYP4B1,CYP4F2, CYP4F3, CYP4F8, CYP11B1, 2, CYP17, CYP19, CYP21A2, CYP27などが含まれる。

【００２９】

(13) ATP-結合カセットは、トランスポーターで薬物の吸収や組織内濃度を調節するものであり、例えば以下のものが挙げられる。

ATP-結合カセットサブファミリーAメンバー1～6、8

ATP-結合カセットサブファミリーBメンバー1～11

ATP-結合カセットサブファミリーCメンバー1～6，8～10

ATP-結合カセットサブファミリーDメンバー1～4

ATP-結合カセットサブファミリーEメンバー1

ATP-結合カセットサブファミリーFメンバー1～3，

ATP-結合カセットサブファミリーGメンバー1

【００３０】

(14) その他の酵素には、ガンマ-グルタミルトランスフェラーゼ１、トランスグルタミナーゼ１、ジヒドロピリミジンデヒドロゲナーゼなどが含まれる。

【００３１】

３．遺伝子多型情報

遺伝子多型情報は、一般的遺伝子多型検出法を利用して得ることができる。例えば、PCRによる方法、アレル特異的オリゴヌクレオチドを鋳型としてハイブリダイゼーションを行う方法（例えばTaqMan PCR法、インベーダー法）、プライマー伸長反応を利用する方法、シークエンス法、MALDI-TOF/MS法 、DNAチップ法等が採用される。PCR法やシークエンス法はいずれの遺伝子多型の検出法にも使用することができ、他の方法は、主としてSNPの検出法に使用することができる。

【００３２】

TaqMan PCR法とは、蛍光標識したアレル特異的オリゴとTaq DNAポリメラーゼによるPCR反応とを利用した方法である（Livak, K.J. Genet. Anal. 14, 143 (1999); Morris T. et al., J. Clin.Microbiol. 34, 2933 (1996)）。インベーダー法とは、SNPのそれぞれのアレルに特異的な2種類のレポータープローブ及び1種類のインベーダープローブの鋳型DNAへのハイブリダイゼーションと、DNAの構造を認識して切断するという特殊なエンドヌクレアーゼ活性を有する酵素によるDNAの切断を組み合わせた方法である（Livak, K. J. Biomol. Eng. 14, 143-149 (1999); Morris T. et al., J. Clin.Microbiol. 34, 2933 (1996); Lyamichev, V. et al., Science, 260, 778-783 (1993)等）。

【００３３】

また、プライマー伸長反応を利用する方法として、例えばSniPer法を採用することもできる。SniPer法とは、RCA(rolling circle amplification)法と呼ばれる手法を基本原理とするものであり、環状の一本鎖DNAを鋳型としてDNAポリメラーゼがその上を移動しながら相補鎖DNAを連続して合成していくものである。この方法によれば、DNA増幅が起こった場合に生じる発色反応の有無を測定することによってSNPを判定する（Lizardi, P. M. et al., Nature Genet., 19, 225-232 (1998); Piated, A. S. et al., Nature Biotech., 16, 359-363 (1998)）。

シークエンス法とは、遺伝子多型を含む領域をPCRにて増幅させ、Dye Terminatorなどを用いてDNA配列をシークエンスすることで遺伝子多型（特に一塩基多型）の頻度を解析する方法である。

【００３４】

MALDI-TOF/MS法とは、質量分析機（mass spectrmeter）を用いた方法で、基本的には異なる一塩基の質量の違いを利用してSNPジェノタイピングする方法である。PCR増幅を利用した方法とmultiplexを利用した方法がある（Haff,L.A., Smirnov,I.P., Genome Res.,7,378-（1997）；Little, D.P. et al. Eur. J. Clinica. Chem. Clin. Biochem., 35, 545-（1997）；Ross, P., et al. Nat Biotechnol., 16, 1347-（1998））

DNAチップ法とは、ガラスなどの基盤上に多種類のDNAプローブを整列化し、固定し、その上で標識DNAのハイブリダイゼーションを行い、プローブ上の標識（蛍光など）シグナルを検出する方法を利用して、ハイブリダイゼーションで完全マッチと一塩基ミスマッチを分別検出する方法である。

本発明の方法において使用することができる遺伝子多型情報、特にSNP情報は表１の通りである。

【００３５】

【表１】

遺伝子名	No.	存在位置	配　　列	配列番号
ABCB2	1	5'flanking − 673	agctaagagtcaaagcaccc G/C ctttttccaccagcctcgcg	1
ABCB2	2	5'flanking − 646	ccaccagcctcgcgtgcctg T/G tcccttcacggacactctag	2
ABCB2	3	5'flanking − 563	ttgcaagcgctggctgctac A/C ggcgacctcoctgcgctccc	3
ABCB2	4	5'flanking − 236	gctttgcgcgcggcgctaac G/T tgtgtagggcagatctgccc	4
ABCB2	5	Intron3 + 408	aaggaaactgaggccaagac C/T ctaaatgctgaaactgcaca	5
ABCB2	6	Exon4 + 153	cctcaccatggtcaccctg A/G tcaccctgcctctgcttttc	6
ABCB2	7	Intron4 + 289	gtatttctttagcatccaag G/T ggcatagctgtgtctctttc	7
ABCB2	8	Intron4 + 291	atttctttagcatccaaggg C/G catagctgtgtctctttctc	8
ABCB2	9	Intron5 − 63	ttccttcaggttaatgactg C/T ggttctttgtgtcccctcca	9
ABCB2	10	Intron7 − 185	gtctctgccctttgtctttgc C/T gcttcttctatctctactcc	10
ABCB2	11	3'flanking + 71	agcgcacttttcagctgcgg G/A tgtctcctcttttatcatcc	11
ABCB2	12	3'flanking + 129	aactgcatcaccttttccct T/C aagcttttaattcctatga	12
ABCB2	13	3'flanking + 459	cattcagggaggcccaggtc G/A tgtgacgtcgacagttgctg	13
ABCB4	1	exon3 + 3	aacacccttattttatagat C/T caatgactgagtcaagaatt	14
ABCB4	2	intron3 + 45	cagcatctctacttatacca T/C gctctgctttaaggttctct	15
ABCB4	3	intron3 + 498	actcaaataggtggtaggag C/T agagacaattcaatacagac	16
ABCB4	4	intron3 + 515	gagcagagacaattcaatac A/G gacagaagtcttagatgaga	17
ABCB4	5	intron6 + 1030	tagttttgccatgtagaatt G/C aaaaagtgatagatggtgtt	18
ABCB4	6	intron6 + 1437	gttaagcctgcttcaatcaa G/A ttagttatattcttgttcta	19
ABCB4	7	intron6 + 2449	ttgacttagcgacactgtta G/A catacttatctttcctgtgt	20
ABCB4	8	intron7 + 451	ccttgctgcacctgtgctgt A/C taagtttggcttattatagt	21
ABCB4	9	intron7 + 530	agtagagacaggctggcgat C/G acacccgacagagctaactg	22
ABCB4	10	intron7 − 152	aacagaatcatgaaattaag T/C tgttaatgatttgaaggcct	23
ABCB4	11	exon8 + 40	aggataaattgtttatgtcg C/T ctgggtaccatcatggccat	24
ABCB4	12	intron8 + 130	ctggttgactccagatatca T/C agaaggagttgtaaaattct	25
ABCB4	13	intron8 + 248	aatacacaggaagcttctaa A/G taaagtaaggaagtcactct	26
ABCB4	14	intron8 + 531	ctaaagagtgaatggattca A/G tacgtcccttggaactcacc	27
ABCB4	15	intron8 + 4240	ctgaggttccagcttatctc T/A tagagatgtttacttagtct	28
ABCB4	16	intron8 + 4343	tgttagaagaaaaaaaggtt C/T atattacaagagggtctgac	29
ABCB4	17	intron8 + 4677	cccaagatatcttcataact G/C tccatagtgcctagggtgcc	30
ABCB4	18	intron9 + 113	tttacccagattcacctatt A/G ttatcatttttgctcccaaa	31
ABCB4	19	intron9 + 982	tgtcctatacagtttttgtt T/A taagtttagtaaattgatta	32
ABCB4	20	intron11 + 457	tccagcttgggtgacagagt A/G agacttcatctcaaaaaaaa	33
ABCB4	21	intron11 + 1337	tactcttggggagcctatca C/G cagggtgggtcagatatagc	34
ABCB4	22	exon12 + 3	tgtttctttttctgtccaget A/T ctctcggcatttagtgacaa	35
ABCB4	23	intron12 + 1288	cagaccacactaaccctcag T/C tggacctcaggatgtcagtg	36
ABCB4	24	intron13 + 206	tgtggataagaaaatagcat G/A tggttagacoatttgtgaaa	37
ABCB4	25	intron13 + 988	cagtcggtttggaagcttgc T/C acccttttcttcacttcctca	38
ABCB4	26	intron13 + (1413−1414)	tttatcttcacttatgtttt (T) ctcagttaagttatgctaat	39
ABCB4	26	intron13 + (1413−1414)	tttatcttcacttatgtttt　　ctcagttaagttatgctaat	40
ABCB4	27	intron13 + 1931	cttgcaaatgttgctcttcc A/G caaaaaaaaaaggaaaggat	41
ABCB4	28	intron23 + 784	agtatctcctaaactcttgc T/C atgcaggaaaaattatttta	42
ABCB4	29	intron25 + 158	gaaatattttactgtattaa T/C gtctagaacttaaatataag	43
ABCB4	30	intron25 + 2920	ctgagtcttcctatacatct T/A ttccattcctcggatgctgt	44
ABCB4	31	intron29 + 411	cttctcttaccttgaattct A/C ggctctcgaactttgacttt	45
ABCB4	32	intron32 + 458	agaaaatgaaattgccctac T/C gagctaactctgaaagcaca	46
EPHX1	1	intron1 + 110	tgcaaaatgtgtcttactag C/T ttctagtgcataaaatattg	47
EPHX1	2	intron1 + 143	aaatattggtggagctcttc G/A ctgtgctgggccagtcacca	48
EPHX1	3	intron1 + 1097	aatccagagagggagataga T/G tggaagttcaagggtggaca	49
EPHX1	4	intron1 + 1717	ttccaagacagagcgagggg T/C gctgctggggcgtggtttgc	50
EPHX1	5	intron1 + 1772	aactcgatgctttctcctcc G/T tctgggtcctaactgcagtg	51
EPHX1	6	intron1 + 2054	gaaatgtaacaggcaacact A/G tggacacagaaagtagatta	52
EPHX1	7	intron2 + 1414	atttccaaaatctgtttggg G/T gtaactgaaacacttgggaa	53
EPHX1	8	exon3 + 174	taccctcaottcaagactaa G/A attgaaggtatgtttgcaaa	54
EPHX1	9	intron3 + 6583	ctgtcaataccatgaagggg G/C ggcgggggcactaagggtgg	55
EPHX1	10	intron4 + 34	agaggttccataactgcccc G/A tcctcgccaagggtgggccc	56
EPHX1	11	intron4 + 63	aagggtgggcccggtgttcc C/T aocaggctctccttccggcg	57
EPHX1	12	intron5 + 154	gcagtgcctgaggcacgttg G/A cttggatcctcctgtctgta	58
EPHX1	13	intron5 + 276	tgctggaccaagctctggga T/C agccctgagcagaactcccc	59
EPHX1	14	exon6 + 130	gatgtggagctgctgtaccc C/T gtcaaggagaaggtattcta	60

遺伝子名	No.	存在位置	配　　列	配列番号
EPHX1	15	intron8 + 206	ggtgcctggctcccgggcgg C/A cctcagtaccgctccccagt	61
EPHX1	16	intron8 + 353	tggccctcccagaaaagaga A/G ggccctcagtgaggggagag	62
EPHX1	17	3'flanking + 708	aggtgcagactcatgcactc A/G gccctgaagaggtgagagag	63
EPHX2	1	5'flanking - (523-522)	aaagtcactggatatgcccc (C) tccccgcccccaacacgg	64
EPHX2	1	5'flanking - (523-522)	aaagtcactggatatgcccc tccccgcccccaacacgg	65
EPHX2	2	5'flanking - 522	aaagtcactggatatgcccc T/C ccccgcccccaacacggt	66
EPHX2	3	5'flanking - 521	aagtcactggatatgcccct C/T ccccgcccccaacacggtc	67
EPHX2	4	5'flanking - 516	actggatatgcccctcccc G/C ccccccaacacggtcttatg	68
EPHX2	5	5'flanking - 515	ctggatatgcccctcccccg C/G ccccccaacacggtcttatgt	69
EPHX2	6	Intron1 - 74	tggctgcttctcaatgaata T/C gaacagtgtctgtttccatg	70
EPHX2	7	Intron3 + 72	gagcattaggtcagaatcca T/C tgaagtgagctttgagatca	71
EPHX2	8	Intron4 + 473	gtgtgtctctactttaatct A/G caaaaggtgattgaatggag	72
EPHX2	9	Intron5 + 276	caagagtgggatgttcaagg C/T catcctgacctcacttttga	73
EPHX2	10	Intron8 + 8	tctgctcctcccggtgggtg T/C gctgtcttgcagctgtctta	74
EPHX2	11	Intron9 + 1573	atgtcgtgaagactgatgaa C/T gatggacggctgcactgctc	75
EPHX2	12	Intron10 + 207	gaacaggatggagatgagct T/C gtttatttgtcttttaatga	76
EPHX2	13	Intron12 + 911	tgaagagacctcgacatgtc G/T catcccacatactacaggga	77
EPHX2	14	Intron12 + 2425	atcttctcagctgagcaaac C/T gaggctcagaggcttaacc	78
EPHX2	15	Intron12 + 2460	ttaaccccaactggcccaag G/A ccaggtacatgattgggtca	79
EPHX2	16	Intron12 - 281	aagtcctttcaagagattat T/C staagtgtacottotoatt	80
EPHX2	17	Intron12 - 268	agattattataagtagtacc T/G tctcattataggaatattga	81
EPHX2	18	Exon13 + 50	cctgagtcggactttcaaaa G/T cctcttcagagcaagcgatg	82
EPHX2	19	Intron13 + 1739	ttgtcgtaacagggttttca G/T atgagcatatttcctttgta	83
EPHX2	20	Exon14 + 33	atgcatcaagtctgtgaagc G/A ggtaagagacatgcttggga	84
EPHX2	21	Intron14 + 314	ggattgagagcttacctcta T/C gggggtcacctcgtgtatgc	85
EPHX2	22	Intron14 + 878	attcccttattccttcacac C/T gtctgtcactcattcattca	86
EPHX2	23	Intron14 + 948	gcacaggctgggtatgaagc T/C ggggctgcatgctcagctac	87
EPHX2	24	Intron15 + 259	agagggttttcactactttt C/T agtcatggctcctcagagaa	88
EPHX2	25	Intron16 + 459	tcctcatttgtcaagcagaa G/C atgagtttccaatctctggg	89
EPHX2	26	Intron16 + 645	gtaagtgaacacactgctac G/A tgccagacttcctgccagac	90
EPHX2	27	Intron16 +985	gtcattatcatcatatgacc G/A atgaaaatgaccaaactgca	91
EPHX2	28	3'flanking + 12	aggtggccttacacacatct T/C gcatggatggcagcattgtt	92
EPHX2	29	3'flanking + 374	tgttcacggagaatgcacgg C/T atggggatgaaccctttccc	93
EPHX2	30	3'flanking + 544	tagccacctgccttttctccc G/A gcttccctagcagagtttgc	94
GAMT	1	intron1 + 429	ctcggaaagctgagctcagg G/A agacagctgtccccgggtg	95
GAMT	2	3'flanking + 626	cactgacctccttgccctga G/A agaaggccggctcctgtgct	96
NNMT	1	5'flanking - 228	ataattttcctgacgagctc A/T agtgctccctctggtctaca	97
NNMT	2	intron1 + 44	ccccactaatgtgagtcata T/C agatggagtctcagggcacg	98
NNMT	3	intron1 + 149	ggataaaaacgaatattggt A/G tagcgattccacagtttaca	99
NNMT	4	intron2 + 158	agataggcccatgtgtgtgc G/A tgttagtaaatttgtgtatg	100
NNMT	5	intron2 + 433	gctgtagccatccaagccta T/C agaacttggctgtgagtgtg	101
NNMT	6	intron2 - 3064	atcatctgactggtaagttc C/T agttctgtggtaactcaagt	102
NNMT	7	intron2 - 260	atttcatggagggaagtcca T/G ggtagaagcaggctgctagg	103
NNMT	8	3'flanking + 71	ggctcagtggttggggccca A/G tggttcatctaggacgggac	104
PNMT	1	5'flanking - 390	aagaggtgaatggctgcggg G/A ggctggagaagagagatggg	105
PEMT	1	exon2 - 4	agctcagcagacctcctggc C/T gtggtgggtagctcctttcc	106
PEMT	2	intron4 + 39	actgtccagacgggagtatc C/T cactgcttggtgagccccac	107
PEMT	3	intron4 + 1317	accgtccccagctggcccca G/A cctcctgacatgggcctctg	108
PEMT	4	intron4 + 1355	ctggagccaggctgcagccg A/C agtgcctggccatcctggcg	109
PEMT	5	intron4 + 5925	gtccaggcactgtggcccta C/T gtgggagtctccagtctcca	110
PEMT	6	intron4 + 6028	ggcagtggtccaaggaccag G/C atggactccctcttctcacc	111
PEMT	7	intron4 + 6078	atctgtcccctcgcggactc C/T acctggcttcgtgccatcac	112
PEMT	8	intron4 + 6089	cgcggactctacctggcttc A/G tgccatcaccccgccagat	113
PEMT	9	intron4 + 6379	tcaggtgtcccctcccctcat G/A cctcctcaccctgccctctc	114
PEMT	10	intron4 + 7339	tgtaaggaatcctgccaaga C/T ggcagatgcacacggggtca	115
PEMT	11	intron4 + 7619	ctcctgcacatgtgctccag A/G gaggaaaggcatttgacagg	116
PEMT	12	intron4 + 8858	ggcatgtgtgtgtgtgtgta T/G gtgtgtgagtgtgtgcatgt	117
PEMT	13	intron4 + 9029	tttctggaccagaaagcgtc G/A tcctctgccagggcctcttg	118
PEMT	14	intron4 + 9056	gccagggcctcttgcacttg C/T gggaaggctgagctgagctg	119
PEMT	15	intron4 + 9512	ctgagctgggcagcagcatt A/G ctctgtgtgctgctggcact	120

遺伝子名	No.	存在位置	配　　列	配列番号
PEMT	16	intron4 + 9523	agcagcattactctgtgtgc T/C gctggcactggcctggtggg	121
PEMT	17	intron4 + 9622	gacaaagtgtacaacaaggt G/A tctcgaactgggtcagctca	122
PEMT	18	intron4 + 10776	ccattcctgggtcttctttg G/A aggctgaatgaaattccatg	123
PEMT	19	intron4 + 10912	tctgccccactttgctcaga G/C gtgcaacaaggccttcagga	124
PEMT	20	intron4 + 11590	ggacactggcctgatgcaga G/C gtgtggtctctctcctgcag	125
PEMT	21	intron4 + 12090	ggccagggcaccccctaccag G/C ctgagtcccacctgtccagc	126
PEMT	22	intron4 + 12263	tacccgccttcccagatgga G/A cgggctgctcatgggactta	127
PEMT	23	intron4 + 12448	tctggtcccctctcctgctt G/A tagtttcctgggctaaaatc	128
PEMT	24	intron4 + 12730	tgggaccagtgccgccacca C/T ggcccaaggacctggtgttc	129
PEMT	25	intron4 + 13240	gggctccaggcacacagcgg T/C cccagtacacctgtcgcttt	130
PEMT	26	intron4 + 13494	tcogtggaactcagagatgg T/C acctccctgcgagtggggc	131
PEMT	27	intron4 + 13817	aactctcccctgctgctgag A/G cagatcttggagcctcggcc	132
PEMT	28	intron4 + 14773	ccgccctgtgcttcatgccc C/T ctatgcctctcactgcctgg	133
PEMT	29	intron4 + 14951	gtcctgaggcccctcocacc G/A gagcctgcggtgcccctcaca	134
PEMT	30	intron4 + 16896	gotgtgactgtcttggagac T/C gggtcttggcgggcctggtg	135
PEMT	31	intron4 + 19439	ccaggagcctctgaggcagc G/A ggggcttctcaaccacacaao	136
PEMT	32	intron4 + 19559	attttgtcagcatgtcacgt C/T cctttcatcatgaagcaagg	137
PEMT	33	intron4 + 20051	acagcactgcgggagccacg A/G catotgcagacgcatttgat	138
PEMT	34	intron4 + 20816	tggactctctggcgtccatc C/T agccacttcagtgcgacgtg	139
PEMT	35	intron4 + 21196	ggctggctgggcoctgggat C/G atcgtgacaggctttagtgg	140
PEMT	36	intron4 + 21528	acaggtgggagccgaggctc G/T ggaggtggccgggctgagc	141
PEMT	37	intron4 + 21596	ccgcttcccogtgctctggc C/T gtagcagaaagtgtcccact	142
PEMT	38	intron4 + 22672	agcctccoactgccttgtgg C/T tgaggggagggggccgggtc	143
PEMT	39	intron4 + 22713	tctaacgctgtcttctttgt A/T ctgaaaaccaaacaccttct	144
PEMT	40	intron4 + 23010	tgccgggcagcggggaggga G/A ggcgagtggttcccccaagt	145
PEMT	41	intron4 + 23588	gtgcaggcgccctgcatccc C/T gcagccaagttctgggcgga	146
PEMT	42	intron4 + 23627	gacactgccctgagccagga C/T ggtgaggtgggacgccttcc	147
PEMT	43	intron4 + 23941	tgaggggttgggactctaca G/A aggagagtggactcacgggg	148
PEMT	44	intron4 + 24091	gacacctcttcactgtcagc G/T ctgagacacgcccctgccct	149
PEMT	45	intron4 + 25348	caggccagttggaatcctac G/A tagagtgaaagcatctcagc	150
PEMT	46	intron4 + 25603	taagcagttaacactgatgc G/A tgatgaaaattccaacagca	151
PEMT	47	intron4 + 31540	cctccaggtggcaggaacac T/C gtgaggagcatgcaacgtgc	152
PEMT	48	intron4 + 31637	gtgggctgggacgccaggac G/A gtgaggggcttcaaggtgtg	153
PEMT	49	intron4 + 31642	ctgggacgccaggacggtga G/A gggcttcaaggtgtgtttgt	154
PEMT	50	intron4 + 35593	ggaggagctgaaagagctgg G/A gctcgggatcaggtggttca	155
PEMT	51	intron4 + 35647	actttgaggcaccaccgcac C/A tgtccgtgcgtgagggagac	156
PEMT	52	intron4 + 35862	tcccagtggtggctctgtcc C/T cgtctcagccgagcactcag	157
PEMT	53	intron4 + 35862	ccgtctcagccgagcactca T/G cggccagggtggctggactc	158
PEMT	54	intron4 + 37141	ccacaggccggatgccttga T/C acttctcagctgcagggctg	159
PEMT	55	intron4 + 38862	tggagagaccacctcagaca C/G caaggacgggcatgccatgg	160
PEMT	56	intron4 + 38872	acctcagacagcaaggacgg G/T catgccatgggtcccggcag	161
PEMT	57	intron4 + 39140	atgtctcaaatctccctccc C/T gggaaatctaggcacaggtc	162
PEMT	58	intron4 + 39635	caggcccaggagcaggtggg G/T cctcctcacaggagcagggc	163
PEMT	59	intron4 + 39713	actctgagcatgctggctcc C/T tccttctttccagggcagca	164
PEMT	60	intron4 + 40436	cctggttgtgcttcggaccc G/A gaggcagacagaggaggcct	165
PEMT	61	intron4 + 47485	acaatgactgttggagccct C/T gagcaggctgtgtcacgtgg	166
PEMT	62	intron4 + 48131	actgggggatcctgaatccc G/A cctcctgatgccagtggagc	167
PEMT	63	intron4 + 48558	cacagtgtgaactgttaggc C/G acagccacatcttgccggag	168
PEMT	64	intron4 + 48702	gagatgggggcggttcggga G/A gcaaaagcaggaaggcagaa	169
PEMT	65	intron4 + 50302	gcatgtgcatgggcagaggc T/C gttcccatctgagtgggacc	170
PEMT	66	intron4 + 54102	ggccgcgtgctcctgcagcc A/T tgggctcctctggcagttct	171
PEMT	67	intron4 + 54220	cccagggacagatcttctcc G/A ccagacgtctctttctgcct	172
PEMT	68	intron4 + 54371	gcagataatgtgcagctggg G/A tgcatgtggttgttgctccc	173
PEMT	69	exon5 + 79	tggcctgctactctctaagc G/C tcaccatcctgctcctgaac	174
PEMT	70	intron5 − 6796	ggaggaagtcagcttcttac A/C gatggtggctcccagctttc	175
PEMT	71	intron5 − 6636	ttttctcctctcacctttttg T/C gttcagaggcagaggtgtgc	176
PEMT	72	intron5 − 6448	gttgggcoaggctctgacag G/A accctcgggaccagctcctg	177
PEMT	73	intron5 − 5218	ggagcoctggctgaagaagc C/G ttacgaccaaggcctggagg	178
PEMT	74	intron5 − 4824	ggacaggccgggggttgagc G/A gctgcatgaaggaggggagg	179
PEMT	75	intron5 − 4249	tcaccagagtgatttcctcg C/A ggcaggtgcctggggtagcc	180

遺伝子名	No.	存在位置	配　　列	配列番号
PEMT	76	intron5 - 4230	gaggcaggtgcctggggtag C/T cactgggcggggtccatgag	181
PEMT	77	intron5 - 4182	ggagagtaaggggtgggggg G/A cacttaggacagggaagctg	182
PEMT	78	intron5 - 3369	ccaggtgggccgtgtgcct G/C tggcctggtgtgtggcccag	183
PEMT	79	intron5 - 2625	cagggaagctgggccctgaa C/T gagctgggcttttgggccac	184
PEMT	80	intron5 - 1200	attattgtgagcatgggaag A/T gcacatttggtcacacatgt	185
PEMT	81	intron6 + 606	gcctggctagacgcccacca A/G tgaccctgatgatggcagca	186
PEMT	82	intron6 + 1229	tttggtccaggaaggggac G/A gcagccaggagcgtctggat	187
PEMT	83	intron7 + 716	atggagatgtgctcccccgg C/G gggtcagaggacctgcggtc	188
PEMT	84	intron7 + 1537	ctctgggggacgcataagcc G/A cctccagaggacatcagcca	189
PEMT	85	intron7 + 1718	gggcttccaggtgtctgagc T/C ccccggcatgtaggacccca	190
PEMT	86	intron7 + 2695	ggctttgggggaccctggac C/T catttctagaaaacagcctt	191
PEMT	87	intron8 + 140	ccaggctcccaggtcagag C/T ggccatggtagcttacaatg	192
PEMT	88	3'flanking + 179	tacttaggaggcgtcagggg C/T tcacctggccatggccatgg	193
PEMT	89	3'flanking + 394	gatgacactgtcattcctaa A/G tgaatggccttgtgtgacc	194
GSTM3	1	5'flanking - 144	ccaacgccggccattagtcgc G/T cctgcgcacggccctgtgga	195
ALDH5	1	5'flanking - 2808	cgttgcactgtaggactctc C/T ccacgtcccctaatcccatc	196
ALDH5	2	5'flanking - 2575	gcagttcccgcggatagagg A/G ggtccggtccttcccgctgt	197
ALDH5	3	5'flanking - 2537	tgtgggtgaactgtaaaaaa C/T tgcctgtattcaggaggata	198
ALDH5	4	5'flanking - 940	cttcaactaatctgggaaca C/T tacactctgtttaatttta	199
ALDH5	5	5'flanking - 785	tgggaaagctgaaaagggat G/T ctgagacctgtggttgggg	200
ALDH5	6	exon1 + 183	ccgacggtcaaccctaccac T/C gggcaggtcattgggcacgt	201
ALDH5	7	exon1 + 257	cgtgaaagcagcccgggaag C/T cttccgcctggggtccccat	202
ALDH5	8	exon1 + 320	gcgggccggctgctgaacc G/T cctggcagacctagtggagc	203
ALDH5	9	exon1 + 605	acttgccccggcactcgcca C/T aggcaacactgtggttatga	204
ALDH5	10	3'flanking + 1527	aaagtgcaactgtaagaccc G/A tagagaaaaactctggttcc	205
TGM1	1	Exon2 + 179	tgccgaaatgcggcagatga C/T gactgggggacctgaaccctc	206
TGM1	2	Intron9 - 611	acttaccactctgtcctctc C/T tgccaggcctcttcctgtca	207
TGM1	3	Intron9 - 272	ccgcacatctgtaccctgcc C/G ccatcctccagcagagcagc	208
TGM1	4	Intron10 + 54	tcagtcatgggttctctggt C/T ccaacttcaccgctgactga	209
TGM1	5	Intron10 - 51	aggaggccgggagtcaggcc A/G ccctcagaccctctggctca	210
TGM1	6	Intron12 - 47	gggagtccctgggggaagcc T/G catgtagggaagcaggcctc	211
TGM1	7	Intron13 + 72	ggataaggacatcagaggtg G/A gcgctaagccagcagcaggc	212
TGM1	8	Intron14 + 1671	atctcttacccacaccccca C/G catggtggggaggttcctca	213
TGM1	9	Intron14 + 1691	ccatggtggggaggttcctc G/A tcctaagggatccgcagagc	214
TGM1	10	Intron14 - 1634	tccctgcctccctccttcag G/A gagctcagaaacaccttcaa	215
TGM1	11	Intron14 - 1459	ggaaacccctcagaaccagg T/C tccaagccaaatgctttgcc	216
TGM1	12	Intron14 - 801	cagaatacaaaagtgggatg G/C gaggcaaggagtcccgttag	217
TGM1	13	Exon15 + 233	ctcgaggtggagcttagccc T/C gtgccaggagcaatgggact	218
TGM1	14	Exon15 + 369	ggagtcagtcttcacttgca C/A tgggggaacagatgctaata	219
GGT1	1	intron1 + 85	ttatccagtaaggtggctcc G/A tcacctcttttcctggtggg	220
GGT1	2	exon3 + 68	gacggccaggtccggatggt G/T gtgggagctgctgggggcac	221
NQO1	1	1 intron 1 80	aggaggttgtaggggcttgg C/A ctgaattttgttccttgact	222
PIG3	1	5'flanking region -47	gggaaggaggaaaggaaaga G/A ggggagggtggttctgctta	223
PIG3	2	intron 2 243	taacaccggacgcccagcag A/G agtcccagcttcttagaatc	224
PIG3	3	3'flanking region 282	agcaggccccagccctgccc G/A ctactcacctgggccccacc	225
NQO2	1	5'flanking region -434	tttctgttgcaccacggacc C/G tcattctgtaaccgggatac	226
NQO2	2	5'flanking region -406	gtaaccgggataccagccag A/G gatggggagcgggaggcgca	227
NQO2	3	5'untranslated region -102	tcctgcggctcctactgggg A/G gtgcgctggtcggaaggtga	228
NQO2	4	intron 1 1919	tcactcaaatagagctgagt T/C agtcactcagctcttggacc	229
NQO2	5	intron 1 2004	acaaactcacatgccaccag C/G catatgatgtaaacatgtaa	230
NQO2	6	intron 1 3391	aaagcagagggctgtgcagg C/T gcccctgccccctaggctagg	231
NQO2	7	intron 1 3456	caaaggcctcatcctcaggg C/A ggccaactcttctgttttag	232
NQO2	8	intron 1 3595	actgcccagctttaggttca T/C tcttgtaagtgttgctggtg	233
NQO2	9	intron 1 3596	ctgcccagctttaggttcat T/C cttgtaagtgttgctggtgt	234
NQO2	10	intron 1 3598	gcccagctttaggttcattc T/C tgtaagtgttgctggtgtca	235
NQO2	11	intron 1 3651	ccctgcgctttgaagggatg A/G atgtgacctctcccacattc	236
NQO2	12	intron 1 6036	tggtgtggcggttcactgat C/T cccagccttctgctcgatc	237
NQO2	13	intron 2 14	atggcaggtaatgattcact A/G ttgtggagtaagacttttt	238
NQO2	14	intron 2 192	gccacgtggaagtgtataaa C/T tatctggaattatcttgttt	239
NQO2	15	intron 2 635	cacccctgtttagcacctagc A/C ccatcccctggcctctgccca	240

遺伝子名	No.	存在位置	配　　列	配列番号
NQO2	16	intron 2 685	agtagcacccctccccccacc G/A gctgtgacaaaccaaaatgt	241
NQO2	17	exon 3 139	ctgatttgtatgccatgaac T/C ttgagccgagggccaccgac	242
NQO2	18	intron 3 36	aatgctctatttataaaaac T/C atctttatgttttttacttt	243
NQO2	19	intron 3 728	aacgtgggcataaaccacca T/C ctagtgccaaaaagcaggtg	244
NQO2	20	intron 4 1577	tgcctctgcacacccctttcc C/T gacaccagccctttctttac	245
NQO2	21	intron 4 1832	tcggccggccacgtggagcc C/T gctttcctcctcgcacccac	246
NQO2	22	intron 4 2583	tggtgttacgcaacagctcct C/T gtcccctccctgcctgccca	247
NQO2	23	exon 5 330	ctgtactggttcagcgtgcc A/G gccatcctgaagggctggat	248
NQO2	24	exon 5 405	atcccaggattctacgattc C/T ggtttgctccaggtatgtgc	249
NQO2	25	intron 5 21	gtatgtgctcttggataagg A/T tcactatggatagttggagg	250
NQO2	26	intron 5 253	atggcaaacaagggagtggg T/C caggtgtcaggtgacgggggg	251
NQO2	27	intron 6 2435	ccccccttaaatcatttaac T/C gaatggtatgtaacaggtgt	252
SULT1A1	1	5'flanking region -1597	gcagagtaaagggactcact C/G aagaagaggaacgtgggggt	253
SULT1A1	2	5'flanking region -1491	gaggggtatattcatgaaga G/T tccaggaaaaggtaaagatt	254
SULT1A1	3	5'flanking region -1376	cggtttcatatgttactgat C/T atacaatgagatcctaggtg	255
SULT1A1	4	5'flanking region -1375	ggtttcatatgttactgatc A/G tacaatgagatcctaggtga	256
SULT1A1	5	5'flanking region -1370	catatgttactgatcataca A/G tgagatcctaggtgaaacct	257
SULT1A1	6	exon 1B -65	aaccctgcattcccacaca G/A cacccacaatcagccactgc	258
SULT1A1	7	intron 1B 442	gagccaccctgcctaggcct G/A tgcttttgctgagtcatcag	259
SULT1A1	8	exon 1A -197	gctgggggtcccagcaggaa A/G tggtgagacaaagggcgctg	260
SULT1A1	9	exon 1A -159	ctggctggcagggagacagc A/C caggaaggtcctagagcttc	261
SULT1A1	10	exon 1A -95	gagaccttcacacaccctga T/C atctgggccttgcccgacga	262
SULT1A1	11	intron 1A 60	ctggttttcagccccagccc C/T gccactgactggctttgtga	263
SULT1A1	12	intron 1A 69	agccccagccccgccactga C/G tggctttgtgagtgcgggca	264
SULT1A1	13	intron 1A 174	tgtggtggtggtaagggaac G/A ggcctggctctggcccctga	265
SULT1A1	14	intron 6 11	catgaaggaggtgagaccac C/G tgtgaagcttcctccatgt	266
SULT1A1	15	intron 6 17	ggaggtgagaccacctgtga A/T gcttccctccatgtgacacc	267
SULT1A1	16	intron 6 35	gaagcttcctccatgtgac A/T cctgggggcccggcacctcac	268
SULT1A1	17	intron 6 71	ctcacagggacccaccaggg T/C cacccagccccctcccttgg	269
SULT1A1	18	intron 6 108	ttggcagccccacagcagg C/A ccggattccccatcctgcct	270
SULT1A1	19	intron 6 111	gcagccccacagcaggccc G/A gattccccatcctgccttct	271
SULT1A1	20	intron 6 270	ctccctgccaaagggtgtgc C/T acccagggccacagtcatgg	272
SULT1A1	21	intron 6 488	ttttacttttcctgaatcag C/T aatccgagcctccactgagg	273
SULT1A1	22	intron 6 509	aatccgagcctccactgagg A/G gccctctgctgctcagaacc	274
SULT1A1	23	exon 7 600	ccctctgctgctcagaaccc C/G aaaagggagattcaaaagat	275
SULT1A1	24	exon 7 645	gagtttgtggggcactccct G/A ccagaggagaccgtggactt	276
SULT1A1	25	exon 8 902	gctgtgagaggggctcctgg G/A gtcactgcagagggagtgtg	277
SULT1A2	1	5'flanking region -547	tgttctttcttggttctatg G/C atccatgctctgctccaccc	278
SULT1A2	2	5'flanking region -425	tgtgggttgcactgggccag G/A accoctggcaccttcaagac	279
SULT1A2	3	5'flanking region -358	ctttccagggcctgcctatc C/T cagctttctcottottgcct	280
SULT1A2	4	5'flanking region -355	tccagggcctgcctatccca G/T ctttctccttcttgcctggg	281
SULT1A2	5	5'untranslated region -28	actgcgggcgaggagggcac A/G aggccaggttcccaagagct	282
SULT1A2	6	intron 1A 85	ctgactggccttgtgagtgc G/A ggcaagtcactcagcctccc	283
SULT1A2	7	exon 2 24	gagctgatccaggacatctc T/C cgcccgccactggagtacgt	284
SULT1A2	8	intron 2 34	gccacccaccctctcccagg T/C ggcagtcccccaccttggcca	285
SULT1A2	9	intron 5 77	cagcaaccctgtgtcggcac T/C ccctgcccgcttctccagtg	286
SULT1A2	10	intron 6 684	actggggtcccaggggtcga G/C gagctggctctatgggtttt	287
SULT1A2	11	3'untranslated region 895	gctctgagctgtgagagggg T/C tcctggagtcactgcagagg	288
SULT1A2	12	3'flanking region 98	cctcccgctccagctcctc A/T acttgcctgtttggagagg	289
SULT1A2	13	3'flanking region 817	ccactgactcggggcttgcc A/C eggctgccaggctgcaaaa	290
SULT1A2	14	3'flanking region 1006	cctctcccctggaggctgct T/C tacccgctgtgggggcgcat	291
SULT1A2	15	3'flanking region 1464	tcccgtagcccaggcaagtt C/T ggtgaccagagagcagcccc	292
SULTX3	1	intron 1 332	cctgcttctccctttacctg G/T ctggctgtgtgaccttggac	293
SULTX3	2	intron 1 1167	taggaatggctaagcgtgtc G/A ttggcttctgtggccactca	294
SULTX3	3	intron 1 2872	cattctcactgatgcagacg G/A aagcttctgggcctgggcgt	295
SULTX3	4	intron 1 6242	caccccttggcttttaccagc A/G tggaaacattttacctgaat	296
SULTX3	5	intron 1 6601	gcgtgggcttctggagggag C/T gagaggagagtggagggccc	297
SULTX3	6	intron 1 6768	agcttgaaatgagccagact C/T tcctgggacctgttgacccc	298
SULTX3	7	intron 1 6905	agtactttgttttatcctcc C/T catcctcacaactttgccat	299
SULTX3	8	intron 1 7464	gccaggatcccttgagagac G/A acatgaacacagccaggagc	300

遺伝子名	No.	存在位置	配　　列	配列番号
SULTX3	9	intron 1 7833	tgcttcgggctgggcttggc G/A ggggcagctgtgctccaggc	301
SULTX3	10	intron 1 8189	caaactggggccottaatgc C/T gcacaccagagcctcctttc	302
SULTX3	11	intron 1 8316	ctctcacacaagggcggagc C/G tcttcccctgaggcagagc	303
SULTX3	12	intron 1 8617	agacagaggctggggccaag C/T cagggttgccggagcttcct	304
SULTX3	13	intron 1 8631	gccaagccagggttgccgga G/T cttcctggactggtcaggcc	305
SULTX3	14	intron 1 9493	ttttcctcttagagcttccc G/A tcgtgctctgtgtcgagggc	306
SULTX3	15	intron 1 10306	caggcggggagcctgaatgc C/T gcagtcgtgaggtggccag	307
SULTX3	16	intron 1 11987	tcataaaataatgatatcag T/C acacttttggaaatttgag	308
SULTX3	17	intron 1 13085	ctctgtgcccggtgttgaga C/A aggcccatgcctagagtcct	309
SULTX3	18	intron 1 13108	gccatgccctagagtcctgg G/A gagttccacccccagaacagc	310
SULTX3	19	intron 2 700	gaaccatctgggagtcgttc C/T gtactgccgtgccgagggcc	311
SULTX3	20	intron 2 818	agccatagtagctagccagc G/A atcagcgctgggagggggagc	312
SULTX3	21	intron 2 1677	actccacttcccctgaaccc C/T acccctcctcctcctctg	313
SULTX3	22	intron 4 4954	gcgtgccgaaggcgggaggg C/T tgggatggctcaagacgtga	314
SULTX3	23	intron 5 3632	ccagctgactcccacaccag C/T ggtcagagaacattgtcttt	315
SULTX3	24	intron 5 3862	acattgtcttttaaggttcc C/T gaagtgctgcaataaagaaa	316
SULTX3	25	intron 6 1874	tctgatctcagagagctgac A/G atggaaagaattctaaacga	317
SULTX3	26	intron 6 2133	agaccggtgcctgcagttta T/G cccacagctcagccctccct	318
SULTX3	27	intron 6 2524	ggaagggccagggctgcctg T/C gatgcccagagcagtgcact	319
SULTX3	28	intron 6 2573	agatcatactcgctcctggg A/G tgtttattaaacacctgcca	320
SULTX3	29	3'flanking region 12	gttcccggcgttgcgtcgag C/G gtttctgcttgtgggggtag	321
SULTX3	30	3'flanking region 445	tccaaagcctgtcttcctga T/G ttcctgtggaaggagagtcc	322
TPST1	1	5'flanking region -298	acccgccaccatgcccagct A/C attttttttgtatttttttt	323
TPST1	2	intron 1 3520	agaaaagcagattaatgtaa C/G agtgacgcttagacaacaag	324
TPST1	3	intron 1 3610	ggcagaaagagaatatagca A/G ctattaaacacaaataaatt	325
TPST1	4	intron 1 20828	tattgctgtccacctggtca A/G tgtgtcctgctgataagtgc	326
TPST1	5	intron 1 -6761	aatacaatacttattctgta T/C aattctagagggcccagaga	327
TPST1	6	intron 1 -544	tagaacaagtgaatatttta G/T gttcttagtggtttatggtt	328
TPST1	7	intron 1 -526	tacgttcttagtggtttatg G/T ttggcagttttccccccaaca	329
TPST1	8	intron 1 -234	tcaagacatttaataatgca C/T atgtttcagctaacccttttt	330
TPST1	9	intron 1 -48	ttatagtgggtttaagcatg A/G tttctaaaaaaatttaaataa	331
TPST1	10	intron 2 -18944	aaaacattagaactgggaag G/A ttaaaaaatctttagtcttt	332
TPST1	11	intron 2 -18687	tatgtgcaccctaataacat A/G tttccttaaaactagtacta	333
TPST1	12	intron 2 -18501	ttggaaggtaacttaatgta A/G gtgcctgaaaaacagggata	334
TPST1	13	intron 2 -159	gaatggggatttccctcagt C/G ctgcccactggctgctcttg	335
TPST1	14	intron 2 -19	acctgttgccttaaactcac G/A cctgctttgttttccaggt	336
TPST1	15	intron 3 158	tgctggggaagaaagatcag C/G gtotgggacttgttgatttt	337
TPST1	16	intron 3 3779	agcagggcacgtcaccctcc C/T ggcacacccatgtgttcacc	338
TPST1	17	intron 4 292	ttgttattttcattatgaac C/T atgaaatatttcagctgaaa	339
TPST1	18	3'untranslated region 1518	gttgtctgtacatgttctaa T/G gttttgtagaacacgtgtgc	340
TPST1	19	3'flanking region 264	acggtgcttggcctgcatta C/T cattttgtagtgaagtttct	341
TPST2	1	intron 2 578	tcacctatcatcctcactgc G/A aggatgccaggatacctccc	342
TPST2	2	intron 2 789	cttaagccatcgtgcaggtc A/G ttgctgtcttctgctcactt	343
TPST2	3	intron 3 2009	cccaggctggagtgtagtgg T/C gtgatctcggctcactgcaa	344
TPST2	4	intron 3 2017	ggagtgtagtggtgtgatct C/T ggctcactgcaacctccgcc	345
TPST2	5	intron 3 2035	ctcggctcactgcaacctcc G/A cctcccgggttcaagcagtt	346
TPST2	6	intron 4 104	aatgttcagtctctcaattc C/T tggtcatctgattgttcct	347
TPST2	7	intron 4 379	taaataaataaactattggt C/T cattttcttgtattataaggt	348
TPST2	8	intron 4 588	tactgcagcctgatacttct C/T ggcttaagccatcctctcac	349
TPST2	9	intron 4 626	caccccaggctcctgagtag C/T taggactgcaggtgcacgcc	350
TPST2	10	intron 4 718	cccaggctggtctagaacto C/G tggcogtaagggatgcccct	351
TPST2	11	intron 4 873	gttgatggccttatttatac G/A tttccattacagcttctagt	352
TPST2	12	intron 4 949	caaatatttgaaaatgggac C/G caggcctgaggaagagcttt	353
TPST2	13	intron 4 1033	taagctcagcatttctgagc G/A tgtgctgattttaggaaata	354
TPST2	14	intron 4 1051	gcgtgtgctgatttaggaa A/G taaacagttatcgtattgaa	355
TPST2	15	intron 4 1356	gattcaacgtacataccagc C/T gacattgacaggtgaatggc	356
TPST2	16	intron 4 1707	gtctccttaaaaggtggctc G/T ctgccoctggcttgccccag	357
TPST2	17	intron 5 215	aagaccagcctgaccaaaac G/A gtgaaaccccgtctctacta	358
TPST2	18	intron 5 341	tgggaggcagaggtcgcagt G/A agctgagatcacgccgttgc	359
TPST2	19	intron 6 31	ggacttcactgggggttccc G/A ctgcttctgggtggcccccgg	360

遺伝子名	No.	存在位置	配　　列	配列番号
TPST2	20	intron 6 273	gtttgtctgacactggggac A/G gggcaggaagcaccactatg	361
TPST2	21	intron 6 693	aaagggatttttttgaactt G/C gtaattcaaagatttaagat	362
TPST2	22	intron 6 1635	tcctgggtacagagttggcc T/G tgaacaaacatgagtccttc	363
TPST2	23	3'untranslated region 1147	cttcccccactttcagatctc C/T gcaaatgacttcattgccaa	364
SULT1A3	1	exon 8 843	cgcttcgatgcggactatgc G/A gagaagatggcaggctgcag	365
CST	1	intron 1b 6302	agagctccccagagaggact A/G tgaggctgcatgatgcatga	366
CST	2	intron 2a 1004	gagtgagacccccatctctca C/T aaaatttttttaaaaagta	367
CST	3	intron 2a 1395	atgcctaagtttacagtagc T/C aggcaggaaaggcacaacca	368
CST	4	intron 1d 473	ccagagcctgaggttggtgc T/A ggggccccctccatggctgcc	369
CST	5	intron 2b 726	ctatctctccagtgcctctc T/C gtcoctgtctggacoctgct	370
CST	6	intron 2b 745	ctgtccctgtctggacoctg C/A tgggggccacagagcaggc	371
CST	7	exon 3 85	tcactagtttcctgctgctg G/A tgtactcctatgccgtgccc	372
CST	8	intron 3 308	tcgtctgaggtcaggagttc G/A agaccagcctggccaacatg	373
CST	9	intron 3 853	ttttgtcctataaaatggca G/A tttcatgtggcccaagctga	374
CST	10	exon 4 198	gaggcagtgatccgggccaa C/T ggctcggcgggggagtgcca	375
SULT1C1	1	intron 3 2280	gcaaatttttggtatttttta G/T tacagtcagggttttaccat	376
SULT1C1	2	intron 3 3742	gcagatctcactttctggca G/A attcoctgaatttgctcccc	377
SULT1C1	3	intron 3 4453	ttcatagggcttttccctca C/T ttgttttgtaattttgtata	378
SULT1C1	4	intron 3 5234	gaaaagagactagaggcagg A/G gagctttgcagttcttctaa	379
SULT1C1	5	intron 3 6175	tggotggcaggaaggtgagg G/C agtcotctcttctctggtcc	380
SULT1C1	6	intron 4 205	acatgaaggcaggatccaga T/C tgaatgtttggagggaacta	381
SULT1C1	7	intron 4 408	ggctcaogcctgtaatccca G/C cactttgggaggccgaggcg	382
SULT1C1	8	intron 4 429	cactttgggaggccgaggcg G/C gtggatcacaaagtcaggag	383
SULT1C2	1	5'flanking region -110	tcctgttaactcaoagagca C/T ggaaggcotggaacggcaco	384
SULT1C2	2	exon 1 15	acactaatggccttacacga C/G atggaggattttacatttga	385
SULT1C2	3	intron 1 297	gtagacttgtttatttattc A/C ttcccaatctaggcccttat	386
SULT1C2	4	intron 1 363	gagtgtgtgagctagaaagg T/G gatcctgagtctgatttggg	387
SULT1C2	5	intron 1 2300	gggctactatcagcagccac C/T acctcaggaaggatgacttc	388
SULT1C2	6	intron 2 455	aagacttggaagcaaataga T/G aaaaaaaaaatcgtagaaat	389
SULT1C2	7	intron 4 55	caaaatctccaaacacccta G/A aaggaaagaatctttttctt	390
SULT1C2	8	intron 4 111	ctgcattctttaatggaaca T/C tctcacttctcttcaggaat	391
SULT1C2	9	intron 5 1657	ctttgtgtttactttgtttt T/C acttggtacaaaagtgttgt	392
SULT1C2	10	intron 5 2082	tctgctcctagagatggagg C/A gtcccacagccacagtgatg	393
SULT1C2	11	intron 6 933	agctactgaacctctcccac A/G taactgtatttcaggggcag	394
ST1B2	1	intron1 80	acttgtccataaaatcatta C/T cattctaaataaagttaata	395
ST1B2	2	intron 2 -352	aacatttaaatagtcattta T/C agcaatgcacaggtataata	396
ST1B2	3	intron 2 -85	attacataatgctcaaaaat G/A tcttgaaaaactggttggca	397
ST1B2	4	intron 4 460	gtacttgacattaaaaaata T/C ctgatgtttatatatccata	398
ST1B2	5	intron 4 470	ttaaaaaatatctgatgttt A/G tatatccataaatagctaat	399
ST1B2	6	intron 4 518	tttaagattgtcctcatatt C/G ttacttcctttggttactaa	400
ST1B2	7	intron 4 616	aatgtttatgaaaatagact T/C ttatctggttttagtggcct	401
ST1B2	8	intron 5 58	ctgcatcatgctgtaaaagg G/A ttgatatttgctttccaact	402
ST1B2	9	exon 6 612	taatagaatocaaaggagga A/C atcaagaagatcattagatt	403
ST1B2	10	intron 6 582	aatacattacttccatttaa G/A tagtctgtttattgtggctt	404
ST1B2	11	intron 6 3130	agatgtaaaaaattattcaa A/T ttttaaaagcctgaaaaatt	405
ST1B2	12	3'untranslated region 907	tttaaagtgtctaaatcaca C/A atctgaagaagtaagagatt	406
ST1B2	13	3'flanking region 50	tcagatcccagttttgttcc T/G ttgattctgagtttccaaat	407
ST1B2	14	3'flanking region 328	tttgacccaggacactgtgt T/G ccactgctgtctaccgagtt	408
ST1B2	15	3'flanking region 446	gtagttcagattttggaaat G/A ttttttctatatcatacctа	409
CHST2	1	5'flanking region -260	agccggacagtccgccgggc G/A gtgatccgggggccgctccc	410
CHST2	2	5'flanking region -56	gcgctggggaccagccgccg C/T gcccgcctcggagtcgcggc	411
CHST2	3	3'flanking region 218	aggagtgaaacacatctttg T/A attctaaaggcagaaaccaa	412
CHST2	4	3'flanking region 383	gcagagaccaatgttttggt G/C ctgaggctggttcagaaaaa	413
CHST2	5	3'flanking region 952	tactgaaacattctgcagaa T/C gttatactatgagaagaaat	414
SULT2A1	1	intron 2 478	ggactgggctctgtacacac T/C tcgtcttactgtgtgtaaat	415
SULT2A1	2	intron 3 382	caaaaccctcttaatattct G/A tttctatctgtctcagaact	416
SULT2A1	3	intron 3 409	tctgtctcagaactgattgc A/G tgactctaggatcgctatat	417
SULT2A1	4	intron 5 249	agctggaaattacaggcaca C/T gccaccacacccagctaatt	418
SULT2A1	5	intron 5 395	aggcatgagccacggcgccc G/A gccaatttatcagctttaat	419
SULT2A1	6	3'flanking region 33	ttccttgttaaaagttacca G/C ggttggccaggcacggtggt	420

遺伝子名	No.	存在位置	配　　列	配列番号
SULT2A1	7	3'flanking region 46	gttaccagggttggccaggc A/G cggtggttcatgcctgtaat	421
SULT2A1	8	3'flanking region 199	ttagccaggcgcattggctc A/G tgtctgtaatcccagcactt	422
SULT2B1	1	intron 2 4162	ttctcccctctcctcaccat C/T cgcacacaggtgatctacat	423
SULT2B1	2	intron 3 879	gagggcatccagctctgggg G/A ctggacctgggggtttgtgg	424
SULT2B1	3	intron 4 3882	ttccacgctccttccttggc C/T gagtgccctcccctccgctga	425
SULT2B1	4	intron 5 1780	cctgcagaaaggggtcccctt C/T catgtccaagcagtaatggc	426
SULT2B1	5	intron 5 1814	taatggctgcagcatggagc G/A ttgtgggggcattgagacag	427
SULT2B1	6	exon 6 789	ccctcttctccagggtctg C/T ggcgactggaagaaccactt	428
CHST4	1	5'flanking region -1092	atgaagccttgtgccatctc G/A ctgtgtcgtgccagcacctg	429
CHST4	2	5'flanking region -941	ctgccagagagaaacaggaa G/A ggaggaagagccacacaatt	430
CHST4	3	intron 1 -150	caggaaatgatttggagaag G/T actggtgccattgttggcac	431
CHST5	1	intron 1 -144	ggcctcttaggtttcagcca A/C gacaggtgactcttagcacc	432
CHST5	2	intron 2 17	caacgtaagagcgcttctca T/A tgtccagctcctttgtttct	433
CHST5	3	intron 2 139	aatcccagcactttgggagg C/A ggagatgtgcggatggatca	434
CHST5	4	intron 3 1829	gactgtatgtctgctattca T/C ataggaacaaataattcatg	435
CHST5	5	intron 3 2037	aaatgaaaccaacaccaaca C/G tgcagagaagcaaacaaaag	436
CHST5	6	intron 3 2134	aagcagctaaattgtgttcc G/A tacaggtgcaattaggcagg	437
CHST5	7	intron 3 2528	atggtaaagttcgcctgggt G/A cagtatgtcagcatcctgct	438
CHST5	8	intron 3 2674	gcacttatcctagaaaggcc A/G tttctgaagactcagcagga	439
CHST5	9	intron 3 7039	ctggctcccgccggccaccc T/C gggaccgcagccacgtctga	440
CHST5	10	intron 3 7211	gtagccccaggacaccccca T/G cctcaacatcccattctggg	441
CHST5	11	intron 3 7294	ggagcttccagtggcttggt T/C acccccgactcttcgtccat	442
CHST5	12	intron 4 108	gcagggtcctgcactctgca G/A ggggcaatcacaggtgggag	443
CHST5	13	intron 4 402	agcactggaaaaagtacagt T/C gcacttgtagcggaggtggg	444
CHST5	14	intron 4 547	ctcctgtccccgcattgagg C/G gaaggagcagaggtgagatc	445
CHST5	15	intron 4 1142	gccccaggtctcatagctcc C/G cattggcagtgctgggattt	446
CHST5	16	intron 5 1187	caatgggcagtaattggggc A/G tgggatgggcatgagggccc	447
HNK-1st	1	intron 1 139	gtgttttggcgacttgaaga C/T ctccctagttcgcgggagta	448
HNK-1st	2	intron 1 1020	acctgagcagaaaattctct T/C cttcgctgaaatgaaaattg	449
HNK-1st	3	intron 1 1091	aagaatttgtaaacatcaca G/A gcaacttgcagttatattcg	450
HNK-1st	4	intron 1 1971	ctataactatttcaaacata C/T gaaacaggcataattggatt	451
HNK-1st	5	intron 1 2096	atttagaatattcatttacc A/C agaaatccaaatataacctg	452
HNK-1st	6	5'untranslated region -91	ctatccagtgacaagaggaa C/A caagaacctcagttcagggg	453
HNK-1st	7	intron 2 -530	agtgggcggaggcgagaagc G/A tcagtgttcattcctttgct	454
HNK-1st	8	intron 2 -466	gctacatcttgtcagccagt C/T agaattttaaacacagccag	455
HNK-1st	9	intron 2 -92	acggaaatatttgtgctgat A/T cttactgactgaaatcacct	456
HNK-1st	10	intron 3 152	catggcctccgttccttcat G/A ttacagaggtgtgaggggag	457
HNK-1st	11	intron 3 312	cacagtggccttatgccttg C/T agcagggcgcctctcaggct	458
HNK-1st	12	intron 3 1948	tcctttgatgtatcaagttt T/C gtgctgaatgttttcagtgt	459
HNK-1st	13	intron 3 2140	ttacacctggagaggagcac C/T gcagcggtccttaatactgc	460
HNK-1st	14	exon 4 187	agcagcacattcctgaggaa C/T tgaggtgggcacagccagg	461
HNK-1st	15	intron 4 581	cctgatcattccctagctgg G/A atgaggggtgcactctggaa	462
HNK-1st	16	intron 4 615	tctggaaggcctctcacttc G/C taacccccattctggatcta	463
HNK-1st	17	intron 5 7	gattgttctaaatggtgtgt G/A tgggtctactgaatgtccac	464
HNK-1st	18	intron 5 123	acctgaagggactggtggcc G/T tccagacaggcctgtttttg	465
HNK-1st	19	intron 5 721	ataattatgggctctgctta T/C gaaatttagcttcagacagg	466
HNK-1st	20	intron 5 867	tgctgcccacagagtcggtg G/A tcactcctggccactgtttg	467
HNK-1st	21	exon 6 444	ccaggagcattttcttccat T/C gaggagatccccgaaaacgt	468
HNK-1st	22	intron 6 94	ctgagttctgtacttggcag A/G ttgatcggaggaccacagag	469
HNK-1st	23	intron 6 247	catgaaggtgacatcatttt G/A ttaatagaaattagcaggca	470
HNK-1st	24	exon 7 696	aggaggaaccggacagagac C/G cgggggatccagtttgaaga	471
HNK-1st	25	exon 7 870	gagaccctggaggacgatgc G/T ccatacatcttaaaagaggc	472
HNK-1st	26	3'untranslated region 1110	tcaaatatctttattagacc T/C ggggctaaccaggtgaagat	473
HNK-1st	27	3'untranslated region 1178	ccacacccctcctttgagga C/T gcccggggtctcccacaggc	474
HNK-1st	28	3'untranslated region 1393	ggaagcatcacacagcgtta G/A gagccgtttccttcaggtgt	475
HNK-1st	29	3'untranslated region 1452	tgaggttctcctggctagtc A/G gggtggcttcaacccatcaot	476
HNK-1st	30	3'untranslated region 1540	gcaaggggctgctgaaatc G/C cagagacttttgcagcatca	477
HNK-1st	31	3'untranslated region 1696	gggtggtgtggtgtccaggg G/A tccatctttccagaatccat	478
HNK-1st	32	3'untranslated region 1829	aggggaggctttttctacct G/A agaaggggagtgtctttgag	479
HNK-1st	33	3'untranslated region 2211	tccagcagtgcggcttcctg G/T caacaaggtaggccctggtg	480

遺伝子名	No.	存在位置	配　　列	配列番号
HNK-1st	34	3'untranslated region 2212	ccegcagtgcggcttcctgg C/T aacaaggtaggccctggtgc	481
HNK-1st	35	3'flanking region 1016	cacacgaaggtgtgcactca C/T ggcctgcagggcacccaggt	482
HNK-1st	36	3'flanking region 1152	gcatgctttgctcatctgga A/C tctccagaagcagggaacag	483
HNK-1st	37	3'flanking region 1291	gccgagaccctcagcaggat A/G gtgcagttacagggctgagc	484
STE	1	5'flanking region -605	caggtttctaaaataataat C/T gaaaggtgagtgatgtttac	485
STE	2	5'flanking region -536	taaaattttcaggtctgctt A/G agagttaaaggcaaagagtt	486
STE	3	5'flanking region -231	ccttcttccccaaccccctga C/T ggcagacttgggaatttgaa	487
STE	4	5'untranslated region -64	tgcagcttaagatctgcctt G/A gtatttgaagagatataaac	488
STE	5	intron 1 69	aaatatagaatgaaaattat G/A tattacaaagctcttaaaaa	489
STE	6	intron 1 311	caatgagaaaaataaagcaag C/G agggtagaaggaggtagaat	490
STE	7	intron 1 655	tctaagaaagtagggactat G/A agaaccctatgtatctata	491
STE	8	intron 1 671	ctatgagaaccctatgtat C/T tatatcaaccatagtattct	492
STE	9	intron 1 772	aaaaggcaggttggaagatg C/A aggaggggagtatgcagaaa	493
STE	10	intron 1 1715	taaccatcttgcttaacctt A/G tcatttttagccaagtcatt	494
STE	11	intron 1 1928	aaatgataaatattcaggaa A/G tcaaaaatctctgacttaga	495
STE	12	intron 1 1953	aaatctctgacttagatacc C/T ggcaataataatcaaatgta	496
STE	13	intron 1 2087	aattttgaaagaaattgaag T/G tctgtggtttttatttatca	497
STE	14	intron 1 2323	taggtatgtaggagggtccc G/C ttatatacatagttgttaat	498
STE	15	intron 2 165	tctattccatgaccacaatt T/G ttacctgtaacttgaatagt	499
STE	16	intron 2 1707	cctaggacccaacatgagac A/G taatataccatcagtaaaat	500
STE	17	intron 3 850	ggtgtccattccctcaagaa T/G ttatacttttgtgttacacac	501
STE	18	intron 4 1653	agtaacaggctagtagataa T/C ataaataactgaggccaacg	502
STE	19	intron 4 1899	tacatgaacttagagaatca A/G gtagatcacacacaccaaca	503
STE	20	intron 4 1930	cacaccaacaataaaattac A/G cagaatgataaaagaatttg	504
STE	21	intron 5 666	ttctgatcatgtagtaacaa T/C tataaagaaaataataatgt	505
STE	22	intron 5 982	aggcaaagcagaacctttttg A/C ctcacacaacattatattat	506
STE	23	intron 7 369	agattttattcctctctctt T/C ttgagttgaagaaataagtt	507
STE	24	intron 7 447	caccttttcaagggtaagtgg C/A aaaaaatagaaattcaaata	508
STE	25	intron 7 672	aatcttgctctttgaaccat A/T ctgtcagtgagagtcaggga	509
STE	26	intron 7 856	tgttacagaggacttaaaac A/G gttgtcttgcttgcaaacgg	510
STE	27	3'flanking region 218	cagcctcccaagtagctagg A/G ctacagacatgtgcaaccat	511
ADH1	1	5'flanking region -55	atcatgtgtggaactggaat C/T gggtgttattcaagcaaaaa	512
ADH1	2	intron 1 268	acatttgcggtaaagcgata A/G tttattccaagctaatcatg	513
ADH1	3	intron 3 442	aaatggaggctacatggcta C/A ggctgaatgagcatgacctt	514
ADH1	4	intron 6 56	tacaacttggaggatgcatt T/G aggctgcagaatatatgttt	515
ADH1	5	intron 8 74	gtctagcagaaaatgaaaag G/A tggaaggatggagaaaatta	516
ADH2	1	intron 2 340	ctatttttttaaagcgtgcat T/C cttacataagacttaaatat	517
ADH2	2	intron 3 91	aaggcaatgagagacgaaag T/G gcttgcacaaggtcaccgcg	518
ADH2	3	intron 3 205	atgtattgtaccccttcaacc A/G ttatgtaccgagtatctact	519
ADH2	4	intron 7 108	acaattgacaaggcaagatt T/C tgaaaacaaatcaaaaataa	520
ADH3	1	5'flanking region -254	tgagagaagagaagcaggaa C/G ttgagagaggaggaagagag	521
ADH3	2	intron 2 355	tatgcattcttctatattat A/G caagacaaaaattttaggat	522
ADH3	3	intron 3 32	acactcagggaacatgcctt G/A gttcaccatcacaagattag	523
ADH3	4	intron 4 6	ctgcttgaaaaatgagtaag C/T ttctgatgctttctttgcac	524
ADH3	5	exon 5 453	agcaccttctcccagtacac A/G gtggtggatgagaatgcagt	525
ADH3	6	exon 6 815	ttcgtttgaagtcatcggtc A/G gcttgacaccatggtatgat	526
ADH6	1	intron 3 249	tgaaactggacttgaaagta C/A aaatgagacaaaaatttatg	527
ADH6	2	intron 6 1072	taacccctatactgtattgc A/G tcactttctaacaggcagct	528
ADH6	3	exon 7 885	gtctgtgtggttgttgggat G/A ttgcctgccagtgttcaact	529
ADH6	4	intron 7 1292	gttgagaaacactgcctagt C/A ccgtctgtggtcctagaatt	530
ADH6	5	intron 7 1616	ctatcacagaataatccgca T/C agaacactaagcagattccg	531
ADH7	1	5'flanking region -528	tgtgcagacacagaaagttt T/C acttaactttctacccctaa	532
ADH7	2	intorn 1 361	tcagtagcatgtgctgcaat C/T gctgcagtcgttcaatggga	533
ADH7	3	intron 3 183	aacctcaacctttagaaggc A/G aaccttacggtgtttataaa	534
ADH7	4	intron 4 76	tgaattgaattaattaatac G/A tgtatttgatgtatcaaaca	535
ADH7	5	intron 6 615	tggctagcgtaaagagact T/A ggaaaaatggaataaagcca	536
ADH7	6	intron 8 532	aagtctaaccatctcaccaa T/C ttagtatgccattgtactat	537
ADH7	7	intron 8 651	gctgctatttatttcaagta G/A gccacaaaatttccttattt	538
ADH7	8	intron 8 760	cattttagatgaagaccaa T/G gttgtgaaagcaaataaata	539
ADH7	9	intron 8 1207	tctccacatttggtctagcc T/C acaggatcatcatattatga	540

遺伝子名	No.	存在位置	配　　列	配列番号
ADH7	10	intron 8 1691	tccctcatctcattgcccac G/A ctcattgctttaattcagtc	541
ADH7	11	3'untranslated region 1364	atttacattttgtaaggcta T/C aattgtatcttttaagaaaa	542
ADH7	12	3'untranslated region 1498	gatatagtaaatgcatctcc T/C agaglaatattcacttaaca	543
ADH7	13	3'untranslated region 1584	aaacacttgttatgagttaa C/G ttggattacattttgaaatc	544
ADH7	14	3'untranslated region 1818	aatataaacatagagctaga A/G tcatattatcatacttatca	545
ADH7	15	3'flanking region 865	tacatcaaaagaaataaatc C/T aagaaggaataaacacattt	546
HEP27	1	5'flanking region -191	tcagcactctgtgtctagct A/T aaggtttgtaaatgcaccaa	547
HEP27	2	5'untranslated region -163	gaacccatcaattccgtaca C/A attttggtgactttgaagag	548
HEP27	3	intron 1 1941	aaatttaccctaaccagcct G/C actctctgccactttctgtt	549
HEP27	4	exon 3 289	ttgtgtgccacgtggggaag G/A ctgaggaccgggagcagctg	550
HEP27	5	intron 4 1070	tgtctcagttcacaggatca T/C gactcttttctcgaaactg	551
HEP27	6	3'flanking region 362	ggctttgtgtgtgctccatt A/G tctgaactgggcctgctggg	552
L1CAM	1	intron 1 + 767	tttgacttccttacatgggt G/A actgtgtgagtcactctgtt	553
L1CAM	2	intron 1 + 862	gcattgggtcatgtgtatgt G/C tgagtggggctgaatgtaag	554
L1CAM	3	intron 1 + 1332	cagggatgaaggagcagagc C/T gctgagaggccacacaggtg	555
L1CAM	4	intron 4 + 502	tttccctggggttttcccttt T/C gcattccatcctccctgagc	556
L1CAM	5	intron 18 + 147	agcgacgttatgaaattccc C/A acacttcacatttctataat	557
L1CAM	6	intron 24 + 221	ctccttagccccccagaggg C/T cccaactttaagagcatact	558
AANAT	1	5'flanking-542	aggggtgcaggatgggtgt G/T agctggagggcaggggtag	559
AANAT	2	5'flanking-263	cccccacataagaggtggg C/G ttgtccaagactccgaggga	560
AANAT	3	intron3 39	cgcccagctccagggaggcc T/A ctgaagacagaggtcagcca	561
AANAT	4	exon4 150	cagccggccgtgcgccgggc C/T gcgctcatgtgcgaggacgc	562
ARD1	1	intron1 + 317	ccgtcggtctgctcggcccc C/G ctccctcggggctgggcagg	563
ARD1	2	intron6 + 322	gctcctcagcatctgctcac G/A ccagggacccacacctctct	564
ARD1	3	intron6 + 1095	aaggctccatcctgagacaa A/C aagtccagtgtgacctgccc	565
ARD1	4	intron6 + 1179	aggaggaagacctgtatccc A/G gggacaccctcctccactcc	566
ARD1	5	intron7 + 159	cctccaggctgctaggcaga C/T ggcctcctctaaagcccagc	567
ARD1	6	intron7 + 295	tgaccagccctgccacccga G/T gagccttgggcagaaccctg	568
ARD1	7	intron7 + 416	actaccatggaggcccccac G/A acagagcgctgccccttgac	569
NAT1	1	3'UTR 215	aataataataataataataa A/T aaatgtattttaaagatggc	570
NAT2	1	exon2 867	cgtgcccaaacctggtgatg G/A atcccttactatttagaata	571
NAT2	2	3'flank 521	ccatccatactttgccacaa G/A agaaggaacatgagctttat	572
NAT2	3	3'flank 573	gatttgaaatcctgtggaca C/T ggggtgaattacttttaaaa	573
NAT2	4	3'flank 918	attttctgtttgtaaattcc A/G gtatcagggctatagtttaa	574
NAT2	5	3'flank 979	actattctccctcttcgact C/T gtgatgactataataatctt	575
NAT2	6	3'flank 1958	tacctattgaagtaagccta C/T gtcatatccacctatttgtt	576
NAT2	7	3'flank 2034	ccactgattcccagagctag T/G tcattaagaagacagtgcct	577
NAT2	8	3'flank 2201	cagattactggagggctact G/A tttgctcaccaatgcaaatg	578
NAT2	9	3'flank 2818	gggatatttgtctcctttct C/G cccagtgcatgttggaaacc	579
NAT2	10	3'flank 3237	atatatattccaattaaaaa A/Δ caaaataaatttccgaaact	580
NAT2	11	3'flank 3386	caacaaagagatttttaaa G/A ctttttaaaacaccagacag	581
NAT2	12	3'flank 3660	cagcactattcgcaatagca A/G agatgtggaatcaatctaaa	582
NAT2	13	3'flank 3973	agcagaaaaaataaataatg C/T gtactaggcttactacctgc	583
NAT2	14	3'flank 4029	caaaacaaacccccatgaca T/C gagtttatctatataacaaa	584
NAT2	15	3'flank 4118	ataagattaatatctgcata C/A aaatctttgtttacagcttg	585
NAT2	16	3'flank 4146	tgtttacagcttgttatata C/T tgaattatgtctgctcccc	586
NAT2	17	3'flank 4279	ttaatctgataggattggtg G/C ctttataagaaaaagaaaag	587
NAT2	18	3'flank 4323	ttgctctctccccagtgcag T/G taccaaggaaaggccatgtg	588
NAT2	19	3'flank 4446	tcaattggctttatctgcga T/C tctggaatcaggcaatactc	589
NAT2	20	3'flank 4462	gcgattctggaatcaggcaa T/C actccatttcataaaacaga	590
GZMA	1	5'-flanking -462	cctcagcttgcacttggcct A/G ctaattcttatataatccaa	591
GZMA	2	5'-flanking -172	agcctgcctgctggcagtga G/C ccatcatccaccattctcac	592
GZMA	3	intron1 1949	gacataaggttctctctatc A/T gcatgtatggtttgccttgt	593
GZMA	4	intron2 + 683	gactgcgtgaccaggtggaa C/T tagcctcagcatggaagggt	594
GZMA	5	intron2 + 1250	gttggtgtagtttatactag G/A ttatgaatgatagccttaat	595
GZMA	6	exon4 + 105	tgccaagttgcagggtgggg C/G aggactcacaatagtgcatc	596
GZMA	7	intron4 + 696	atagagccttacctgaagaa A/G ggtgtgcagtatgcatggtt	597
GZMA	8	intron4 + 1141	ctgttcagggaggatccogg G/A ttccaacatggttctttatt	598
GZMB	1	5'flanking + 529	gcctccgtctcacaccaaca A/G gcagatttccccaccacggc	599
GZMB	2	intron3 + 141	gagggaagattgtgcagccc C/T atcactgtgtcggggcccag	600

遺伝子名	No.	存在位置	配　　列	配列番号
GZMB	3	3'flanking + 448	ttttcagggcctgtccctcc G/A atgggggcaggcttctccca	601
ESD	1	5'-flanking -333	gtcttgggacagaggagttg G/A gggagttgaaattaggcccct	602
ESD	2	intron 1 603	gtcatttctgatgggggtcat C/T agggaaatgggattgagcgc	603
ESD	3	intron 1 717	tgtgtggtagaagcagcatt C/T taagcactacgtgaattaac	604
ESD	4	intron 1 1864	gctttcatgcaggattgatc G/C tagtgggatgtattaggaag	605
ESD	5	intron 1 2389	ttttgggaacacctgtctag G/A tgttaagagccagtggaata	606
ESD	6	intron 2 21	taaacttgttttattgttta T/C atgttactctgaacattgaa	607
ESD	7	intron 2 588	taaaattagtatctctctct G/A taagttcattatttaagata	608
ESD	8	intron 2 1498	tagaaaaatgtgtatcacac C/T gtaagtgttcagtaatgtta	609
ESD	9	intron 3 92	ctttatctagatattatagt C/A cctcattttacttttaaact	610
ESD	10	intron 3 422	gtaaagagattaaacacaca C/T gcacacatacatatacctat	611
ESD	11	intron 3 581	agaaaacctgagaaatgaca C/T aatttatttaaagccatagt	612
ESD	12	intron 3 2270	gccagtaattacatgtagcc G/A tttacatcaaattagctaat	613
ESD	13	intron 3 2951	taatgaaagtaaatgtttca A/G cttccctaacaaaagttgaa	614
ESD	14	intron 3 3001	aaatgtcagaaatttttttgt G/A ccgtcagtcatcaacaagaa	615
ESD	15	intron 3 3096	cagggagcatacagaaaactt G/C ccatgatgggggcctttgtgg	616
ESD	16	intron 4 2611	tctaatagtccccagtatta A/G tggtgcacatcttcatgtcc	617
ESD	17	intron 5 390	tctttttttcatctctgttaa C/T atcaaccatacagttaaaca	618
ESD	18	intron 7 107	ttagtattggaactaaactt T/C tctagtgttgagaactttgg	619
ESD	19	intron 8 1090	aaattctaactaattaaagg G/T ttcatcctttagtaactaga	620
ESD	20	intron 8 1651	tataaagttgtggttaatga A/G tatatatgaataagaatatt	621
ESD	21	intron 8 2047	agaaggaaaaaggccatttt G/C ttaagaatccctgagatatg	622
ESD	22	intron 9 -3490	atagaaggagaggctatact A/G cctccttaagtctcaggacc	623
ESD	23	intron 9 -2596	actaaggataaaaatatggc A/G tactcagtccattggaact	624
ESD	24	intron 9 -666	aggccttaatgacatatttc T/C cctcacataaagatacaaca	625
ESD	25	intron 9 -660	taatgacatatttcccctca A/C ataaagatacaacatgcttt	626
ESD	26	intron 10 799	tatggtaactgaagaaaatg A/G cattaagttcctaaagttat	627
DDOST	1	intron2 629	attctgttaagaagttctta T/C attaagaaatattgtctcct	628
DDOST	2	intron2 3125	gagaatataggagcttctgc G/A tatgcctgaaagtcagtcag	629
DDOST	3	intron2 3920	attactcatttaatgaataa A/G tggattactgagcactgtct	630
DDOST	4	intron3 189	actgctgtccagggtccat C/T tggggctgagcccagctgga	631
DDOST	5	intron6 185	ctgtcctcttgttcgggagg C/T gtggcagcttttcccttact	632
DDOST	6	exon8 37	aactatgaactagctgtggc C/T ctctcccgctgggtgttcaa	633
DDOST	7	intron9 37	tcctgcccaagaatgctgcc A/Δ aaaaacggccccaggcctca	634
MGST1	1	5'flanking - 5	tctggacoctgaacaggagg G/C gacatcgtgacaaagcaaat	635
MGST1	2	intron1A+330	atcagcaggcgatggttact C/G tgggcgggtaaatcaggtga	636
MGST1	3	intron1C+1428	gtaaagggaaagggcgttcc T/A caactgagaagtgaagattc	637
MGST1	4	repeat	attatttgctctacctcagg G/A tttttcgggtcaagcgagat	638
MGST1	5	intron1C+2914	ctcatcaggtgtgtgtcaga G/T ggcttggtgctggccagtct	639
MGST1	6	intron1C + 4274	attgtaatagattaacaaag G/T tgatgaaagtagtgtacata	640
MGST1	7	intron1C+4276	tgtaatagattaacaaagtt T/G atgaaagtagtgtacataat	641
MGST1	8	intron1C+4306	gtgtacataatgtacatagt A/G tagttgaacacatagcaagc	642
MGST1	9	intron1C+4406	gatggctatatgaccaataa T/A gatacatataaatgtataga	643
MGST1	10	intron1C+4464	agaaagattgcagctgatag A/G tgtcaggctaataaggacac	644
MGST1	11	intron1C+4683	aatggcagaggactggaaat G/T tacattttaagctttaccct	645
MGST1	12	intron1C+4767	gccttcctcttcagcacatt C/T ccaattatacttccaattcc	646
MGST1	13	repeat	atttcaatttttttttttgg G/A gggggagacagagtctcact	647
MGST1	14	repeat	aattacctcccaaaggcctc A/T tatcccagatactatcacat	648
MGST1	15	intron2+2379	ttctcaaatttcattatаca C/G tattcttcaacccaaagttt	649
MGST1	16	intron2+2767	tttaactatagatgccttct T/G ctcctcttgtgtttgattta	650
MGST1	17	repeat	tcactgcagcctcaacctct C/T gggctcaggtgatcctccaa	651
MGST1	18	repeat	aaaaaaatttgtagatatgg T/G tactccctatgttgcccagg	652
MGST1	19	repeat	ctccctatgttgcccaggct A/G atcttgaattcttgggctca	653
MGST1	20	intron3+1495	gtcagacaatggccttcagc G/A tcctctctttgcagaatatg	654
MGST1	21	intron3+2528	ttttggagacactttttcaga G/C agagcgtttccagcatcttc	655
MGST1	22	intron3+2567	tcccttccatttttaagtt A/Δ gacttttttttttcacctct	656
MGST1	23	intron3+2731	atacacatatggaacaatta A/C ctaaaaacttaaggtaatat	657
MGST1	24	intron3+3288	gggtttatagtgttccccccc C/Δ tccccgccccccaaaagaccc	658
MGST1	25	intron3+4288	ccattctatttgtcaactgc G/A taacacaggcgtgcaagtgg	659
MGST1	26	intron3+4378	aaatgtctgtcctttttggca T/C gttgtgaaggagaacactaa	660

遺伝子名	No.	存在位置	配　　列	配列番号
MGST1	27	intron3+4429	attggaggtgacgatatctc T/C gtgatgctgggggagaaatc	661
MGST1	28	intron3+4817	attgctatagaagagagtaa C/T gtaaagcagaaatagttttc	662
MGST1	29	intron3+6077	tttgaaattagtgtctttaa T/C agttatctttttccacagag	663
MGST1	30	exon4+304(3'UTR)	aagaattctgtacttccaat T/G tataatgaatactttcttag	664
MGST1	31	3'flanking+1581	totgtgtgoatgaacatgca C/T gogtgoaogcgcaocacacac	665
MGST1	32	3'flanking+1729	tatgtggagcaatttgaaaa A/T agtatattctaagccattaa	666
MGST1	33	3'flanking+3407	ggatcactgctaaagatccc G/A gagtcactccatgtcccagt	667
MGST1	34	intron1B+36	ggagaaggggaccgcatgca G/A agggtggcaggcagggaggg	668
MGST1	35	3'flanking+25	gggtaaacccatttgaata T/C tagcattgccaatatcctgt	669
MGST1	36	exon4+266(3'UTR)	aaagaaaatcatacaactca G/A catccagttggctttttaag	670
SULT1A2	1	intron 4 1728	tcagcttcctcctttgccaa A/Δ ccaagagatgagctggcctg	671
SULTX3	1	intron 1 6415	tgacctctccctgttagtgt G/Δ ggggcagctctttccagtgt	672
SULTX3	2	intron 5 2457	gccottaaagggaagttcat C/Δ cttctctgccttccaggctc	673
PIG3	1	5'untranslated region-93	tccgcgaggatacagcggcc (CCTGY)n cagacaatatgttagcogtg	674
ADH2	4	intron 7 + 108	acaattgacaaggcaagatt T/C tgaaaacaaatcaaaaataa	675
ADH2	5	intron 3 +(1721-1723)	actgcatagaaatttaagaa GAA/ Δ cttgttttattcctctccag	676
ADH2	6	3' untranslated +(2305-2306)	gttaatgctttcccactctc AG/Δ gggaaggatttgcattttga	677
ADH5	1	5' flanking - 115	taactgctgtaaagttacac G/A gggaagccctttcccgacaa	678
ADH5	2	5' flanking - 114	aactgctgtaaagttacacg G/A ggaagccctttcccgacaaa	679
ADH7	16	intron 8 + 727	ttcagatccctgtaagccag G/A tattatttttaccatttta	680
GSTM1	1	5' flanking - 694	tacgaagtggctaatttaca C/T agtacttagccagatgaccg	681
GSTM1	2	5' flanking - 661	gatgaccgaaggactcagta C/T ccgagggcccctaacagaaa	682
GSTM1	3	5' flanking - 658	gaccgaaggactcagtaccc G/A agggcccctaacagaaaaca	683
GSTM1	4	5' flanking - 656	ccgaaggactcagtacccga G/A ggcccctaacagaaaacaca	684
GSTM1	5	5' flanking - 537	tagaggggagactaagccct G/C ggagtagctttcggatcaga	685
GSTM1	6	5' flanking - 525	taagccctgggagtagcttt C/G ggatcagaggaagtcctgct	686
GSTM1	7	5' flanking - 465	aattaaattcccaggttggg G/A ccaccacttttagtctgac	687
GSTM1	8	5' flanking - 383	gcggagagaaggctgaggga C/T accgcgggcagggaggagaa	688
GSTM1	9	5' flanking - 382	cggagagaaggctgagggac A/T ccgcgggcagggaggagaag	689
GSTM1	10	5' flanking - 378	gagaaggctgagggacaccg C/T gggcagggaggagaagggag	690
GSTM1	11	5' flanking - 343	agggagaagagctttgctcc G/A ttaggatctggctggtgtct	691
GSTM1	12	intron 2 + 118	tgctggagctgcaggctgtc T/C cttcoctgagcoccggtgag	692
GSTM1	13	intron 3 + 233	agtgagtgcccggtctccto T/C otgctcttgcttatgggaag	693
GSTM1	14	intron 4 + 26	tgtgggtggctgcaatgtgt G/A gggggaaggtggcctcctcc	694
GSTM1	15	intron 5 + 140	actatcagcagttattctca C/T gactccaatgtcatgtcaac	695
GSTM1	16	intron 5 + 577	ctgccaccccattagaagga A/G ctttctactttccctgagct	696
GSTM1	17	intron 5 + 645	gctggtctggatccagaggc T/A gccaggtgcttgggcgctcc	697
GSTM1	18	exon 7 + 519	caccgtatatttgagcccaa G/C tgcttggacgcctccacaaa	698
GSTM1	19	exon 7 + 528	tttgagcccaagtgcttgga C/T gccttcccaaatctgaagga	699
GSTM1	20	intron 7 + 2421	cagcaccgtgtagaatcttc A/G taagtgttagctgttactgt	700
GSTM1	21	3' flanking + 42	atttgctcctggccatctac C/T cagactgtctgtctgtctgt	701
GSTM2	1	intron 1 + 7	ggaacatccgcggggtgagc C/G agggtccgctgggcggtggg	702
GSTM2	2	intron 1 + 45	gggacgggggtgcgtgggggg C/T ggggaagtgtgggagcagctg	703
GSTM2	3	intron 3 + 70	gactgcatctcctctcccca G/C cttagaggtgttaagatcag	704
GSTM2	4	intron 3 + 224	agcaggccctggtctcctct T/C tgcccttgcatatgggaagg	705
GSTM2	5	intron 5 + 100	ttgattccttctggtgagtt C/A ttggtcttgctgactctaag	706
GSTM2	6	intron 5 + 341	tcctcttggtgggttcatgg T/C ctggctggcttcaggagtga	707
GSTM2	7	intron 5 + 696	accttttagctagaacacagag C/T gctgatttgtgcatttaoaa	708
GSTM2	8	intron 5 + 723	ttgtgcatttacaatccttt A/G gctaggcagaaaagttctcc	709
GSTM2	9	3' untranslated + 1006	ctcagcccgagctgtcccc G/A tgttgcatgaaggagcagca	710
GSTM2	10	3' flanking + 139	ttctgctgggcatagtaagg C/T gcttgagaattcttgctccc	711
GSTM3	2	5' flanking - 144	ccaacgccggccattagtcgc G/T cctgcgcacggccctgtgga	712
GSTM3	3	intron 7 + 165	agcctaacttctatacottg A/G aggcactgtctacaaaaaaa	713
GSTM3	4	intron 7 + 257	ctgttggactgggtgggtc T/G ttataagattggtgtatttt	714
GSTM3	5	exon 8 + 91	cccagtgggcaaacaagcct A/G tatgctgagcaggaggcaga	715
GSTM4	1	intron 4 + 67	ttggctggattgggtgctc T/C gctcagagtgagtctgtgtt	716
GSTM4	2	intron 7 + 77	gatgctttcocagtcctgga T/G ctgcataaagaataacttgc	717
GSTM4	3	intron 7 + 80	gctttcccagtcctggatct G/A cataaagaataacttgcatt	718
GSTZ1	1	5' flanking - 546	agcagggcccaccagccgac C/A gcctcgaagcgccgtgagcc	719
GSTZ1	2	5' flanking - 321	tgtctgaccagccgccccgc T/C aaggagtcacaagagggcag	720

遺伝子名	No.	存在位置	配　　列	配列番号
GSTZ1	3	intron 1 + 2890	aaaatactgcatcaaaacca G/A gccacgctctgttgggggga	721
GSTZ1	4	intron 1 + 2896	ctgcatcaaaaccaggccac G/A ctctgttgggggacaccaa	722
GSTZ1	5	intron 2 + 255	tctcccaacactgctctcca A/G agcccctggcaaccatgtt	723
GSTZ1	6	intron 2 + 1560	caccactgtttaaggcctg G/C gggggcagagttaaacacaa	724
GSTZ1	7	exon 3 + 94	ccttgaaaggcatcgactac G/A agacggtgcccatcaatctc	725
GSTZ1	8	intron 4 + 297	agaaggaggagtttgctggc C/T ctgtcccctctggtccaggg	726
GSTZ1	9	intron 6 + 94	tatctgaaccagcctcccag G/A ctgctttgggcctgacagtt	727
GSTPi	1	intron 1 + 269	ctccccgggctccagcaaa C/G ttttctttgttcgctgcagt	728
GSTPi	2	intron 2 + 134	ccccgggcctccttcctgtt C/T cccgcctctcccgccatgcc	729
GSTPi	3	intron 5 + 438	gtgtgtgcgcgtgcgtgtgc G/A tgtgtgtgcgtgtgtgtgtg	730
GSTPi	4	intron 6 + 162	cccgctggctgagtccctag C/T cccctgccctgcagatctc	731
GSTT1	1	5' flanking − 103	taaagagtgtcccaggcgtc C/T gtgccgcccaatggggcaca	732
MGST1L1	1	5' flanking − 105	tgctgccgctgccgtgggcc G/A gggcgtgggcggtgctgcct	733
MGST1L1	2	intron 1 + 277	agtgtctgtgagagaagcag G/A ttctggagggtggagtgtgg	734
MGST1L1	3	intron 2 + 8030	ggggttatacagagcccctc C/G gccccccaccacacatatgca	735
MGST1L1	4	intron 2 + 8499	gtatggcaggagtggggtcc C/T ggcaagccatagaggtatgg	736
MGST1L1	5	3' untranslated + 468	cgccacctgtgaccagcagc T/G gatgcctccttggccaccag	737
MGST2	1	5' flanking − 46	ggtcagcattcaaagtcaag A/T agcgccatttatcttcccgt	738
MGST2	2	intron 1 + 176	ggtcacccatgccgcctgct A/C ccctccttcccaggggcaag	739
MGST2	3	intron 1 + 204	tcccaggggcaagcagagac T/C gagaacattccagagattag	740
MGST2	4	intron 1 + 373	ttacaagtgttccaaaggaa A/T cgtgcctgcttctaaacctg	741
MGST2	5	intron 2 − 3245	cctcgtgatttgcccacctc G/A gcctcccaaagtgctgggat	742
MGST2	6	intron 2 − 1998	aggccgaggtgggcggatca T/C gaggtcaggagatcgagacc	743
MGST2	7	intron 2 − 1640	tgtttattccttgcatagcc A/G taatataaagtatgaatttt	744
MGST2	8	intron 3 + 41	actgtgttctaatgatgact A/G tgatgcttaaacgattaagg	745
MGST2	9	intron 3 + 453	atcagagtgctatgttgcag A/G tatatgaactttggcttcat	746
MGST3	1	5' flanking − 520	acaaaaaggccctaacagcg A/C taaatccattcacttcggga	747
MGST3	2	5' flanking − 355	cgcctaaaaccgctacggtg G/A ctctgctggggacaaattat	748
MGST3	3	5' flanking − 234	ctgggggagtagatatatgt T/A tttgagaatgagaggagtaa	749
MGST3	4	intron 1 + 74	agcctttgcgcaggcactcc C/T atatttcagcctatgcgagc	750
MGST3	5	intron 1 + 682	agaaaatgcccttctttat G/C tggggtggcagcacggagcc	751
MGST3	6	intron 1 + 832	cgagtttacaagctacataa T/C agcgtcgggggcaagtaagt	752
MGST3	7	intron 1 + 1919	aataaaattcctgagtttct G/C tcactcgctcttacagtacc	753
MGST3	8	intron 1 + 1991	tgtaattaggcaacaggaaa A/G ttgtactatctttcaaatgc	754
MGST3	9	intron 1 + 4458	tcttccatcctcctaacata T/C agttagcttccactctccaa	755
MGST3	10	intron 1 + 4676	tgaatatgcaatgcaattgt C/G gggggatagttacttttcat	756
MGST3	11	intron 3 + 278	cagcatgacccatctaaacc G/C atgttgactctcccaggcct	757
MGST3	12	intron 4 + 423	cttgccttttttgttgtgggg T/G gtgggtggtcacagagaag	758
MGST3	13	intron 4 + 506	gtgcagagaagaaaacaaag T/C ggggaaggtggaaaggggat	759
MGST3	14	intron 4 − 162	tcacagatattttatttcc C/T gactgaaactaacttaattc	760
MGST3	15	intron 4 − 130	acttaattctacctaatttg C/G gtggggagtagttggccaaa	761
MGST3	16	intron 4 − 105	ggagtagttggccaaatcat C/G aaattgttaacttttgcta	762
MGST3	17	intron 4 − 65	aacatattgtgtaatcaacc C/T taggtgttaaaaaaggtttg	763
MGST3	18	intron 5 + 105	atcccagcactttgggaggc G/C aaggcaggcagattgcttga	764
MGST3	19	intron 5 + 197	aaaaaatacaaaaattagcc G/A gatgtggtggtgcacacctg	765
MGST3	20	intron 5 + 222	tggtggtgcacacctgtagt C/T ccagctacttgggaggctga	766
MGST3	21	intron 5 + 374	tcttatgctactatattttt T/C ttcttgggaatttgagaaaa	767
MGST3	22	3' untranslated + 517	atgacttacctttatttcca G/T ttacatttttttctaaata	768
MGST3	23	3' flanking + 166	agtctgattgtggtgatgta G/T gtatagtcatgccacagtga	769
GSTA1	1	5' flanking − 266	ttgcaaaaagagcaaaatct C/A ggtgaaatgtattgtgtaaa	770
GSTA1	2	intron 2 + 1220	gagacacaggctttcctaag A/C tatgacaacaccataactag	771
GSTA1	3	intron 4 + 1813	aaaggcacccactggaggtg A/C attattttgccatcacctga	772
GSTA1	4	intron 5 + 732	gaagagtgttgtcatgaagg T/C ggagtcactgcccaagggag	773
GSTA1	5	intron 6 + 333	ttatcccatatgtgcccaca A/G tgagccggtctgagcagagc	774
GSTA1	6	3' flanking + 412	ctttcttatgcatttgcaaa A/C caatgattctgtctgctgtg	775
GSTA4	1	intron 1 + 280	gcattggtggaaggtgggct C/T ggatcgtccccgggcctggc	776
GSTA4	2	intron 3 + 176	ggeaatcacttcttattcaa T/C agttccataaaagctggccg	777
GSTA4	3	intron 4 + 94	acaccacatttacttttatgt C/G ttacatagttagtgagatca	778
GSTA4	4	intron 5 + 1062	cacacttgtgcacatgcaga C/T acccatgggcatccaagagt	779
GSTA4	5	exon 6 + 487	cagatgtgattttactccaa A/G ccattttagctctagaagag	780

遺伝子名	No.	存在位置	配　　列	配列番号
GSTA4	6	intron 6 + 595	tgagctctgagagcaaatga G/A agatgttagcaccctaaaca	781
GSTA4	7	intron 6 + 630	taaacatcaccccaaaggat T/A cctaccattctccttctgag	782
GSTA4	8	intron 6 + 3943	tcttcgtagtatctaatacc T/C tttttgttagccttaaagtt	783
GSTA4	9	3' untranslated + 1099	taataacaaccgaatgtcta G/A taaatgactctcctctgagc	784
GSTA4	10	intron 5 +(370-371)	gttgtcgaacagctgtctca (TA) gctgacatcctccctgataa	785
GSTA4	10	intron 5 +(370-371)	gttgtcgaacagctgtctca gctgacatcctccctgataa	786
NDUFA1	1	5' flanking - 1437	agggctaaaaatcctgatta T/A acctaccttgaagcttttaa	787
NDUFA1	2	intron 2 + 3071	aataaaagtacatggcatat C/A tttgatgggaacagacttgt	788
NDUFA1	3	3' flanking + 1218	aactccatgtgtataaagca A/G caccacagatgacacttcca	789
NDUFA1	4	3' flanking + 1411	ggattgtgccatcccttgat C/T/G ggcaatgacctttttacttttt	790
NDUFA1	5	3' flanking + 1411	ggattgtgccatcccttgat C/T/G ggcaatgacctttttacttttt	791
NDUFA2	1	intron 2 + 1087	aacatacaaaaattagccgg A/G tatggtggcgggcacctgta	792
NDUFA2	2	intron 2 + 1089	catacaaaaattagccggat A/G tggtggcgggcacctgtaat	793
NDUFA2	3	intron 2 + 1356	ttccctgaaacaacccattg T/C ggccatccagaatcagccaa	794
NDUFA2	4	3' flanking + 467	cacagcctcatgggtcagcc C/T actccagagggtgcattccc	795
NDUFA2	5	3' flanking + 744	ggaagcaggggcccctggcca C/T agccgctggcagtaagcagg	796
NDUFA2	6	3' flanking + (844-845)	tatagtctacaaagaatgaa (ACAC) aaagatcataacaatagcta	797
NDUFA2	6	3' flanking +(844-845)	tatagtctacaaagaatgaa aaagatcataacaatagcta	798
NDUFA3	1	intron 2 + 2656	tccctgctgcccctcccctgc G/A cactttatcttccctttgcc	799
NDUFA3	2	exon 4 + 241	agggccccagcctggagtgg C/G tgaagaaactgtgagcacct	800
NDUFA3	3	3' flanking + 1019	tccttacctgcactggcacc A/G gctctggagccccagtccct	801
NDUFA5	1	intron 3 + 2155	agactctagcatggtacctg G/C aacataaggttccttagaaa	802
NDUFA5	2	intron 3 + 2493	ggcatattgctagttttctc G/T gtctcaatttcatcatctat	803
NDUFA5	3	intron 3 + 2712	acaaattttgaactgttcac C/T taacacaggctttttctgaa	804
NDUFA5	4	3' flanking + 1296	aggtatctaaaaggtattgc A/C atttggtcattggttctttc	805
NDUFA5	5	intron 3 +(30-31)	aagtcagttttgttgtcttg (GATTTGTGGTATCCAG) tgtaa catttaaccaaaaaa	806
NDUFA5	5	intron 3 +(30-31)	aagtcagttttgttgtcttg tgtaa catttaaccaaaaaa	807
NDUFA5	6	intron 3 +(427-428)	attaagtagcagttaataaa AG/△ tctagactgctgattcatac	808
NDUFA5	7	intron 3 +(4733-4734)	tataggaatttttaaaatata TA/△ ggatattgaaacattcagtt	809
NDUFA6	1	5' flanking - 1148	tttataatttatatatgtta C/T gtgctttcttttgtatagct	810
NDUFA6	2	5' flanking - 363	actaccaaggagcgcggcgg G/A cagccggatagcaggacgct	811
NDUFA6	3	exon 1 + 26	ggggagcggcgtccgccaag C/T tacttctaccgccagcacct	812
NDUFA6	4	intron 1 + 1318	attcagcagtttgaaaacat A/G atgtttgcctggcagaatac	813
NDUFA6	5	intron 2 + 562	agttaaagaatctgaaaagt G/C tcagaaatgatttaccctga	814
NDUFA6	6	5' flanking - (861-862)	ctgtaaaatggggatgctga (T) ggtacctacctgacctatga	815
NDUFA6	6	5' flanking - (861-862)	ctgtaaaatggggatgctga ggtacctacctgacctatga	816
NDUFA7	1	5' flanking - 731	accaaccaaaggtctatcaa A/G ggggtgtcctctttgcaccc	817
NDUFA7	2	5' flanking - 434	aaagggaaccatcagaaccc C/T gtgatgaaatgagaatcggc	818
NDUFA7	3	5' flanking - 395	gctcccggattccggctggc A/G ggggttagggcagggtagag	819
NDUFA7	4	5' flanking - 100	agaggagtcacgtgcttcgg G/A gagagcctttataggacgtt	820
NDUFA7	5	intron 1 + 92	tcacctcctcctaagccgg G/A accettcgctctccccgaat	821
NDUFA7	6	intron 1 + 133	ctcccgggaaccccagct A/C gtcacccttcagcccggga	822
NDUFA7	7	intron 1 + 136	cctgggaacccccagctagt C/G acccctcagcccgggaccc	823
NDUFA7	8	intron 2 + 89	tcctttagacccctgaaacg G/C agggctgacatcctgccacc	824
NDUFA7	9	exon 3 + 196	gccgccgggaatctgtgccc C/G? cttccatcatcatgtcgtcg	825
NDUFA7	10	intron 3 + 4203	gcctccacccctggggcgcc T/G cctccatcaccccaccctcc	826
NDUFA7	11	intron 3 + 4604	gggccttgtgtacgctggag A/G ccaaaagtgggaagggagga	827
NDUFA7	12	5' flanking - (1360-1353)	agggtccagggtcccctgct (CAGAGGCT) aacactggccg aagagaaag	828
NDUFA7	12	5' flanking - (1360-1353)	agggtccagggtcccctgct aacactggccgaagagaaag	829
NDUFA7	13	5' flanking - (1240-1239)	tgatagagccctgatccacc CA/△ ctctctgaaacttctttgct	830
NDUFA7	14	intron 2 +(4142-4143)	cattttgtgactgaggtgac AG/△ gggcccacagcggggccatg	831
NDUFA8	1	intron 1 - 75	tttgtgttctctattctgac C/T cgcatgaggtaaagctgaga	832
NDUFA8	2	intron 2 + 790	caaacctagacaaagtgtgc C/T ctttatccagaagtgagcag	833
NDUFA8	3	intron 2 + 900	ttcaggagataaaaagctct G/A attgctcaggcctgagatgg	834
NDUFA8	4	intron 2 + 3837	gaagttgtcttgtaagtgag A/G taagaatatgtactcacata	835
NDUFA8	5	intron 2 + 3942	tcattgttttgcaaagagat G/T cccctaacccagctttcttt	836
NDUFA8	6	intron 3 - 66	gaggagacaccaggaggcgc A/G ttgatggttacagattcctc	837

遺伝子名	No.	存在位置	配　　列	配列番号
NDUFA8	7	3' untranslated + 520	tttatttctggaccaagtaa A/G gatgggtccgtggcccacac	838
NDUFA8	8	3' flanking + 367	gtcatacaagggagcctcc A/G ggatagaagtgcagaaactt	839
NDUFA8	9	3' flanking + 777	attctttttttcactactagg C/T tgtttcctccacatctgact	840
NDUFA8	10	3' flanking + 1053	aaagaaaaagcactgtgtga T/A ctgccatggccgcttctgca	841
NDUFA8	11	3' flanking + 1190	gattctctaatgaaaaataa G/T actttttttgcatttttt	842
NDUFA8	12	intron 2 +(449-453)	ggtcattgtgcatgatacttaa (GTAAA) aaaaaactaagctgtgtaat	843
NDUFA8	12	intron 2 +(449-453)	ggtcattgtgcatgatacttaa aaaaaactaagctgtgtaat	844
NDUFA8	13	intron 2 +(707-708)	ctcattttggaaagactctc (A) accttgctgtaccaaaaatg	845
NDUFA8	13	intron 2 +(707-708)	ctcattttggaaagactctc accttgctgtaccaaaaatg	846
NDUFAB1	1	intron 1 + 8451	cagcacccctgtagaggcctc G/A ggatgctgaagatgccatga	847
NDUFAB1	2	intron 1 + 8495	gacacaggcattctgcagac G/A ctagacaattttagtggcag	848
NDUFA9	1	5' flanking - 807	gatggctctttgtagaacaa T/G gcagattctcaaaggtgacc	849
NDUFA9	2	5' flanking - 769	accacagttaaagaaaaagt T/C acaagccattgcgctagaga	850
NDUFA9	3	5' flanking - 353	cacaccctattttggtttct C/G ttctccactttccccctcgt	851
NDUFA9	4	5' flanking - 322	ttcccctcgttcttgtcccc C/T cttttctctctcctgggccc	852
NDUFA9	5	intron 1 + 447	attcatatgagcacaatgga A/G atgataatattacaatacca	853
NDUFA9	6	intron 1 + 1039	ggcttgatgttcagcctgag G/A caagaattaggagtgtttag	854
NDUFA9	7	intron 1 + 4010	aatgtatccaaaagagattc T/G cattcctgccatatgaagaa	855
NDUFA9	8	intron 3 + 49	gacaaatataaattactaag G/A tcatttttaggagtgatagg	856
NDUFA9	9	intron 3 + 107	aatttcttcccagaatggac C/T aaaggcatcctctgttccca	857
NDUFA9	10	intron 3 + 1183	atctctggtaatattcatac A/G gattattgtaatcccttta	858
NDUFA9	11	intron 3 + 1395	attcctagttctttgtccct C/T aagtttgttggtcaccttgt	859
NDUFA9	12	intron 3 + 2363	agaaaatagtcatgaatggc C/T ccaactaacactagtcttta	860
NDUFA9	13	intron 3 + 2608	gtcatttgattacctgagta A/C agtgtactgttaactgtttg	861
NDUFA9	14	intron 4 + 561	attttataaattctttgatg A/C cttgggggtcttattcaact	862
NDUFA9	15	intron 4 + 860	attgtgtagagtaatgacag C/T agagctgtcaactttttaa	863
NDUFA9	16	intron 4 + 879	gcagagctgtcaacttttt A/T aaaaaataattttagcttaa	864
NDUFA9	17	intron 4 + 893	ttttttaaaaaaataatttt A/G gcttaaaaaaattaaaaatt	865
NDUFA9	18	intron 4 + 1090	atcattgctgtttaaaagtt T/C aagtagtgtgaatttcagta	866
NDUFA9	19	intron 4 + 1188	aaccaatccttttattttttt A/T tcttccagaaactttgattt	867
NDUFA9	20	intron 5 + 161	gggtgtgtgtgatgttttga C/T gttttgattgattgccttct	868
NDUFA9	21	intron 5 + 373	ctttctcaccccttgcactg C/T agtggttttgtgccactctt	869
NDUFA9	22	intron 5 + 457	gccagggaagatgcctattc A/C cacagtgcttatgctccttt	870
NDUFA9	23	intron 5 + 3113	gatttttctccttcttcaat G/A taagcttcccttaaaataaa	871
NDUFA9	24	intron 5 + 3339	tctaaactcaaaacaggttt G/A tttggttattgtttaggctg	872
NDUFA9	25	intron 6 + 414	tatagttttgccttttccag G/C atattacatatatggttaga	873
NDUFA9	26	intron 6 + 518	ctttcatttcttttcatagc T/C tgatagctcatttctttata	874
NDUFA9	27	intron 7 + 974	ggattatgcgtacttggaaa A/G tacttggatagcggtgatta	875
NDUFA9	28	intron 8 + 368	acattaatttttgatggagta T/G cacaatgcctccagaggctg	876
NDUFA9	29	intron 8 + 954	gcatgcaatcagttatatag T/C ctagataagaattacaattc	877
NDUFA9	30	intron 8 + 1253	tcctcttgaaattgtagata G/T gtatctacacatttctcatc	878
NDUFA9	31	intron 8 + 11608	gaaaagatagatgtataaat G/A accaaaaattcgtgaagaaa	879
NDUFA9	32	intron 8 + 11930	ctacaaatatattctaaatg C/T gtaatcatggataagtacaa	880
NDUFA9	33	intron 9 + 1998	tgtttttcaagcctttaaac G/A gctgtggaaccctgtgctca	881
NDUFA9	34	intron 9 + 2238	ccagctacttgggaggctga A/G gtgggaggatcacttgagcc	882
NDUFA9	35	intron 9 + 2885	acagcggtctgtcttcctgc A/G gttctcataggctagcttac	883
NDUFA9	36	intron 10 + 801	tacactaaagtgtctcttac G/A tttatacttgagaaagtgtt	884
NDUFA9	37	intron 10 + 910	tgcagactttcaggtgggta G/C gatgagggattgctgctgct	885
NDUFA9	38	intron 10 + 1180	aaaactgagtcagaacgccc G/A tgctcagaaaacaggggcgt	886
NDUFA9	39	3' flanking + 554	gtgccagcacttaggaatta T/G gaccttctaatgaagttctt	887
NDUFA9	40	5' flanking - (1129-1128)	taaacagtaggggcaagata (TC) gagtggaaacagccaagatt	888
NDUFA9	40	5' flanking - (1129-1128)	taaacagtaggggcaagata gagtggaaacagccaagatt	889
NDUFA9	41	5' flanking - 341	tggtttctcttctccacttt T/Δ cccctcgttcttgtcccccc	890
NDUFS1	1	5' flanking - 3	tcctaggggtcgtcgtggt C/G cagacagtttagcagaacag	891
NDUFS1	2	intron 1 + 445	gtgttagcaatggctcacgc T/C tctgtttgttgtccttgttt	892
NDUFS1	3	intron 1 + 470	tttgttgtccttgtttgttt G/T gtccattgaccacgttggac	893
NDUFS1	4	intron 1 + 502	acgttggacagcatttttttt A/G ttcctttaactaacgggaaa	894
NDUFS1	5	intron 1 + 557	ttttgaaaagttagcccagg A/G ttgcattgcaaataacaaaa	895
NDUFS1	6	intron 1 + 5218	tatctcagaatatctcagga A/G catttagtagacagctatgc	896
NDUFS1	7	intron 3 + 1371	aagccctaaaatagatagtg T/G caatgggaatgaaaacaaga	897

遺伝子名	No.	存在位置	配　　列	配列番号
NDUFS1	8	intron 5 + 414	ttttgaaacgaggtctcact A/G tgttgtccaggctgggcttg	898
NDUFS1	9	intron 10 + 812	gagtgcggtggcgcgatctc G/A atctcgggtcactgcagcct	899
NDUFS1	10	intron 11 + 233	ggaggccaaggcaggcagat C/T gcctaagtgcaggagtttga	900
NDUFS1	11	intron 11 + 283	ggccaacatggcgaaacccc G/A tctctactaaaaatacaaaa	901
NDUFS1	12	intron 11 + 585	ctgtatgtcttaattttaaa G/T taaatttgcattttatatat	902
NDUFS1	13	exon 12 + 1251	gcaccactgtttaatgctag A/G attcgaaagaggttggtaat	903
NDUFS1	14	intron 13 + 5159	attacttttagaaaacgtgt T/C ttagctgatactcaggcata	904
NDUFS1	15	intron 14 + 250	aaaaattgttatattagtta C/T accttggttcaaaaattgca	905
NDUFS1	16	intron 14 + 550	gataaagtctcactatgttg C/T ccaggttgatctcaaactcc	906
NDUFS1	17	intron 14 + 2429	ctgaaaatacaaaaattagc C/T gggtgtggtggcatgtgcct	907
NDUFS1	18	intron 14 + 2530	ttacagtgagccgagatcac G/T ccactgcgctccagcctggg	908
NDUFS1	19	intron 14 + 2659	acacatttaatttttacat T/C gaaaatactgcagttatggt	909
NDUFS1	20	intron 16 + 150	agaaaacatgtattcagaaa C/T aggaattcaaggttacagtg	910
NDUFS1	21	intron 18 + 279	cactgtgtagcaatttatgg T/C gaattttccaaagtggcaaa	911
NDUFS1	22	3' flanking + 182	tctaggataattataattaa T/A aataatcatagtaacaatgg	912
NDUFS1	23	intron 11 + 3226	aaatgtattgtctgtgcttt T/△ aacattttgtaatagtaaat	913
NDUFS3	1	5' flanking - 194	tctgccacaaggagctagga C/T cacgctcacctcacgatttc	914
NDUFS3	2	intron 1 + 46	cggggtcaggcgcagcggcg T/C gcccagtgcagagagctcct	915
NDUFS3	3	intron 6 - 439	aaagctgtgtcaaatgtact G/A ctttagatctggactgtgaa	916
NDUFS3	4	intron 6 - 280	ggtgggtgagcagtcagttc G/A gagctcctgatgtgggagtg	917
NDUFS4	1	5' flanking - 439	aactgaatacagccctgtcc T/A gagggcttgcaaagtgaatc	918
NDUFS4	2	intron 1 + 1829	gaaaaaaaatcttaatgcca G/T ggaagacgtttttaaatac	919
NDUFS4	3	intron 1 + 2057	attaatgggaaaatctaaat C/G taaaattcattttattgtaa	920
NDUFS4	4	intron 1 - 521	ttcattttaactaatttttt T/G tctcccattttgtgaatggg	921
NDUFS4	5	intron 3 - 1259	ataaaattatgatattatta G/A tactaatatagcaagccata	922
NDUFS4	6	intron 3 - 1174	aatatatataattataggaa T/C ctcagagtagcaaccatggt	923
NDUFS4	7	intron 4 + 10682	cacaatataggcacaaactt A/C ctaccaaagcaactaacaagt	924
NDUFS4	8	intron 4 + 12299	tttactatatagatatatgg A/T atagactatagagtatctct	925
NDUFS4	9	intron 4 + 12560	accaaataaggtattatgca G/A gctcatctttttatataaga	926
NDUFS4	10	intron 4 + 18801	ggaaagaattgctttgccag T/C gtatccgaaacctctgttat	927
NDUFS4	11	intron 4 + 19888	tcgcacagctgagaagagca A/G ggggctggttttcagtaccc	928
NDUFS4	12	intron 4 + 20178	agaaaagatgagtataattc G/A tctaacttacccattcttaa	929
NDUFS4	13	intron 4 + 23016	ctactctgtgaaagtaaggt T/A atgttgaacaagtaaattaa	930
NDUFS4	14	intron 4 + 23124	actttctttggagatggagt T/A ccagcagttgggaatgtaat	931
NDUFS4	15	intron 1 + 766	tgtgatgatttttttttttt T/△ ggctgtattaaccttccatt	932
NDUFS4	16	intron 1 + 1261	tttctttctctttttttttt T/△ gagatacattctcactctga	933
NDUFS5	1	intron 1 + 388	ccaaacatagccagcacttc C/T ggctgtaactccgggctgtt	934
NDUFS5	2	intron 1 - 13082	agtgagccgagattgcacca G/A tgcattccagcctggcaac	935
NDUFS5	3	intron 1 - 12905	gttttcaacaaaggactcca G/T agtagtgagagaagtttctgt	936
NDUFS5	4	intron 1 - 12564	attttcatcacacctcaact T/G aaggtataacagccttaaga	937
NDUFS5	5	intron 1 - 12561	ttcatcacacctcaacttaa G/A gtataacagccttaagaatg	938
NDUFS5	6	intron 1 - 10561	aacaatgtggtatagtgggg C/G gggtggtgagcaggtgtcat	939
NDUFS5	7	intron 1 - 9065	cctgatgctcctggctccag G/A gtagacctttccctttaga	940
NDUFS5	8	intron 1 - 8871	tcaccacgtgtctgtagata T/C aggaccgcagaccttcgctt	941
NDUFS5	9	intron 1 - 7312	aaatccttggcttctagaat G/T ggtcactgatggtatataat	942
NDUFS5	10	intron 1 - 6827	aacctctgcctcccccgattc A/G cgccattctcctgcctcagc	943
NDUFS5	11	intron 1 - 6725	agtagagacggggtttcacc G/A tgttagccagcatggtctcg	944
NDUFS5	12	intron 1 - 6631	aggcgtgagccactgcgccc G/A gcctagaccttcttcttata	945
NDUFS5	13	intron 1 - 6531	cccaacagctcccaatgtaa A/G acagatctattaatattctg	946
NDUFS5	14	intron 1 - 6346	gcaacagatcttgacctata T/C cccatagggtacagctgagg	947
NDUFS5	15	intron 1 - 6327	atcccatagggtacagctga G/C gactttaatcagaaaaggag	948
NDUFS5	16	intron 1 - 6122	tagccttgcttttactctac T/C gttcctcccaaatcacaccc	949
NDUFS5	17	intron 1 - 2512	acaaactcttaatgcgaatt T/C tgcagatcaaagtgggctta	950
NDUFS5	18	intron 1 - 1945	tttaatctccttaaatttc G/A caatttcacaacctagggta	951
NDUFS5	19	intron 2 + 75	ttttttttttttttgagac G/A aagtctcactcttgtcccct	952
NDUFS5	20	intron 2 + 148	ctgtagcctctgcctcccag G/A ttcaggcgattcgcgtacct	953
NDUFS5	21	3' flanking + 150	cagattcaagtggttctcct G/C cctcagcctcccaagtagct	954
NDUFS5	22	intron 1 - (10682-10681)	attataaacactaaacaaac AT/△ gtgtggtctctttagagggg	955
NDUFS5	23	intron 1 - 10272	aggaacaagtgactaccctg A/△ aaaaagaagagatgaaacaa	956
NDUFS5	24	intron 1 - 2069	accagacagagttcccttta C/△ ttgttttcctgtggcaaaga	957

遺伝子名	No.	存在位置	配　　列	配列番号
NDUFS6	1	intron 1 + 26	ggccgctgggtacaggatgc A/C ccttcctccagccgcccctc	958
NDUFS6	2	intron 2 + 1076	ggatcatggtggtggagagg G/A gcttgtgtctggtgggtttg	959
NDUFS6	3	intron 2 + 1260	cagttgtcgagtaagtggtg T/C atagggtaagtgctctttct	960
NDUFS6	4	intron 2 + 1413	caaaggagctcatggcattg C/T gaatgggacatttcttccgt	961
NDUFS6	5	intron 2 + 1568	tggagaaggggaggtttctc T/C tagtgtggatgcggtatggt	962
NDUFS6	6	intron 2 + 1692	gaccgtggtgacggaggttt C/T ctgggcatcgatgggtggtt	963
NDUFS6	7	intron 2 + 6488	tagcttaaataattattggc A/G ttcatgttcagaatgcctga	964
NDUFS6	8	intron 2 + 6563	tttaaacttttattttaaat G/A tccatgaatggggtcggtat	965
NDUFS6	9	intron 2 + 6740	aaagatttaaacctacatat C/T tttatgcccaatcatttgat	966
NDUFS6	10	intron 2 + 6832	gcgagggactcatttttacag A/T ggttggacacttcactgtgt	967
NDUFS6	11	intron 2 + 7054	ttcactgccggagcttggcc G/A tgtgaacccggagccgggct	968
NDUFS6	12	intron 2 + 7186	ggtcagggtcacccttgagc T/C gcgcacactaaatgacggga	969
NDUFS6	13	intron 2 + 7225	gagggcatcccgcgtcagtc G/A ccagtgtcgaggcgtcagca	970
NDUFS6	14	intron 2 + 7810	cttccactctggggcgggga C/T gctgtagaaggagcacaaag	971
NDUFS6	15	intron 2 + 11080	gtaactgttcagtgctttct C/T ctttggatttcatgtaaatc	972
NDUFS6	16	intron 2 + 11657	gggacagaacgatgtggtgg G/A gagaagaggcgtggcagag	973
NDUFS6	17	intron 3 + 208	cgaaaaccccctttcaactg T/C gaagtggtgggcggcatgtt	974
NDUFS6	18	intron 3 + 1031	ctagagtgggactgggcacc C/T ggcatgtcccctcctgggct	975
NDUFS6	19	3' flanking + 270	gcttcagagagccaaggtgg G/C tcttgaggtgcatagtgaag	976
NDUFS8	1	5' untranslated − 45	agtgtagcctccgcctcccg A/C ttgactggcctgcttggcaa	977
NDUFS8	2	intron 1 + 163	aggtgcagcggggagccggc T/C ctcagggcgcatgcgccgcc	978
NDUFS8	3	intron 3 + 123	tctctgagcctgtttccact T/C ttaaaatgattatggtgatg	979
NDUFS8	4	intron 6 − 505	aggcaaggcaggccgggcac G/A gtggctcacgcttgtaatcc	980
NDUFS8	5	3' flanking + 491	ggcoctgagctggcctgcgt C/A cagccacatcctctttcctg	981
NDUFS8	6	3' flanking + 693	ttcacttcatttgcagtgag G/A aaaccagctccgagaggtga	982
NDUFS8	7	3' flanking + 1267	ttttcccgacgtaaccgcc G/A tcagagcgtggcatggagcc	983
NDUFS8	8	3' flanking + 1362	cgctgggttctttcccttac C/T gtggtctcccaggcacttac	984
NDUFS8	9	3' flanking + 1449	tgtcagaacaggcctatggc G/A cccaaccacaagtcccccaa	985
NDUFS8	10	3' flanking + 1572	cagccccacaggcctgtgct C/A gctgtgtggggcttagggat	986
NDUFS8	11	3' flanking +(783-784)	cagagaccttgacccccccc (C) atctaccatcatttccaaaa	987
NDUFS8	11	3' flanking +(783-784)	cagagaccttgacccccccc　　atctaccatcatttccaaaa	988
NDUFB3	1	5' flanking − 1439	ttaaaagttgacttttttct G/A ccgggcacggtggctcacgc	989
NDUFB3	2	5' flanking − 1436	aaagttgacttttttctgcc G/A ggcacggtggctcacgcctg	990
NDUFB5	1	5' flanking − 213	ggcggatgaaactctcctac A/C aagaagggccaaaccggccg	991
NDUFB5	2	intron 1 + 6288	ggggatgttgattacctagg T/C cagtaaagtaaagaaggcat	992
NDUFB5	3	intron 1 − 1581	cttctgggccactgtatcct A/G tttcttccctgttaccct	993
NDUFB5	4	intron 1 − 1487	ccctcttagacgtatatag T/G tctagcataggatctgcaca	994
NDUFB5	5	intron 2 + 556	ttgtctggaccatctgccac G/A gtagataaagctctgaatca	995
NDUFB5	6	intron 3 + 467	ggcgccatcgcactccagcc C/T gggcaacagagtgagactct	996
NDUFB5	7	intron 3 + 497	agtgagactctgtcccccccc C/G caaaaaaaaactataatcct	997
NDUFB5	8	exon 5 + 397	atgatagtcctgaaaagata T/C atgaaagaacaatggccgtc	998
NDUFB5	9	intrion 1 +(231-215)	attgcatttctaaaacgtt GTT/△ attcaccatcccaattaatg	999
NDUFB7	1	intron 1 + 68	cctgaacacctggcacccca G/A ggctggcaccccagggctgg	1000
NDUFB7	2	intron 2 + 266	gggctctctaggggcctgtt T/C gatgggacagggcaggtgg	1001
ABCA1	1	5' flanking − 278	gggcccgggcggggaaggg G/C acgcagaccgcggaccctaa	1002
ABCA1	2	5' flanking − 99	acataaacagaggccgggaa G/C ggggcggggaggagggagag	1003
ABCA1	3	intron 1 + 159	gcggtgttaaatggggagac G/T atgtcctagtacgagctctg	1004
ABCA1	4	intron 1 + 506	gaattggctatatgctcccc G/C ggactggagcggcacagtcc	1005
ABCA1	5	intron 1 + 5897	gtacaaaaccctttagcttt T/G gcaaacctcctttaagaccc	1006
ABCA1	6	intron 1 + 5929	ttaagacccgatttaaatgc C/T tcctcctcatgaagctctt	1007
ABCA1	7	intron 1 + 5962	aagctcttctggatccactc T/C ttcccatcactaagttgaaa	1008
ABCA1	8	intron 1 + 5985	cccatcactaagttgaaagt A/C agatcccctctctttactt	1009
ABCA1	9	intron 1 + 11416	ttacagtgccctttatagga G/A agaaagaagaaattgtgtct	1010
ABCA1	10	intron 1 + 11935	tctctgtggagcaaatagag G/A gctgtctgacacttggttcc	1011
ABCA1	11	intron 1 + 12281	gaatgtttgatttgtgaaaa T/A cttaataacagtagtttttt	1012
ABCA1	12	intron 1 + 12924	gtgctgacaatcttatactc T/C aggttgaacctccggggaag	1013
ABCA1	13	intron 1 + 13002	gagcctcaatcacagattct C/G tctagctcacatgaagttaa	1014
ABCA1	14	intron 1 + 17715	ggagcatgactttgtggaag C/T ctctcctcttccacccagag	1015
ABCA1	15	intron 1 + 17848	gagggctgactgtcaccctt T/C gataggagcccagcactaaa	1016
ABCA1	16	intron 1 + 21384	gtgggtgggaggaattggag G/C aggaagcttgcctaagtgtg	1017

遺伝子名	No.	存在位置	配　　列	配列番号
ABCA1	17	intron 1 + 22145	gtagcttctaaatcaacgaa C/G tgattcctggagagcagctt	1018
ABCA1	18	intron 1 + 23063	ggaggcaactgtgacaccca G/A cggagtagggggggcggtgtg	1019
ABCA1	19	intron 1 + 23131	agtgtgcatatgtgctgacc G/A tgggagcttgtttgtcggtt	1020
ABCA1	20	intron 2 + 156	ggacacaggactgtgtggtc T/C ggatatggcatgtggcttat	1021
ABCA1	21	intron 2 + 384	gctgtgggtgaagtgagtta A/G tggccccactcttagagatc	1022
ABCA1	22	intron 2 + 1081	agtgcagccaaaattgcaaa G/A tcataccattcaaattaata	1023
ABCA1	23	intron 2 + 2801	aagaaaagtgatttatttca A/G gttgctgatgcttagattgt	1024
ABCA1	24	intron 2 + 2830	tgcttagattgttagagttg C/G aaagatctggcttgcatctt	1025
ABCA1	25	intron 2 + 2856	tctggcttgcatcttgtaca A/G ctgacagaactggggctcag	1026
ABCA1	26	intron 2 + 3187	tgatagctgttgcctgcagc A/G tacggacgttcattgcgcag	1027
ABCA1	27	intron 2 + 3190	tagctgttgcctgcagcata C/T ggacgttcattgcgcagttc	1028
ABCA1	28	intron 2 + 3194	tgttgcctgcagcatacgga C/T gttcattgcgcagttcctgt	1029
ABCA1	29	intron 2 + 3204	agcatacggacgttcattgc G/A cagttcctgtctcctgagat	1030
ABCA1	30	intron 2 + 3401	acataaagcctgtgtgctgc T/C gccaggaagactagaaacgc	1031
ABCA1	31	intron 2 + 13927	gtcaccacatacctggcact A/G tgctaaggctgggaatgcag	1032
ABCA1	32	intron 3 + 4163	ccagcccacttcatcttacc G/A tagttacctccttagagtat	1033
ABCA1	33	intron 3 + 4262	tgtcaaagaggaactaagga T/C gccagggactttctgcttag	1034
ABCA1	34	intron 3 + 4306	ccctctcatcacttctccaa C/T gctggtatcatgaaccccat	1035
ABCA1	35	intron 5 + 240	gacagaagaaaagtccccag G/A gaagaatactacagacttgg	1036
ABCA1	36	intron 5 + 490	gatgggcatttgaacttgtt G/A tctttaaaaagtgaaatctt	1037
ABCA1	37	intron 5 + 583	tatctggggagtgggcattt T/G ctgactgaggcattggctgc	1038
ABCA1	38	intron 5 + 1051	ggctacaaaactgtgctttc C/T ttgggcagtaaaagaggcaa	1039
ABCA1	39	intron 5 + 3051	tagagaacaagtctaattct G/A ttttccttgaaatagtcgaa	1040
ABCA1	40	intron 5 + 3127	aagtccatgatttttttaggc A/G aaatggcctcctttcctctt	1041
ABCA1	41	intron 5 + 5924	ctttctttcacaaaattgcc C/T cccagagctttctggaaggg	1042
ABCA1	42	intron 5 + 6831	ccagtccctcagccttgcca T/C tgcttatgctggtctggaaa	1043
ABCA1	43	intron 5 + 12678	gctcaccgctctgctcaccc G/C accctctggccatctcctct	1044
ABCA1	44	intron 5 + 14214	cagcttggtcccagaggcct G/A gacctgggtcccagaggtcc	1045
ABCA1	45	intron 5 + 14257	gctggttccccggcttggtc C/T cagaggcctggatgtgtggc	1046
ABCA1	46	intron 5 + 18078	cctaccacacccatgcacgtg C/T acagccaagggttgttgact	1047
ABCA1	47	intron 5 + 18795	ctgggctcttcctggacctg G/A ccagctaaaaggaaatctcc	1048
ABCA1	48	intron 5 + 18948	gcattggtggtactaagaac G/A catattccctatcctatagg	1049
ABCA1	49	intron 5 + 19063	ctcccccaacattaaaagtg T/C aagggatgcttattcaaatg	1050
ABCA1	50	intron 5 + 19148	ggcccaagaaactgcatttt C/A gcatgctccctaaatgaagc	1051
ABCA1	51	intron 5 + 19229	atgctaacagtgtagagtca C/T atgtgatgggaagcatcagg	1052
ABCA1	52	intron 5 + 19405	cttgctcaatttattctgtc T/C atataactcaatattactga	1053
ABCA1	53	intron 5 + 19534	catgtgaccctcttagctcc G/A cggattaactcctgtcctca	1054
ABCA1	54	exon 6 + 474	gaaaccttctctgggttcct G/A tatcacaacctctctctccc	1055
ABCA1	55	intron 6 + 210	gcaacctggcgtcatgggcc A/C gctggttaaaataaaattga	1056
ABCA1	56	intron 6 + 334	acagttctgaggcaataacc G/A tggttaagggttattgatct	1057
ABCA1	57	intron 6 + 2288	cttctttcaaagcttgtggt C/T cactggaccacgtatgaagt	1058
ABCA1	58	intron 6 + 2322	atgaagtggaatagtttagg T/C ccagaaaggcaattaagtaa	1059
ABCA1	59	intron 6 + 2820	gtgctttgatacattctgag T/G ttcagtaaagagacctgatg	1060
ABCA1	60	exon 7 + 656	tgagctttgtggcctaccaa G/A ggagaaactggctgcagcag	1061
ABCA1	61	intron 7 + 416	catcataaagatgacattgt G/A ggctgtcacagttggaaggc	1062
ABCA1	62	intron 7 + 471	agaccacactatttagctta C/T ttagtaataacattgcaaag	1063
ABCA1	63	intron 7 + 504	ttgcaaagaaaaattccgac G/A aagtttttcagcctaggaa	1064
ABCA1	64	intron 7 + 679	gctctggtgaaattcctctc G/C ctaccccaaacatcatcatt	1065
ABCA1	65	intron 7 + 1740	acaaatgctcacccttcag C/T tggaatgattgaaattttgg	1066
ABCA1	66	intron 7 + 2122	tgattaaggtggctactacc A/G ggtgctttctgcatatctcg	1067
ABCA1	67	intron 7 + 7753	taggaattccaagctgtgaa T/C tttttactgaagctctttgg	1068
ABCA1	68	intron 7 + 8973	atggaaatttgtttatattg A/T ctacagattgccaatattat	1069
ABCA1	69	intron 7 + 8976	gaaatttgtttatattgact A/G cagattgccaatattattag	1070
ABCA1	70	intron 7 + 11327	ctaacaatcttatttccatt G/C agtccttataaaagaagtgg	1071
ABCA1	71	intron 7 + 11738	ctgacgtttaagggagacgg C/T gtaggtccctttgaggactg	1072
ABCA1	72	intron 7 + 12295	agtctgtaaattattgttct T/A ttttttctttagcttatgct	1073
ABCA1	73	intron 8 + 387	tagcaaggccaatcatttta C/G caacacacatgcttgctaac	1074
ABCA1	74	intron 8 + 697	ggaactgtctggtgtcccccc A/T gcataggaagctgagccagg	1075
ABCA1	75	intron 8 + 1312	attgctctgcagatcccctc G/A cagccctctgtcccttgttc	1076
ABCA1	76	intron 8 + 3036	ctttatgtgggaagaaattt T/G ttttttgattgggagtgg	1077

遺伝子名	No.	存在位置	配　　列	配列番号
ABCA1	77	intron 8 + 3176	aaatggcctggttototgtc C/A cctttctgtctgtatgcctc	1078
ABCA1	78	intron 8 + 3364	ggcagaaggcaaagcttagg A/T cctagagagtgctggaccac	1079
ABCA1	79	intron 8 + 3373	caaagcttaggacctagaga G/A tgctggaccacgccactcac	1080
ABCA1	80	intron 8 + 3561	cagggatttattaatgattt C/A ttgtgaaatgtttggaaata	1081
ABCA1	81	intron 8 + 3654	agtgcoggaatacatttgca T/C gteagacagaacgctgcctg	1082
ABCA1	82	intron 8 + 4715	ggcagaggggtctcagaatc C/T gcatttccaacaatgtctcc	1083
ABCA1	83	exon 9 + 936	cgtattgtctgcgggcatcc C/T gagggaggggggctgaagat	1084
ABCA1	84	intron 9 + 2309	cccctcaagagtcagtttaa A/G tgttggtcatgttagttgtc	1085
ABCA1	85	intron 9 + 2392	atgggagggcttgtgcttca T/C gaaaacatttttccagatca	1086
ABCA1	86	intron 10 + 228	tggggatggggaggactggc A/G cagggctgctgtgatggggt	1087
ABCA1	87	intron 10 + 319	ttctgcggtccctggctccc C/T acctgactccaggtgaacaa	1088
ABCA1	88	intron 11 + 377	gaaagaagtgtgggagcaaa A/C gcatgatgttacatgtagac	1089
ABCA1	89	intron 11 + 521	agtgctctagagacaattgg G/A ttcaaatgtggagcaggctg	1090
ABCA1	90	intron 11 + 2850	ctctatacaatcattatgct G/C ccattgaaataataaataca	1091
ABCA1	91	intron 11 + 2976	ctccaattcggtagaaccag A/G gcttcatcttctctgtcgaa	1092
ABCA1	92	intron 11 + 3056	gtttgcagctgctgtttttc C/T ggcagcacatctgtgcaggc	1093
ABCA1	93	intron 12 + 340	ggcattatttgtgaaactta T/C ctaaaatcgaattcgggtcc	1094
ABCA1	94	intron 12 + 381	aattaaatttttgaaatttt A/G tattaaaaattatattagta	1095
ABCA1	95	intron 14 + 1728	caggctcagaggccttggcc C/T atcaccctggctcacgtgtg	1096
ABCA1	96	exon 15 + 2040	atgggcctggcaacagcat C/A ctctggtttagctggttcat	1097
ABCA1	97	intron 15 + 1382	cttttagacagaaaagttac G/A tgggatattatctcccacag	1098
ABCA1	98	intron 15 + 1453	tatataaggagaaaccagtt G/A aaattacctattgaagaaac	1099
ABCA1	99	intron 15 + 1567	ttctgcgtagttttgggtaa G/A tcacttatcttctttaggat	1100
ABCA1	100	intron 15 + 1617	cagttgcctcatcagaaaga T/A gaacagcattacgcctctgc	1101
ABCA1	101	intron 16 + 95	agttgagaacagaagatgat T/A gtcttttcoaatgggacatg	1102
ABCA1	102	intron 16 + 452	tggtgttttgcttgagtaat G/A ttttctgaactaagcacaac	1103
ABCA1	103	intron 16 + 657	ctgttgcctcagtctgggct T/C cataggcatcagcagcccca	1104
ABCA1	104	exon 17 + 2473	gcttcaatctcaccacttcg G/A tctccatgatgctgtttgac	1105
ABCA1	105	exon 18 + 2649	ggttccaaccagaagagaat A/G tcagaaagtaagtgctgttg	1106
ABCA1	106	intron 18 + 1730	tgaaagttcaagcgcagtgc C/G ctgtgtccttcacctccact	1107
ABCA1	107	intron 19 + 428	aggaccttacagtgggtagt A/G tcaggaggggtcaggggctg	1108
ABCA1	108	intron 19 + 468	aaagcaccagcgttagccto A/G gtggcttccagcacgattcc	1109
ABCA1	109	intron 20 + 876	ccctcctcatctaaagtgaa C/T acatggggctcatgtgcagg	1110
ABCA1	110	intron 22 + 118	catgggatactcttctgtta T/G cacagaagagataaagggca	1111
ABCA1	111	intron 22 + 560	aaagctttgccattctaggg G/A tcatagccatcacagggtgaa	1112
ABCA1	112	intron 23 + 102	accccctttgccatgttgaa A/G ccaccatctccctgctctgt	1113
ABCA1	113	intron 23 + 287	gtcaaagaaaagagacttgt C/T aagaggtaagagccttggct	1114
ABCA1	114	intron 23 + 1063	accttcaccctcaggaagc G/A aggctgttcacacggcacac	1115
ABCA1	115	intron 25 + 321	otctttacttaagtacagtg T/G gaggaacagcggcatcagga	1116
ABCA1	116	intron 25 + 376	gttagaaattcagcaacttg G/C gcccagctcagacctactga	1117
ABCA1	117	intron 25 + 478	catacataggaaatgacaaa C/T gtttatggatggatagtcta	1118
ABCA1	118	intron 25 + 579	tcatttaattctcaaaaaaa G/T atgaaaaaatgaacactcag	1119
ABCA1	119	intron 27 + 153	aatggtaaaagccacttgtt C/T tttgcagcatcgtgcatgtg	1120
ABCA1	120	intron 28 + 1058	actatcatgggagataatga C/T tatggttgtccatgattgga	1121
ABCA1	121	intron 28 + 1317	caggacccagtgttctgagt C/T accctgaatgtgagcactat	1122
ABCA1	122	intron 30 + 372	tatatgatttttaggttttg T/C ttatcagcttcttcgctttt	1123
ABCA1	123	intron 30 + 506	ccttttaaaaagtaagcagt A/G gataaataaattcagtgaag	1124
ABCA1	124	intron 30 + 1033	ctggatttcatggtgccttt G/C attttccacatgaaggttgt	1125
ABCA1	125	exon 31 + 4281	tcttcccttgcagagacac G/A ccctgccaggcaggggagga	1126
ABCA1	126	intron 33 + 626	ggctccttgttactgatttc C/T gtcttttctctctgccttttt	1127
ABCA1	127	intron 33 + 719	taatagccctcatgctagaa G/A ggagccggagcctgtgtata	1128
ABCA1	128	intron 33 + 726	cctcatgctagaagggagcc G/A gagcctgtgtataaggccag	1129
ABCA1	129	intron 33 + 889	cttcctcaatgtctcagct A/G tctaactgtgtgtgtaatca	1130
ABCA1	130	intron 33 + 1097	ctgtgcacccactgtctgg G/C ttttaatgtcaggctgttct	1131
ABCA1	131	exon 35 + 4760	tatgacaggactggacacca G/A aaataatgtcaaggtaaacc	1132
ABCA1	132	intron 35 + 234	aacctatctaaacctcagtt T/C cctcatctgtgaaatggaga	1133
ABCA1	133	intron 37 + 411	aactctgtacatttttatcag C/T agcttatccatccattgcaa	1134
ABCA1	134	intron 37 + 1224	caggcataggtgattcagag A/G tgaaaggtcaagtcoctgaa	1135
ABCA1	135	intron 37 + 1720	aaattaaaattactctgact G/T ggaatccatcgttcagtaag	1136
ABCA1	136	intron 40 + 251	tgaaggtaaggaaaatagtg T/G tatttgcttggatocactgg	1137

遺伝子名	No.	存在位置	配　　列	配列番号
ABCA1	137	intron 40 + 252	gaeggtaaggaaaatagtgt T/C atttgcttggatccactggc	1138
ABCA1	138	intron40 + 319	agcactggaaaagtcaaacc A/G taactttgagaattaggtga	1139
ABCA1	139	intron 40 + 957	cttgttactcttttttcctt G/C tcatgggtgatagccatttg	1140
ABCA1	140	intron 41 + 146	tgatgtgggcatcccgcagc C/T ccctccctgcccatcctgga	1141
ABCA1	141	intron 42 + 239	cattggttttatatgcttac A/C tttatgtgttagttattaaa	1142
ABCA1	142	intron 42 + 321	aataaatggttgattttgag T/A ttgagtttcatagtccaaaa	1143
ABCA1	143	intron 42 + 322	ataaatggttgattttgagt T/C tgagtttcatagtccaaaaa	1144
ABCA1	144	intron 42 + 533	agatgaaaaattatgtagat G/A ataatgaatgatacggttct	1145
ABCA1	145	intron 42 + 546	tgtagatgataatgaatgat A/G oggttctaaaaagccaggtt	1146
ABCA1	146	intron 43 + 739	tacagccacacttaaaatgg T/A cccattatgaaatacatatt	1147
ABCA1	147	intron 44 + 18	taggtgagaaaagaagtggc T/C tgtattttgctgcaaagact	1148
ABCA1	148	intron 44 + 264	acaatataatttgcttgttt T/C ttaagagtataatttagtga	1149
ABCA1	149	intron 44 + 279	tgttttttaagagtataatt T/C agtgatttttggtaaattga	1150
ABCA1	150	intron 44 + 508	tttacattgctacataaaat C/T ccccatatgtacatgtaccta	1151
ABCA1	151	intron 44 + 1477	gatctcctctcctgtctctt A/T catttttgcagtagcaatgt	1152
ABCA1	152	intron 44 + 1665	tggttgtaagaactgatttg G/A ttggtatagctgtgagggcc	1153
ABCA1	153	intron 44 + 1956	gtgttgctcacactcaaaat T/G tctgggccttctcatttggt	1154
ABCA1	154	intron 45 + 68	aatatatacottatggcttt T/C ccacacgcattgacttcagg	1155
ABCA1	155	intron 46 + 608	ttatactgacttcaatagag G/C tttcagacaaaaagttgttt	1156
ABCA1	156	intron 47 + 336	ttcacaattgtaaacaccac T/C acactgaacagcatcatccc	1157
ABCA1	157	intron 49 + 55	agggtgtggattcctgcccc G/C acactcccgcccataggtcc	1158
ABCA1	158	3' UTR(exon 50)+7949	aacaaaaatgtgggtgtctc C/T aggcacgggaaacttggttc	1159
ABCA1	159	3' UTR(exon 50)+8226	aggagcccactgtaacaata C/T tgggcagccttttttttttt	1160
ABCA1	160	3' UTR(exon 50)+8682	aacttcttccacttttcca G/A aatttgaatattaacgctaa	1161
ABCA1	161	3' UTR(exon 50)+8697	ttccagaatttgaatattaa C/T gctaaaggtgtaagacttca	1162
ABCA1	162	3' UTR(exon 50)+9097	aactattttgaagaaaacac A/G acattttaatacagattgaa	1163
ABCA1	163	5' flanking - (1033-1032)	tgacttaaatatttagacat (AT) ggtgtgtaggcctgcattcc	1164
ABCA1	163	5' flanking - (1033-1032)	tgacttaaatatttagacat ggtgtgtaggcctgcattcc	1165
ABCA1	164	intron 5 + 6368	ttctgatggggttgttgctg C/Δ tgagaatcatgactgggtgg	1166
ABCA1	165	intron 5 + 9709	cattttctgtctgaaccccc T/Δ cacccattcaggcagctgct	1167
ABCA1	166	intron 5 + 13816	tccctacttctcctttttt T/Δ catttgcctcctccacccac	1168
ABCA1	167	intron 10 +(270-271)	cttttcagggaggagccaaa (G) cgctcattgtctgtgcttct	1169
ABCA1	167	intron 10 +(270-271)	cttttcagggaggagccaaa cgctcattgtctgtgcttct	1170
ABCA1	168	intron 20 +(611-612)	tttagcccatcctctcccccc (C) gccacoctccttattgaggc	1171
ABCA1	168	intron 20 +(611-612)	tttagcccatcctctcccccc gccacoctccttattgaggc	1172
ABCA1	169	intron 32 +(391-392)	gagtgccttgggtactctct (T) gatgggggactcoatgataa	1173
ABCA1	169	intron 32 +(391-392)	gagtgccttgggtactctct gatgggggactcoatgataa	1174
ABCA1	170	intron 37 + 847	gctgtatattgtgaatgtcc C/Δ gttttcaaaagcaaagccaa	1175
COMT	1	5'flanking - 1287	cgtatgatattccccattct G/A agtccagaatacctagaaat	1176
COMT	2	5'flanking - 1217	tgtgagtatgggaagggaa G/A cttttctgtctgttgtcccc	1177
COMT	3	5'flanking - 503	caggggctccaggaggacga G/A tgtgtatcctcccattgcto	1178
COMT	4	5'flanking - 425	gagaagttgggaagtctggc C/T agtggggccggtgcctggtg	1179
COMT	5	5'flanking - 277	cccagcccccagtttoccoac C/T tggaaggggggctacttgtg	1180
COMT	6	intron1 + 12058	ctggcccatggaagggaggg G/A aggggcccccgacgggcca	1181
COMT	7	intron1 + 12070	agggaggggaggggcccccg A/G cgggccacagtaaaggagt	1182
COMT	8	intron1 + 18831	tgtgtatgttcttggtaaac C/T agcccttggtcttacacatc	1183
COMT	9	intron2 + 832	cctctcctttggccacccgt G/C actaccccaactccgggcc	1184
COMT	10	intron3 + 90	ggagaagctgttatcacccc A/G tttccaggggggctgggaacc	1185
COMT	11	intron3 + 425	ccccaaggtgggcggttcgg T/G gattcagagagggcagctct	1186
COMT	12	intron3 + 671	ggctcctgctctttgggaga G/A gtgggggccgtgcctgggg	1187
COMT	13	intron3 + 676	ctgctctttgggagaggtgg G/T gggccgtgcctggggatcca	1188
COMT	14	intron5 + 75	tcagcctcagcctctccaaa G/C agccaggcattccagtagag	1189
COMT	15	intron5 + 310	accagacaccagggcagaaa C/T ggcacaggaccaaggagatg	1190
COMT	16	intron5 + 346	agatggggtggggaagggcc G/A ctctgggcccagcctgctct	1191
COMT	17	intron5 + 3023	aaggcagccgccotgctcaa G/A gcctaggccattgtcctcct	1192
HNMT	1	5'flanking - 211	cagaggcagotgacagtctt C/T cgttaaagatttcoctgctg	1193
HNMT	2	intron1 + 5409	aatataactgatataattgg A/G acatttcatgttggcctagt	1194
HNMT	3	intron2 + 2561	cacttgtgcttggacaagaa A/G agaaggcctacaagaaaaag	1195
HNMT	4	intron2 + 2895	caatcagaaatgtaagaaaa A/G ctccaagaaaaatttaagtt	1196
HNMT	5	intron2 + 3977	accaaacttggaagtgtaaa G/A ttatgcatgtatgttcatgt	1197

遺伝子名	No.	存在位置	配　　列	配列番号
HNMT	6	intron2 + 5296	ttaacatagtgagttggag T/C cccaggattttattttcctt	1198
HNMT	7	intron2 + 13317	caacctcatgaattcttag C/T tgggatgggtccctataaca	1199
HNMT	8	intron2 + 14682	gtagatgagcaaatgagttc A/Δ ggagagatttaaatacccta	1200
HNMT	9	intron2 + 15406	gtctatgcattcatgcatcc G/A tctaaccagctgtctaccta	1201
HNMT	10	intron2 + 28943	atgtgacttaaacttcaggt A/G tatcaatatcccttgaatgt	1202
HNMT	11	intron4 + 49	cagaaagaagacttttcaga A/G tatatatataatgaatatct	1203
HNMT	12	intron4 + (1942-1943)	tttgagaaaaatttaaggta (A) tcttctatggcccacttcca	1204
HNMT	12	intron4 + (1942-1943)	tttgagaaaaatttaaggta　　tcttctatggcccacttcca	1205
HNMT	13	intron4 + 2405	ccctgtgaccaagcagataa G/A ctcatgctttatttagtcca	1206
HNMT	14	intron5 + (80-81)	cctgtgtttgaaagaagctt (TT) atatattttgtcttcattat	1207
HNMT	14	intron5 + (80-81)	cctgtgtttgaaagaagctt　　atatattttgtcttcattat	1208
HNMT	15	intron5 + 235	ctttcttttagggaaaatatg T/C ctttgtcttctatatatgaa	1209
HNMT	16	intron5 + (702-703)	tacttacaggttgattttag (AT) acacagcagactctgtcttc	1210
HNMT	16	intron5 + (702-703)	tacttacaggttgattttag　　acacagcagactctgtcttc	1211
HNMT	17	intron5 + 749	ttacaccagaccccatactt T/G aacaccatatgtcacaaaat	1212
HNMT	18	intron5 + 1101	gtaggcagcctattcttgat T/G atattcatcaatcatacaga	1213
HNMT	19	intron5 + 1137	acagaaaaagtattgtagac G/A gaaataacaattcattgcga	1214
HNMT	20	intron5 + 1348	aagggagcatgaatagtcca C/G aagtaactgagaactgatta	1215
HNMT	21	intron5 + 1673	caaaagaaagggagtaaaga C/G tcaacaatcagttagctttt	1216
HNMT	22	intron5 + 2022	attttatttggggctttcta C/T gtctctctctcctaagccta	1217
HNMT	23	intron5 + 2285	tgtcatacttaactcttaaa G/C atccagagtaaatgatggag	1218
HNMT	24	intron5+4159	taccagttgacccagcaacc C/T tcttatagagtagtttaaat	1219
HNMT	25	intron5 + 4501	aatgatccacaaaattccta C/G tcattgttttctttcaatga	1220
HNMT	26	intron5 + 5251	cacacacacacacacacaca C/G caaatggaagcagccagaca	1221
HNMT	27	intron5 + 5802	gaaaaagaaaatctggctta C/T atcatgttgaaaacaaaagt	1222
HNMT	28	intron5 + 6189	tccaattccaccttctccta G/C agcatatcctgcagttacct	1223
HNMT	29	intron5 + 6297	gtcttggttcatctcttgag T/A taaattagatctgggaactt	1224
HNMT	30	3'flanking + 458	tatgtcactctcaagaactc C/T tataagaccaagagtcatct	1225
HNMT	31	3'flanking + 993	ctgaaaatgaacactgaacc G/A ttaatcatactgatatgtac	1226
HNMT	32	3'flanking + 1793	gtggagcacagcattttagg G/A cttgatatttgcttattata	1227
GAMT	3	intron5 + 1411	ggtgacctggtgccatcccc G/A acccaggagcgcaggtgccc	1228
PNMT	2	intron1 + 35	ctgaggcacgagggacaaga G/T gtcgtcggggagtgaaagca	1229
CYP1A1	1	intron 1+1590	ccactcttcaaaaggaggta C/T atgtgacagcagctggaaat	1230
CYP1A1	2	exon2+160	gaatccaccagggccatggg G/A ctggcctctgattgggcaca	1231
CYP1A2	1	5'flanking-731	gcctgggctaggtgtagggg T/G cctgagttccgggctttgct	1232
CYP1A2	2	intron1+371	cttcccctgtgttcacactaa C/T cttttccttctttgaaattg	1233
CYP1A2	3	intron3+44	atagccaggagaagccttga G/A acccaggttgtttgttcagt	1234
CYP1A2	4	intron5+81	tccctgctaggaactgttta T/C ataatgaaggaggggacct	1235
CYP1A2	5	exon6+181	ctggccatcctgctacagca A/T ctggagttcagcgtgccgcc	1236
CYP1A2	6	exon6+295	cggctgcgcttctccatcaa C/T tgaagaagacaccaccattc	1237
CYP1B1	1	5'flanking-3669	tgtatcctgtgaagcatcac G/A gttatccttctctgcacatg	1238
CYP1B1	2	5'flanking-3149	tgacagcacttaccaaccta G/C ttcctctgatttttgagtca	1239
CYP1B1	3	5'flanking-1222	gggggaagccaccccccgccc G/A agcgcctccggcttcccttc	1240
CYP1B1	4	5'flanking-376	ttccgggaagcaagctcaag T/C cgcggagagggaagggaggt	1241
CYP1B1	5	5'flanking-265	ctgggacaccgtgcggcct C/T gattggaggtggctgtgatg	1242
CYP1B1	6	intron1+129	tgcccgcagcgttgtcccca G/A attgcaggaaccgttacgcg	1243
CYP1B1	7	intron1+379	tgagtgtcacgccttctcct C/T tctgtccccagcatgggcac	1244
CYP1B1	8	exon3+(799-800)	agcttctgggagatttttt (T) gagtcaaagacttaaagggc	1245
CYP1B1	8	exon3+(799-800)	agcttctgggagatttttt　　gagtcaaagacttaaagggc	1246
CYP1B1	9	exon3+1284	agtatagtggggttccatga G/T ttatcatgaatttttaaagta	1247
CYP1B1	10	3'flanking+2226	tttctttttctttttttttt T/Δ aaaatttattcctatttcct	1248
CYP1B1	11	3'flanking+(2226-2227)	ttctttttctttttttttt (T) aaaatttattcctatttcct	1249
CYP1B1	11	3'flanking+(2226-2227)	ttctttttctttttttttt　　aaaatttattcctatttcct	1250
CYP1B1	12	3'flanking+2230	ttttttctttttttttttaaa A/Δ tttattcctatttccttaca	1251
PEMT	90	intron1 + (297-299)	attgtgtgagactcagaggt TGT/Δ ccgtgttagtctttgggatt	1252
PEMT	91	intron1 + 817	tcatgaagcctgtaaggcac A/G tctctgccccaagcagcttc	1253
PEMT	92	intron1 + 830	aaggcacatctctgccccaa G/A cagcttctaatccagttctt	1254
PEMT	93	intron1 + 1035	gagttctctgaaggagctaa T/C accagttagtgttttgaaga	1255
PEMT	94	intron1 + 1573	agtgggcaggggagactaac C/T gggtgtgtgaggggtgggct	1256
PEMT	95	intron1 + 1759	gatttttcttaaagaaagaa A/G gaaagaaacatccaaoatac	1257

遺伝子名	No.	存在位置	配　　列	配列番号
PEMT	96	intron1 + 2768	gcatcttgctgtccacaggc C/A ggggcacctccaggattcag	1258
PEMT	97	intron1 + 2785	ggccggggcacctccaggat T/C cagaagatgactccagtagg	1259
PEMT	98	intron2 + 4598	ccgtgggttttttttttttt T/Δ cttcatttctttggttgctg	1260
NAT2	21	exon2 + 288	atgttaggagggtatttttta C/T atcctccagttaacaaata	1261
NAT2	22	5'flank - 2053	ctggattgcaacattttaat T/C ccaggtgtcaggtttccaac	1262
NAT2	23	5'flank - 1299	gaatcaccagtgcgggaggt A/G taacagtgaacccaagacac	1263
NAT2	24	5'flank - 1145	ctgtagaacacaaggatatt C/T ggaggcagtttgtacatgcc	1264
NAT2	25	5'flank - 1036	ccttcccacagagtcccgag T/A tcatgtggcagcatgccaga	1265
NAT2	26	5'flank - 94	aaagatttgctaagagattc G/A cagaggcaacctgaggccct	1266
NAT2	27	5'flank - 643	atgtttatattttatattaa T/C attaatgtaaataaaaattt	1267
AADA	1	5'UTR + 29	attaaagtacactattcagg C/T atatcatgtaggtttacttt	1268
AADA	2	intron1+138	gctgtggcctttgacaatgt G/A ttacttagaaatgttgtttg	1269
AADA	3	intron1+142	tggcctttgacaatgtgtta C/T ttagaaatgttgtttgtttt	1270
AADA	4	intron1+1033	ttccagcagagacaccaaca A/G gtaaaaacaccccagctaca	1271
AADA	5	intron1 + 1253	ttttttttcccctcatatttgc T/C gtctgtgctacaatatgtga	1272
AADA	6	intron1+1366	ctctggtagccttttaattta A/G ttaattcattcatttactta	1273
AADA	7	intron1+1369	tggtagccttttaattaatt A/C attcattcatttacttacat	1274
AADA	8	intron1+2501	ggttacagaaagaatggtgg C/A ttggccaaaaaatgatatgg	1275
AADA	9	intron2+1971	aaatgagagttaagtaggag A/C attttcttttatttttgtgc	1276
AADA	10	intron2+1988	gagaattttcttttatttttt A/G tgcaggagaaatataaacaa	1277
AADA	11	intron2+2341	aggtgccttttctattgtcc C/T atgcagacttaggtgatcct	1278
AADA	12	intron2+2546	gtctgacacagaaggatcaa T/A ggcaaaatgtgcaagacaaa	1279
AADA	13	intron2+2609	taggaggttcactggaaaac T/C tgaattccactgagtcatga	1280
AADA	14	intron2+2663	tataaatacagtgttaaatt T/C gtctctcgtattttaaggta	1281
AADA	15	intron4 + 605	tgtgtcagtaaaatattata T/C taagtaggtgaatgagatca	1282
AADA	16	intron4 + 621	tatattaagtaggtgaatga G/T atcatgtaattgtgagacta	1283
AADA	17	intron4 + 679	ttagagattcagacgaattc A/G tataatcttcgatggtgtat	1284
AADA	18	intron4+1680	gttaaaatgtggataaatac C/T acaatttgcaaaatatttgg	1285
AADA	19	intron4+1748	atttagaagttctatacatc T/C tttatagtatattacacact	1286
AADA	20	intron4+1771	tatagtatattacacacttc G/A aaaacacaaaattatttttt	1287
AADA	21	exon5 + 238	caagtcatctcttcaaattt A/G ttaattggagttccctgctc	1288
AADA	22	3'UTR + 121	ttagaaattggtctttctta A/G aatggtctagttaagttcca	1289
NTE	1	5'flanking - 535	cacgatctgtcctccgattc C/T tgttaactctagactttctg	1290
NTE	2	5'flanking - 15	gtaaatcccggcaaaaacc A/G gcagcgccttgcaagcccac	1291
NTE	3	5'flanking - 748	agcatggcgcggggaggagg G/T gtgggagggtcgggagggac	1292
NTE	4	5'flanking - 690	tgaataatttaaaggggccg T/C gcctgcggagccgggcggaa	1293
NTE	5	intron6 + 605	tcttgccatatacttagtgg A/G ggggtctacatcagggttt	1294
NTE	6	intron6 + 748	agcctccagcctctcttctc C/T gggggttatctcaggcatct	1295
NTE	7	intron6 + 987	ggtgctggctctgggatccc C/T gtgcgtcatgtagtctacct	1296
NTE	8	intron6 + 1882	tggcctcaagcaatcctccc G/A cctcggcctcccaaagtgct	1297
NTE	9	intron6 + 2222	gaatgtttatgtagaacaga G/A agactgtatctgcggtcttc	1298
NTE	10	intron12 + 166	tatctggtaccgaggaagct C/G tggcctcgtccccaagggcc	1299
NTE	11	intron13 + 69	atccaggtccaccgcctgcc C/T gtcttgattgttttaatctg	1300
NTE	12	intron14 + 8	agccccccgctcgggtaaggc C/T tgggaccctgcccggtggtg	1301
NTE	13	intron16 - 113	gccaccgcgcccctgcgcctt T/C atatttttcttaacccttcc	1302
NTE	14	intron21 + 34	agagccggccggcccagagc A/G tgctgggagatgtagtccgg	1303
NTE	15	intron21 + 128	gaagaaatcgtgcccctgag G/A gtttcaaaccctaagtagga	1304
NTE	16	intron21 + 151	ttcaaaccctaagtaggacc C/G aggtgcagagcattctgggg	1305
NTE	17	intron21 + 651	ccactgtactccagccggga C/T gacagagctagaacctgttt	1306
NTE	18	intron21 + 737	tggaaaatagtctgtggatt G/T ttgtttaggactctgggcac	1307
NTE	19	intron21 + 1752	acagctggtctaggctgtta G/C tggagaaactgggaagcaac	1308
NTE	20	intron21 + 1788	gaagcaacagctgggtcaaa A/Δ gtagcttttcttttcttggc	1309
NTE	21	intron21 + 1907	cactgcaacctctgcctccc A/G ggttcaagtgattctcctgc	1310
NTE	22	intron21 + 2065	ctgcctcgttttatgttcag G/T tccccattagacagaggaa	1311
NTE	23	intron21 + 2336	agtctgggagcacaggagca G/A gaatttcagataaggaggaa	1312
NTE	24	intron23 + 41	tggggagggtggtgggtggg G/C ctggagcctcaaattctttc	1313
NTE	25	intron23 + 71	caaattctttcagacctgag T/C tcaagttctcggcttccaac	1314
NTE	26	intron23 + 81	cagacctgagttcaagttct C/T ggcttccaaccacggagcct	1315
NTE	27	intron24 + 150	gtggggcggctggtgacctc A/G gccgtccgtattccgcagct	1316
NTE	28	intron29 + 37	gcctgcagcaaccgctgacg T/C cacgtggggttgggggatg	1317

遺伝子名	No.	存在位置	配　　列	配列番号
NTE	29	intron29 + 370	cgtcccaggtcagcgagccc G/A tcgggccggctgggcctccg	1318
NTE	30	intron30 + 56	acctcccgcaccaacacacac G/A cacacgcgtgggcacacaca	1319
NTE	31	intron30 + 358	aaaaatacaaaaaaattaacc A/G ggctggtggggtgtgcctgt	1320
NTE	32	intron30 + 372	ttaaccaggctggtggggtg T/C gcctgtaatcccagctactc	1321
NTE	33	intron30 + 430	aaatcacttgaacctgggag G/T tggaggttgcagtgagctga	1322
NTE	34	intron30 + 655	gtgtgcacaccagctatata T/C gcaaatgctttctctcaggg	1323
NTE	35	intron30 + 659	gcacaccagctatatatgca A/C atgctttctctcaggggcag	1324
NTE	36	intron30 + 760	tgaaatagggcatttgccaa C/T gcatgccagtctgtcccgtt	1325
NTE	37	intron30 + 835	gcacacacgtagataggatg T/C ggcacctctgaccgagttaa	1326
NTE	38	intron31 + 40	tggtgcctgcataggtggtc T/C ggctaagctttgctacttaa	1327
NTE	39	intron31 + 41	ggtgcctgcataggtggtct G/A gctaagctttgctacttaaa	1328
NTE	40	intron31 + 1329	gtctgtcaagggcaggacag G/A ggatgtgtaggcgagtgtgc	1329
NTE	41	intron35 + 31	aatggcttcctgtcgtttcc G/A gactggggacccaccttctg	1330
DDOST	8	intron2 + 1299	atcttctgatgactgggctt C/T ggtgcagtaactggtgtttg	1331
DDOST	9	intron2 + 1581	gatactgttggtgggagaaa T/C gacagagagtgtaaaacagt	1332
DDOST	10	intron2 + 2822	gttttctcaacaggtgcattc T/G tgacgtttcagactggataa	1333
DDOST	11	intron2 + 3392	cagaaggcgtggaggcctgc C/T gcgcctccctctgttgctgc	1334
DDOST	12	intron5 + 495	attgcttgaacccaggaggc G/A gaggttgcagtgagccaagg	1335
DDOST	13	intron6 + 226	ggaactgcttgggtcacagc C/T tcgttttgttcccagtatcc	1336
DDOST	14	intron8 + 303	aagagaaataggtcattagg A/T tgaatttgttaggcaagaga	1337
DDOST	15	3'flanking + 40	cacagcgtggagacggggca G/A ggaggggggttattaggatt	1338
MRP2	1	exon 1 + 77	catattaatagaagagtcttt C/T gttccagacgcagtccagga	1339
MRP2	2	intron2+192	atcaaagtggctttgatttt T/G gcataagaatggtgactctt	1340
MRP2	3	intron 1 + 413	gataagttctagaactggca A/C ctaatgatatggactagaag	1341
MRP2	4	intron2+3639	gtcatatcccacccccaaat C/A gacccaataggtacaatgaa	1342
MRP2	5	intron2+3989	agttatgaaaccgatttttc C/T gggactggttgttctagtct	1343
MRP2	6	intron2+4078	aggtttccagatgtgttccc T/C aggcattcctggtggtagga	1344
MRP2	7	intron2+4171	cttattctttggtcagttgg C/T tttctaccacctcttagctt	1345
MRP2	8	intron 2 + 5373	gttaaggatatgtgaactca A/G aatttttatacacagtgcaa	1346
MRP2	9	intron2+4436	ggactagtggaagaattaga C/G ctttcctgaataaatagatc	1347
MRP2	10	intron 2 + 3930	aaaactggcaggagaatttc A/G ctggagctgcatgcaggact	1348
MRP2	11	intron 2 + 4257	gggtattggaaagttcttgc G/A gctgctggaggctgcggtgt	1349
MRP2	12	intron 3 + 772	ggtataaggcaagatttttt A/T aaaaaattaattgcttaatc	1350
MRP2	13	intron 7 + 1658	ggactcttaccagcttagtt G/T cctggttttctaatctaaaa	1351
MRP2	14	exon 10 + 40	tggccaggaaggagtacacc G/A ttggagaaacagtgaacctg	1352
MRP2	15	intron 11 + 1672	aacttttaagtcttaagac T/A ggaaggcctgtgtcctaggc	1353
MRP2	16	intron 12 + 148	ccctctcaccgccccatgcc A/G cttttcctcctttgtaccat	1354
MRP2	17	intron 2 + 1020	agtgctgcgattacaagcct G/C agccacctgcacagcctctg	1355
MRP2	18	intron 2 + 5227	taccataatttatgtgtcct A/G tatgacatgaatttcattgg	1356
MRP2	19	intron 2 + 5373	gttaaggatatgtgaactca A/G aatttttatacacagtgcaa	1357
MRP2	20	intron 2 + 5538	ttaatgaggttaagcacatg G/T tcatatgtttaaaagccttt	1358
MRP2	21	intron 13 + 180	catgagttttctgagccccca G/C tttatctaactataaaatga	1359
MRP2	22	intron 13 + 1497	gtgcagggtccccctgatgc T/C atagccagttcctctttaga	1360
MRP2	23	intron 15 + 169	atgagctgaaagcaaaggtt T/C tcagcccattcccctgataa	1361
MRP2	24	intron 15 + 949	ttccaggtgacacatttagt A/G cctaatttgggaaatgttaa	1362
MRP2	25	intron 15 + 984	tgttaatctagtccaatccc A/C ttagtaagaaaggaggggtc	1363
MRP2	26	intron 16 + 4059	catcctgatgcacagttatt C/T aaattaagctccatttgtt	1364
MRP2	27	intron 19 + 10899	atgtatggagtatttatgga G/A taaagtattccatgctgtat	1365
MRP2	28	exon 22 + 51	ccagcaataggattgtttc G/A atattcttcatcatccttgc	1366
MRP2	29	intron23+56	tatactgaggatctttctga C/T agggaggaattattatgtcc	1367
MRP2	30	intron 23 + 734	tgagccaactactgtactag G/A cactggggcactcaatgaat	1368
MRP2	31	intron 23 + 801	atgggccagacccaactcac T/G gatttttttagtgtatctgag	1369
MRP2	32	intron 27 + 124	gggtcctaaagtttccttt C/G ctctaactcaaaggacctaa	1370
MRP2	33	exon 28 + 52	cagattggcccagcaaaggc A/C agatccagtttaacaactac	1371
MRP2	34	exon 28 + 84	aacaactaccaagtgcggta C/T cgacctgagctggatctggt	1372
MRP2	35	exon 28 + 129	agagggatcacttgtgacat C/T ggtagcatggagaaggtagg	1373
MRP2	36	intron 29 + 154	ttccctaggatggacacgtc A/G tttccagaactttgaaatgt	1374
MRP2	37	intron 30 + 91	gtgttaggtgatgcctggca T/C agaattttcatccaggtctg	1375
MRP2	38	intron 31 + 170	gccaaaattttacatcacgc A/G aatgaaaacgaacaaggtta	1376
MRP2	39	intron 26 + 154	ctggctccatctttttaccca T/C ggacgtattccttactcttc	1377

遺伝子名	No.	存在位置	配　　列	配列番号
MRP2	40	3'-flanking + 739	gtgaatttttattataagct C/T gttctccttaaaactttatc	1378
MRP2	41	intron 3 + 1145	acatcctttctcccctcagtc C/T tcggttagtggcagtattct	1379
MRP2	42	intron23+432	tggcagtagagcagggtgag G/A aggattattctgcagaggaa	1380
ABCB1	1	5'flanking-196	gctttggagccatagtcatg T/C actcaaaatttattttatct	1381
ABCB1	2	5'flanking-16	tactctttacctgtgaagag T/C agaacatgaagaaatctact	1382
ABCB1	3	intron1+71660	cttgctggaggaagggtgct A/C gaaaatatgccaaatccaag	1383
ABCB1	4	intron1+80091	gaaataatattcaagttctg A/C aataatatcatgacctatag	1384
ABCB1	5	intron1+103126	gatatgaatcagaattcatc T/C gtgtctcaagaaaaggtcat	1385
ABCB1	6	intron1+103148	tgtctcaagaaaaggtcatg C/T gataaattaagttctgctag	1386
ABCB1	7	intron1+108428	aattaatttatcatcatctg A/G tcaccatttcacacaactca	1387
ABCB1	8	intron1+112042	cataagttgaaatgtcccca A/G tgattcagctgatgcgcgtt	1388
ABCB1	9	intron2+491	gctctctggcttcgacgggg G/Δ actagaggttagtctcacct	1389
ABCB1	10	intron4+36	attaactattcaaaatactt C/T ggaaatttgacatctcctta	1390
ABCB1	11	intron5+1596	ttagctctcttactgcttca T/C agtggaagaatcaaatactt	1391
ABCB1	12	intron8+1789	aaacactctgaatattaaac C/T gctcctggaaccacagctca	1392
ABCB1	13	intron14+24	agttgtccttgccctttgcc T/C ttctagaggtgcaaaaaata	1393
ABCB1	14	intron14+81	tgcaggaagttaggaaacta C/T tataaatcggaagaaggaa	1394
ABCB1	15	intron15+38	caaaccaacctgatttataa A/G cataagaacattctactact	1395
ABCB1	16	intron17+73	gtttggtgggctagggctac A/G gtaggagtgggaacaagaga	1396
ABCB1	17	intron18+564	caacagtaaagttacaatct G/A aaaggaatgctctctgttta	1397
ABCB1	18	intron18+2062	tttccctgaggaatggttat C/T ctctgtgttccttgagtcca	1398
ABCB1	19	intron18+2293	ccacatcaggttttccccag A/G caccttgggacagtttgaaa	1399
ABCB1	20	intron20+557	aaaaccctaaccattgacac G/A tgtgaatgttttcctgggga	1400
ABCB1	21	intron21+24	cgtgcctcctttctactggt G/A tttgtctteattggccattt	1401
ABCB1	22	intron21+2725	ctgacctgtttttggctgac A/G ggttttegttcctccctca	1402
ABCB1	23	intron21+4725	tcttggtattaaaagatcca A/G agagataggaatatgtaatt	1403
ABCB1	24	intron22+8507	tgcacttaggaaaaaaaaaa T/C atggaaatgtgtaaaatata	1404
ABCB1	25	intron22+8537	tgtaaaatatactttttttt T/A aaaaaaaaggacacatttat	1405
ABCB1	26	intron22+8565	aggaacacatttattcagcat T/C atgatcagactattacattt	1406
ABCB1	27	intron22+8952	caccttggtttcatggtttg G/A caaagtactggcctgtacca	1407
ABCB1	28	intron22+9520	caccaacaaaatatcttttttc A/G cagttgggtgggcatctggt	1408
ABCB1	29	intron22+9836	agactctgacttagacatga C/T ggcaggggaaagagagactt	1409
ABCB1	30	intron24+377	taaaatacagatgtgttgta C/A taagttctgcaagcctttgg	1410
ABCB1	31	intron24+1493	ggggaggtgtccaggcacga A/Δ catggagagctggacttgat	1411
ABCB1	32	intron24+1495	ggaggtgtccaggcacgaac A/T tggagagctggacttgatac	1412
ABCB1	33	intron25+342	tgcagccttgatcttctggg C/T tcaagcgatcctcctgcctc	1413
ABCB1	34	intron26+134	cttggataaagtctgagagc C/G taaatatggtctccaagtgg	1414
ABCB1	35	intron26+1272	gtccttcaattttgtggtga A/G cttaaaaacaggactctaaa	1415
ABCB1	36	intron26+1394	tattaagtggtgtgttaaag A/G ttgtgctataatgaattgta	1416
ABCB1	37	intron26+(1987-1988)	aagggctggaagagtgaaag (AAAG) gaggctatttgctcccagac	1417
ABCB1	37	intron26+(1987-1988)	aagggctggaagagtgaaag gaggctatttgctcccagac	1418
ABCB1	38	intron27+59	gcagcctctctggcctatag G/T ttgatttataaggggctggt	1419
ABCB1	39	intron27+80	ttgatttataaggggctggt T/C tcccagaagtgaagagaaat	1420
ABCB3	1	intron3+8	tctcctttggcaggtaggtg G/A tgggcagctgggtccatttg	1421
ABCB3	2	intron4+104	cttcacccgtatgccaggac C/T tggggatgcttttctcttgt	1422
ABCB3	3	intron10+219	gcagcagtggtgctccctcc A/G tgggcagccccgtcaggtcc	1423
ABCB3	4	intron11+(317-319)	atggtgcccaggtggatgtg GTG/Δ tccatctcattcctgtcttt	1424
ABCB3	5	exon12+19	agctgcaggactggaattcc T/C gtggggatogcacagtgctg	1425
ABCB3	6	exon12+(356-357)	aggtgggctgggtgggatg GG/TGGTGGGGTGGA ggctg tctgtgtccaggaaa	1426
ABCB7	1	intron1+220	acgggcaggaggttctggg C/A agaggacacctggagcgctg	1427
ABCB7	2	intron1+480	agttaactcccttgctgaca G/A gcgtgcttcttgataggcca	1428
ABCB7	3	intron1+(512-513)	getaggccaaaaccgtaact AT/Δ ctttccaaaacatagaccgc	1429
ABCB7	4	intron1+1690	agttctccaataaggcagat G/A aagttaagataaaatttgta	1430
ABCB7	5	intron1+5309	aattaatatcatttattgct G/A tattgttgtcagtgttatct	1431
ABCB7	6	intron1-11274	tgcttcttttcaagccagcc A/G gctttaaaaaaaagttagct	1432
ABCB7	7	intron1-11085	caggttttcagggctcatgt A/G gacctgaagaaaaatgagag	1433
ABCB7	8	intron1-10037	attctactttctcaacttct T/C ttattacattatctcatcat	1434
ABCB7	9	intron1-21	ccactctgaaacttcccccc G/A ctttttttccttgtcagcag	1435
ABCB7	10	intron3+(135-136)	ttctctaatgaaaaaaaaaa (A) catattaattgaccatagtt	1436

遺伝子名	No.	存在位置	配　　列	配列番号
ABCB7	10	intron3+(135-136)	ttctctaatgaaaaaaaaaa　catattaattgaccatagtt	1437
ABCB7	11	intron3+333	aaaacaatttgtgtgtgtgc G/A tgtgcttcaaggttaatgtt	1438
ABCB7	12	intron12+524	taaccactctgcccctcagta C/T gaaacacagtgccgaaccca	1439
ABCB7	13	intron13+1543	atcctgtgaggtggggaagc G/A tatggctagcataaatataa	1440
ABCB7	14	intron13+2400	tgttaccttactgcctcatt C/G tcattcttcccacctgctat	1441
ABCB7	15	intron15+2201	ctccttcctaaccttagcaa G/C agtctggagatttacttatc	1442
ABCB8	1	5'flanking-2272	ggcttaggcctaagggctga T/C gttggggccagtaccccctga	1443
ABCB8	2	5'flanking-2070	agctatgaaaacaagaccct G/A tccttctagaggtagcaaaa	1444
ABCB8	3	intron1+25	aaacggaaaaacctactcag A/C gcgggccattgaccgcccgg	1445
ABCB8	4	exon2+308	tgctggtcctgggggtagcc G/A tcgtggtgaggctttcccca	1446
ABCB8	5	intron2+334	ccccccacttaaaacatttgt C/G cctctgtctccccattcca	1447
ABCB8	6	intron4+12	cctgctccggtactgccagc C/T gcagggtgcagagttggggt	1448
ABCB8	7	intron5+547	agttcatagcattctcgctc G/A gccccctcaggcctgctgct	1449
ABCB8	8	exon7+57	ggcaatgtgcggactgtgcg A/T gccttcgccatggagcaacg	1450
ABCB8	9	intron9+1231	tttccgcagctgcatggaca C/T cctcgcgtgccccgtttctg	1451
ABCB8	10	intron9+2164	cctcttggaggtccttctag C/T gctgcctatgtggagattct	1452
ABCB8	11	intron9+2645	ttcctgcctggtgcctcccc C/Δ ggctgcctttagcaagtgct	1453
ABCB8	12	intron9+2646	tcctgcctggtgcctcccc G/A gctgcctttagcaagtgctg	1454
ABCB8	13	intron9+3229	cagggccgagcagggagtcc G/A tgggtcagctgggctcccct	1455
ABCB8	14	intron12+(113-114)	tcctccactgccacaagggg (GG) ccttctttcctgggacaatc	1456
ABCB8	14	intron12+(113-114)	tcctccactgccacaagggg　ccttctttcctgggacaatc	1457
ABCB8	15	intron13+128	tgctctcgggagaccctggc C/T gtcttcacatgtcctcagct	1458
ABCB8	16	intron13+305	atccaggtctagagaagcct A/G tagtggaggtgctgagctgc	1459
ABCB8	17	intron14+135	acagttgtgtcagggaagac C/G agaaccacagccaaagggga	1460
ABCB8	18	intron14+159	accacagccaaaggggacag A/T gtcgttgtgtggggacaggg	1461
ABCB8	19	intron15+747	gttggagccttgggctctgt A/G agggggacagagggaatcat	1462
ABCB8	20	3'flanking+333	cctatccccctggctcacccc G/A ggacccacagtccccatctt	1463
ABCB8	21	3'flanking+1168	ccctctttcaggggtgtgat G/A cagtgcattgatggagcagc	1464
ABCB8	22	3'flanking+(1719-1721)	tagaccgcaggagccgcgcc GTC/Δ ttcctaacctcgcctcggcc	1465
ABCB9	1	intron1+ 69	agggtgccaggccaggcacg G/C gttgggggcgtctgggcac	1466
ABCB9	2	intron1+8873	tggcccagcacgtgcggcc T/C ggaactacctcaaaggcttc	1467
ABCB9	3	intron1+8940	accagctcagcctgcccagc G/A tgcacacggcaccaagctgg	1468
ABCB9	4	intron1+11410	agatccaagggatccagagg T/C tggaatgtgaccctccgtgc	1469
ABCB9	5	intron1+12863	gggaagccagatgcccacaa G/A gctctgtgacttcacttcca	1470
ABCB9	6	intron1+19731	gccaagtgtcaagatcgagc G/A agcggagggcctgacgaggg	1471
ABCB9	7	intron1+29649	cagaatccagatgcccgtaa T/C gttgttaagaagcctgcaca	1472
ABCB9	8	intron1+31793	ggccaggcgcggcagcggtac C/T ggccagaccggtgggcaaaa	1473
ABCB9	9	intron1+37537	agagtcacagggttgcggtg C/A ccccgggaaggtggcatcta	1474
ABCB9	10	intron1+38293	taccagccctgtgctttcag G/A gaccatgtgacctgtcaact	1475
ABCB9	11	intron1+44661	cccgaggtgcctggcttcac A/G gcaggattgccgtcctgcag	1476
ABCB9	12	intron1+49576	aaagtggcccccgtggcttgt C/T cctgaagcccctaaagcacc	1477
ABCB9	13	intron1+64669	ccacagacaagccgggtagc C/A cacctcgcagctcaacacac	1478
ABCB9	14	exon2+448	cctggttttgggccctgttc G/A tgtggacgtacatttcactc	1479
ABCB9	15	intron7+3364	ggtaccaggagtcgggtatc A/G gtgggacaggaacgcgtgtc	1480
ABCB9	16	intron11+113	gggccccaggagctctccca G/T actatcagcctcctgggctg	1481
ABCB9	17	exon12+370	cccaggcctgcagcactgaa A/G gacgacctgccatgtcccat	1482
ABCB10	1	5'flanking-424	tcgcgtctgcgcgctccgcc C/T ggtctgccggcgtgagaaag	1483
ABCB10	2	exon1+491	acaaggggcggttgcgcccc G/T cagcggccggactcccggag	1484
ABCB10	3	intron1+37	ccacttccctccgccgggcc T/G ctccttctccacacgcgggg	1485
ABCB10	4	intron1+217	actcgtttgcagattttaca C/T ttgttttcttgttgacacac	1486
ABCB10	5	intron1+405	gcgtttatacttttttttt T/Δ aaccaaaaacacattatttg	1487
ABCB10	6	exon3+185	agggccggggcccaggcttc C/T gtaggcatcagtatgatggt	1488
ABCB10	7	intron6+1269	caaattcacaactgtgcctt C/G cacagaatgggttggaaaac	1489
ABCB10	8	intron9+632	cccctccccttgggtgag G/A gcaggtggatggtgatgggt	1490
ABCB10	9	intron10+2373	tacctcagggcactcagaca G/C cctcaccaatcagaggctca	1491
ABCB10	10	intron11+108	tcctttcctgtttttttgtt T/G ttttttttttcttggagtgg	1492
ABCB10	11	intron11+2379	cattggtttttagtgtattc T/A gtgttgtgcatccatcatca	1493
ABCB11	1	5'flanking-(2596-2595)	tgtggtttagagctttctct (TT) gagacatttttgctaaggtt	1494
ABCB11	1	5'flanking-(2596-2595)	tgtggtttagagctttctct　gagacatttttgctaaggtt	1495
ABCB11	2	5'flanking-1746	agctgaagtgaattaagcac G/A atcaactcagtactcacact	1496

遺伝子名	No.	存在位置	配　　列	配列番号
ABCB11	3	5'flanking-(326-314)	agggggaaagtttaaaggta (T)9-12 gtcttgttatgtttttaagt	1497
ABCB11	4	5'flanking-135	agagggtttcccaagcacac T/C ctgtgtttggggttattgct	1498
ABCB11	5	intron1+511	aaatatagatgcaaaaaaaa A/Δ tgagctgtggatgcatgttt	1499
ABCB11	6	intron1+581	aatttcagtttttaggtcac C/T caagccagtgggagtcacat	1500
ABCB11	7	intron1+(1938-1951)	aaagacgttttaagggcttt (A)10-13 gaaagaaaagcaaaactgtag	1501
ABCB11	8	intron1+4517	ggtttcccaacatctcatct G/A ataaaaaaaaataatttgcca	1502
ABCB11	9	intron1+5651	aaagagaataggttagtgga T/C tagtattcctgtgcttaatg	1503
ABCB11	10	intron1+(12200-12201)	aagagatggtctctagcccc CT/Δ gtttgatttggggcacttac	1504
ABCB11	11	intron1+13023	gtttggctactttgattaaa G/A aagaaagaagagataataat	1505
ABCB11	12	intron2+739	cctgcatctattctgaccta C/T actgggaaaacagtatgtg	1506
ABCB11	13	intron2+(921-922)	tattttgtagttcaaaaagt (CAGATCTTCTTCAGCT AATTTAGAAATGT) tgctgtccatttgatattca	1507
ABCB11	13	intron2+(921-922)	tattttgtagttcaaaaagt tgctg tccatttgatattca	1508
ABCB11	14	intron3+644	agccacacgtttcttattgc G/A tgggaagtttaaaaaatggg	1509
ABCB11	15	intron3+2231	agtgaacctgagattgagct A/G tactgaaatctctagaagag	1510
ABCB11	16	intron3+2406	aaagggtggtctttaaatcc T/C tatgtttttctcatcaggtt	1511
ABCB11	17	exon4+10	tttctcatcaggttacaaga T/C gagaagaaaggtgatggcgt	1512
ABCB11	18	intron4+434	acaatttatagtatttctca A/G tgccccacacagtttatcta	1513
ABCB11	19	intron4+518	gtagatgagtagctaaaaac G/T aaagtcagctcctgaaataa	1514
ABCB11	20	exon5+120	ggcacaatgacagatgtttt T/C attgactacgacgttgagtt	1515
ABCB11	21	intron5+320	gggaggtgacccatgaattt T/C acttgagtatcatctccaag	1516
ABCB11	22	intron5+16076	agaagaggtaacagtaagcc T/G cctgatttacagcacacatc	1517
ABCB11	23	intron6+303	atttgcaggtgtgtttgtag G/C gggcagttgagtagcttgaa	1518
ABCB11	24	intron7+1141	aaaggattcagcaggcatga A/G gaaagaaaagctttgcaaga	1519
ABCB11	25	intron8+2463	ccattggctaatagcaatga A/C ctatgacatggtctaactta	1520
ABCB11	26	intron8+2677	tcaatgatgttacagtgaga A/C tctaatattgtattaaaccc	1521
ABCB11	27	intron8+2699	ctaatattgtattaaaccca T/A gccacatgttaaatgaatct	1522
ABCB11	28	exon9+24	gtgtccaagtttacggacta T/C gagctgaaggcctatgccaa	1523
ABCB11	29	intron9+108	caccttggtctgtggcctcc A/G gaggaagtacttgttcaaga	1524
ABCB11	30	intron10+2475	taatcattccaaaccacgga C/A tttatttcattaagaacatg	1525
ABCB11	31	intron10+2478	tcattccaaaccacggactt T/A atttcattaagaacatgata	1526
ABCB11	32	intron10+2711	tttacagattggaaaagcca C/T tgaagtattgcaggtccaga	1527
ABCB11	33	intron10+3539	agtgactgtaattagtatca C/G ttgtgcacagagaaaaaatg	1528
ABCB11	34	intron10+3623	tgcagaaggttgttctttca T/C gaccttcctgagtttcagaa	1529
ABCB11	35	intron10+3661	gaattcattaataaaaataa A/T cacataatggagcgtgacat	1530
ABCB11	36	intron10+5100	gggccactctttggcttggc A/G atagactgtggccaatgaaa	1531
ABCB11	37	intron10+5292	gctatttggtaggaacatct G/A ggcatgatcaggtagccttc	1532
ABCB11	38	intron10+5912	gagtaatattcagtaaaaaa A/Δ taaagtggtattttaaatca	1533
ABCB11	39	intron12+116	tgtttccagtaatagggaat G/A gaggtgtctttctctgaaag	1534
ABCB11	40	intron12+326	gataaatgacaaggcaatta G/C aacaatcaggaagcaaaggt	1535
ABCB11	41	intron12+335	caaggcaattacaacaatca A/G gaagcacaggttcttcccaa	1536
ABCB11	42	intron12+2572	cctcatccttgccaatgttt C/T cttttactggttttgatgg	1537
ABCB11	43	exon13+23	tctaaatgacctcaacatgg T/C cattaaaccagggaaatga	1538
ABCB11	44	intron13+70	atggcagtatattgatcaaa C/T agaaaggtgtagcatacatt	1539
ABCB11	45	intron13+(1578-1579)	ttattggcctctatttttttc (C) tgcccattggtcaagtatga	1540
ABCB11	45	intron13+(1578-1579)	ttattggcctctatttttttc tgcccattggtcaagtatga	1541
ABCB11	46	intron14+32	catacattcctgggagaaac C/T aagaggtcatagaaggaaaa	1542
ABCB11	47	intron14+80	cacaattatacacatttctt C/T tcgtatgattcccaagtcat	1543
ABCB11	48	intron14+439	tattgtgtcaaaaacaattc A/G ttgtatatctccattctaag	1544
ABCB11	49	intron14+(1262-1263)	cagcctttgcattatatttt (T) gctgtgttgtctaacaggag	1545
ABCB11	49	intron14+(1262-1263)	cagcctttgcattatatttt gctgtgttgtctaacaggag	1546
ABCB11	50	intron14+1283	gctgtgttgtctaacaggag A/C aaagagacacggatttgctc	1547
ABCB11	51	intron14+1339	tgagatagatatttaggacc G/A tgaccaatttttatttggt	1548
ABCB11	52	intron14+1359	gtgaccaatttttattttgg T/C tgaaaaatcttatttgaagt	1549
ABCB11	53	intron14+1460	tattgattagacaataaccc G/A tctggggaagggatatttct	1550
ABCB11	54	intron15+370	ccttttctaatgtctgcaca G/A cctatttaagaatattccca	1551
ABCB11	55	intron16+(550-559)	aaagtttagtgtttctatca (T)9-12 gctacttctgatggacttct	1552
ABCB11	56	intron17+188	tttctctcccaattcatgg T/G tttttggttagcttctcatc	1553
ABCB11	57	intron17+194	tccccaattcatgggttttt T/G gttagcttctcatcttcttg	1554

遺伝子名	No.	存在位置	配　　列	配列番号
ABCB11	58	intron17+(197-198)	caattcatgggtttttggtt (T) agcttctcatcttcttgggg	1555
ABCB11	58	intron17+(197-198)	caattcatgggtttttggtt　　agcttctcatcttcttgggg	1556
ABCB11	59	intron17+(289-296)	ttagaaaggggacttctttt (A)7G(A)4 tctgtgtttagtgttcctct	1557
ABCB11	59	intron17+(289-296)	ttagaaaggggacttctttt (A)12 tctgtgtttagtgttcctct	1558
ABCB11	59	intron17+(289-296)	ttagaaaggggacttctttt (A)10 tctgtgtttagtgttcctct	1559
ABCB11	60	intron17+1070	tcagacttgggttttcctat C/T tttcttcttgagaacaagtt	1560
ABCB11	61	intron17+1651	tgttaaaatatctcattgta T/C atgctgacggatttttcttg	1561
ABCB11	62	intron17+2226	ccttaagtctcctcctatca T/A gcaccttgttctcaccagct	1562
ABCB11	63	intron17+2979	ctctctcttcctttctcagc T/Δ ctactatttcactgttggct	1563
ABCB11	64	intron17+3288	aatccccatatcctacctta T/G ccatctcatccatgaatctt	1564
ABCB11	65	intron17+3289	atccccatatcctacctlag C/T catctcatccatgaatcttg	1565
ABCB11	66	intron18+97	aatatgagttttctaggtat A/G tatctagcagtgtttcaagt	1566
ABCB11	67	intron18+98	atatgagttttctaggtata T/C atctagcagtgtttcaagtc	1567
ABCB11	68	intron18+892	ctctgaaagttagtgatacа C/T cttatttgtgtttgaatcaa	1568
ABCB11	69	intron18+2681	atgtatgagatcaagtcagg A/G tcaaaatattagacacccata	1569
ABCB11	70	intron18+3780	ggaccatcctgtggggcaat C/G gttccagaaaatgctggtat	1570
ABCB11	71	intron18+5741	ctcaccggtataaatacaac C/T gtagcaaaggttttcttttt	1571
ABCB11	72	intron18+(5882-5883)	tgcgtattccctcagttcag (C) tttttattcaagccacagca	1572
ABCB11	72	intron18+(5882-5883)	tgcgtattccctcagttcag　　tttttattcaagccacagca	1573
ABCB11	73	intron19+10022	tggctaagttaaaaaaaaaa A/Δ gagattcaactataattgct	1574
ABCB11	74	intron21+322	caagattcaatactgcccccc C/Δ agggggtgggtgaacagggc	1575
ABCB11	75	intron22+257	ctgttcaatttcctctcgca T/C agtgattcattccacattcc	1576
ABCB11	76	intron22+552	taattaatatcttgtccttg G/C ggggtaaatgagggatggta	1577
ABCB11	77	intron22+569	ttgggggtaaatgagggat G/A gtagcataaacacttctcaa	1578
ABCB11	78	3'flanking+243	aaacaccacagaatgacata G/A aactaaaggcggcaggaatc	1579
CYP4B1	1	5'flanking-333	gaaacattcacagtgcttgt A/T tgagaegacagtggttatta	1580
CYP4B1	2	5'flanking-18	gagcagctgaaggcaggtca G/T atgaaggctaggtggctgga	1581
CYP4B1	3	intron1+341	tccaaaacctctggatagta C/T atagaagtaggcaatccatt	1582
CYP4B1	4	intron1+542	cctatgggtggctcaggagc C/T gtgacaccttcccaggttca	1583
CYP4B1	5	intron1+2856	gaggactttgcacatagtag G/A tgctcagctatattgttggc	1584
CYP4B1	6	intron1+6086	tttggaatctaaagactggg G/T cacgatgctagttgtgtgac	1585
CYP4B1	7	intron1+6598	ttttggggtgtgggggaggg G/A cccatagtagggagacagct	1586
CYP4B1	8	intron1+6660	acctaagggtgtccatcctg A/G aggagagcagtcctaggggg	1587
CYP4B1	9	intron1+7242	ccctggtctcccttaactca T/C gctggactgttccctttggt	1588
CYP4B1	10	intron2+107	gcctgtgtactaagtctgcg C/G agctgaggttcccaccctac	1589
CYP4B1	11	intron3+361	atggtgtggtggtaggacca C/T ggctggtcaccagaggctgt	1590
CYP4B1	12	intron4-492	aaaggctttcacatctaaaa C/A gtgtctcctcattttctgtc	1591
CYP4B1	13	intron4-315	ggattacttacatatacacc A/G tgcgggggagctcaccacct	1592
CYP4B1	14	intron4-157	ctacccaccctatcctgata T/C tccagcaggatggagggcag	1593
CYP4B1	15	exon5+22	acaagtgggaagagaaagct C/T gggagggtaagtcctttgac	1594
CYP4B1	16	intron5+125	cccagggagccttagcttgc G/A gggagacaggacctgctcat	1595
CYP4B1	17	intron5+(287-289)	tgtctaagccaatccctcct CCT/Δ accctctgcttagcagggac	1596
CYP4B1	18	intron6+54	gcctgggttcctcctcctgg C/T ccctctatgcccccctcccat	1597
CYP4B1	19	intron7+(99-100)	agctcttaagcatttcccccc (TC) tttcctcagcaaatataacc	1598
CYP4B1	19	intron7+(99-100)	agctcttaagcatttcccccc　　tttcctcagcaaatataacc	1599
CYP4B1	20	exon8+114	tcctggtttctctactgcat G/A gccctgtaccctgagcacca	1600
CYP4B1	21	exon8+139	tgtaccctgagcaccagcat C/T gttgtagagaggaggtccgc	1601
CYP4B1	22	intron8+247	agaaagttgtcaacaagagg C/T tgatattttgtgtgctaact	1602
CYP4B1	23	intron8+366	tgtgggggtgaacagagctg A/G gacagctgggagagccagtt	1603
CYP4B1	24	intron8+650	cctttgcttgtggtcagaca C/A cctgccttttctctgtgggct	1604
CYP4B1	25	intron8+844	tcatatgtgagaatcccccc C/A ccacggggtatccagacaca	1605
CYP4B1	26	intron8+1767	tcccattccaagaatgttct G/T gttgtgttgctggcagggat	1606
CYP4B1	27	exon9+53	tgtgcatcaaggagagcttc C/T gcctctcccacctgtgccc	1607
CYP4B1	28	intron9+652	agtcggatgtggtcatgaac G/T ctctgtcactggcagtggtc	1608
CYP4B1	29	intron9+774	cctggtcaccaacctctgtt C/T tgcccacaggaagcctgatc	1609
CYP4B1	30	intron10+33	tgggctgggagatcagacag G/T gtgggggactgggagggtca	1610
CYP4B1	31	exon12+224	ccagatggctcaggctgtga C/A ctcoctgggcaccaccctcc	1611
CYP4B1	32	exon12+270	ctggctgtggaggagttggg G/A cccctgcctcaggaggct	1612
CYP4B1	33	3'flanking+129	tctgtgtctcacagtcacgt G/A gtgctccaggcattcagggt	1613
CYP27A1	1	intron1+295	aggagggagctgtcttggga A/G gagagtggcagaggcaaatg	1614

遺伝子名	No.	存在位置	配　　列	配列番号
CYP27A1	2	intron1+17503	cagtgcataaagcctctgat C/T ctccttagagaaggagggac	1615
CYP4F2	1	intron1+(145-146)	ccaagcccctggcaacctca CA/Δ gtgattcaggctgggccttt	1616
CYP4F2	2	intron1+193	tttaatcagtctctctctct C/T tttcccattctaagtgctta	1617
CYP4F2	3	intron1+324	ccctgctctacctccggcac T/C gcccgtccctgcctctccac	1618
CYP4F2	4	intron1+367	tccctggaggtccctgggcc G/C ttctctgggcctcaggatct	1619
CYP4F2	5	intron1+402	ggatctcaccgtccatcccg T/C ctgccctgcaggatgtccca	1620
CYP4F2	6	exon2+35	gcctgtcctggctgggcctc T/G ggccagtggcagcatcccct	1621
CYP4F2	7	exon2+166	cggtgtttcccacaacccccc A/G agacggaactggttttgggg	1622
CYP4F2	8	intron2+125	ggcagagaagcagaggaggc A/G tcttactcattcctctgctt	1623
CYP4F2	9	intron2+440	gggccgtctcccacttccac T/C acacccgaaggcacctttct	1624
CYP4F2	10	exon3+48	gttctgactcagctggtggc C/T acctacccccagggctttaa	1625
CYP4F2	11	intron3+701	agactccaccccagcttggg T/A cccttttcctgacccctgtg	1626
CYP4F2	12	intron3+742	cttcccatcgttggacgggc G/A aggctgagcaggggaatgg	1627
CYP4F2	13	intron3+1020	gctttagctttctccatgtc G/A cttttcctatcaaggtggcc	1628
CYP4F2	14	intron3+1039	cgcttttcctatcaaggtgg C/A cttttcctcatgatgtcaac	1629
CYP4F2	15	intron3+1040	gcttttcctatcaaggtggc C/G ttttcctcatgatgtcaacg	1630
CYP4F2	16	intron3+1920	ccacctgtctaacctctgtt G/C ctgtttgctcatgtctgggg	1631
CYP4F2	17	intron3+1945	ttgctcatgtctggggcgtg T/A ctctacaatggctgttatat	1632
CYP4F2	18	intron3+2621	agcattctgtagaatgctga G/A ctgtgctcaggggttgcgga	1633
CYP4F2	19	intron3+2665	tgttggatcgtgtaggaggc A/G tgtcaaggcatgctggaacc	1634
CYP4F2	20	intron6+194	gggtttgaactggtgggtgt G/T gtcagagctctgtaggggac	1635
CYP4F2	21	intron7+67	tgtgaaatgtcagatgaaag G/A atttgaacttgattaagagg	1636
CYP4F2	22	intron7+2811	ttccaagggaaattgccatt T/G aattctcctgtaactcaggt	1637
CYP4F2	23	intron7+(3096-3097)	ggggtgggggttgggggggg (G) ttactgccttctctccagga	1638
CYP4F2	23	intron7+(3096-3097)	ggggtgggggttgggggggg ttactgccttctctccagga	1639
CYP4F2	24	intron8+145	ggtgctgtctaccttcgggt G/A ctgcagcagcccagcgaccc	1640
CYP4F2	25	exon9+44	ctctcctgggtcctgtacca C/T cttgcaaagcacccagaata	1641
CYP4F2	26	exon11+48	gaacccatcacaacccagct G/A tgtggccggaccctgaggtg	1642
CYP4F2	27	intron12+108	tggtccaagttccagctctc C/T ttccctcacctcctctggag	1643
CYP4F2	28	intron12+285	gcatggggatccaggcacgg A/T taccccccttctctattcctc	1644
CYP4F2	29	exon13+238	aagtgaagcctagaattacc C/A taagaccctgttccacagtc	1645
CYP4F2	30	exon13+342	tgtgcgtgaatgttcatggc G/A gccctatttcacagtagccaa	1646
CYP4F2	31	exon13+563	tagtgtactgtccttttata T/C gaaatttccagaacaggcca	1647
CYP4F2	32	exon13+707	aaatgttccggacctagata G/C tgacgaaggtagcacgacac	1648
CYP4F3	1	intron2+258	cattaatgcacctctgcggg G/T ctcttgggcaggggttggg	1649
CYP4F3	2	intron2+916	ttagggacatgtcctgagtc C/T acactgctccccacaaacct	1650
CYP4F3	3	intron2+3417	atccaggtctcacacagtgt C/T acttcctctcttggctttag	1651
CYP4F3	4	intron2+4090	gagagcatgaattgggtcct G/A tgtotttctctcoagattca	1652
CYP4F3	5	intron3+89	tgtgctgcctccagcgggtc G/A cgtgcccatgtgcagacagg	1653
CYP4F3	6	intron3+243	tcaagtctgctgtacggcta C/T gtcttgtcacctgtatattt	1654
CYP4F3	7	intron3+502	aggtctgggacccagggtcc G/C taagtgaactgtctgagaca	1655
CYP4F3	8	intron3+755	ttttgtggccatgtcaggac A/T tgtgaacacatgtcagtgtc	1656
CYP4F3	9	intron3+855	gggacagacagggtgtccta G/A gtccttgtgaaggcattctg	1657
CYP4F3	10	intron3+970	cctgacatagctcctacgtg C/T catgttaggcagtgtcattg	1658
CYP4F3	11	intron6+122	gaggagttgttatacctgat C/T gttgaaggactggtatgaat	1659
CYP4F3	12	exon7+159	ggtgcacgacttcacagatg C/A cgtcatccaggagcggcgcc	1660
CYP4F3	13	intron7+2107	caggttgccagtgattttttt T/Δ ctcagaaagttttcatcaag	1661
CYP4F3	14	intron7+2255	gaccaagaagggtctaggag T/A gcaagatgggcttgggtttc	1662
CYP4F3	15	intron8+132	cctcaatgcaaggttgctgt A/C caccctcgggtgctgaagca	1663
CYP4F3	16	exon9+59	taccaccttgcaaagcaccc G/A gaataccaggagcgctgtcg	1664
CYP4F3	17	intron9+13	attgaatggtgagtgcaggt G/A ctggtgccctgttcctgagc	1665
CYP4F3	18	intron9+36	ggtgccctgttcctgagcct G/C tctcattggctctgttcccc	1666
CYP4F3	19	intron9+167	acccatcctgactgtctggg C/G aaaggttataggccctagg	1667
CYP4F3	20	intron9+369	tccctaattcctacccttcc G/A tccagtccagggatttataa	1668
CYP4F3	21	intron9+458	tcattcatccatccagtcct T/C gttcagcaaatactctcata	1669
CYP4F3	22	intron10+46	ctcctgggtaggaagaggag A/C ccctcaggcagggagcattg	1670
CYP4F3	23	intron10+63	gggccctcaggcagggagc C/A ttgtcctgactgcccccttc	1671
CYP4F3	24	intron11+14	ccctgaggtgcgggcccccc C/G tctctgtttttgtccattcc	1672
CYP4F3	25	intron11+84	gatcaggagaatccaacatc G/A cctccctccaagacacacac	1673
CYP4F3	26	intron11+113	caagacacacaccactgtct T/C tccaaggctggcggactggg	1674

遺伝子名	No.	存在位置	配　　列	配列番号
CYP4F3	27	intron11+164	cggcaaccctctctggtctc T/G cctccaggtctatgaccccct	1675
CYP4F3	28	intron11+165	ggcaaccctctctggtctcg T/C ctccaggtctatgaccccctt	1676
CYP4F3	29	intron12+156	gaaaaggcccacagagtagg G/A ttgggttggtcctagaagga	1677
CYP4F3	30	intron12+253	gagctcggctaggctcgcag G/T atatgcaagcccacatgggg	1678
CYP4F3	31	intron12+346	tgggtgtcccaggccaggtt A/C ccggcttgatggggccagga	1679
CYP4F8	1	5'flanking-61	accatgtttacccatcattg G/T tcctggagctccccagcccc	1680
CYP4F8	2	exon1+67	gtggcagcatccccgtggct G/T ctcctgctggtggtcggggc	1681
CYP4F8	3	intron1+707	tacgcagcaggtattcacca T/G tatttccacattatccactg	1682
CYP4F8	4	intron1+857	acacccctaccctcacatc G/A tgacacagctgggccagaag	1683
CYP4F8	5	intron1+907	tgccatctccacccticcccc G/A tgcaggggcatcttctttat	1684
CYP4F8	6	intron2+668	tgtggcacttccaccatatg T/C tcattgccctcttgctccag	1685
CYP4F8	7	intron2+818	gccacagagaccatggctca G/A gccccaaaatgctgagtgac	1686
CYP4F8	8	intron2+1079	tatgcttgggtgttgcagaa C/T atgttggaccatgtaggagc	1687
CYP4F8	9	intron2+1194	ccggtcccctttatgcccca C/A accctcctttcttcttctgc	1688
CYP4F8	10	intron5+45	aacatgggatggagtgggggg G/T gtgggtgtgggggagagcaaa	1689
CYP4F8	11	exon8+(19-20)	ggccatgacaccacggccag (GCCAG) tggcctctcctgggtcttgt	1690
CYP4F8	11	exon8+(19-20)	ggccatgacaccacggccag　　tggcctctcctgggtcttgt	1691
CYP4F8	12	intron8+222	tttatttccccactaacttg C/G tatgcaagcttagtaaaatc	1692
CYP4F8	13	intron8+334	cttggagaattaacggcaaa A/T accgcaatgacttttggacc	1693
CYP4F8	14	intron8+1999	ttctaagtacatttattctc T/C tgcttttagctatgatctag	1694
CYP4F8	15	intron8+4184	caggagggccgtgtatgctc C/T ctggataattgttgggtgtt	1695
CYP4F8	16	exon9+119	acgtggtgctcccagacagc C/T gagtcatccccaaaggtgcc	1696
CYP4F8	17	intron11+282	gggttgggggttccgggcct G/C gttcctggcgcagtgggccc	1697
CYP4F8	18	intron11+340	tgcagtcagaccttccacct C/T ggccccaggaactgcatcg	1698
CYP4F8	19	3'flanking+35	atcacctacctttgcaccaa T/C tacctttcagatttccggt	1699
CYP4F8	20	3'flanking+83	ctgtgttggccctgtgcct G/C agtcccgcggatggccagta	1700
CYP4F8	21	3'flanking+90	ggcccctgtgcctcagtccc A/G cggatggccagtaggggcg	1701
ALDH1	1	intron1+564	cattatttcttcagccaagt T/C tgttgccattggagcagatg	1702
ALDH1	2	intron1+710	gttctgagagtaactctgaa C/T tttgcctgtttcacactgct	1703
ALDH1	3	intron1-3868	ccctttttatatccagaata C/G agcctaaacttctttctctg	1704
ALDH1	4	intron2+2933	taagtatgctatactatatt T/C gatagatatactatactata	1705
ALDH1	5	intron2-1646	caatgtgattaactgaatgc C/T gcaaatatgcactgtatatg	1706
ALDH1	6	exon3+54	caggcttttcagattggatc C/T ccgtggcgtactatggatgc	1707
ALDH1	7	intron3+157	taggccccttaacattgaac T/G attctcaaatagtaatctgc	1708
ALDH1	8	intron3+339	tgagtctcctagaatgatat G/A ttaggtttattcaagcattt	1709
ALDH1	9	intron3+655	agcagttagatgagtcagag C/A ataatatagttgggggaggg	1710
ALDH1	10	intron3+735	gaagccaatttaacataaac C/A aataccaagatcaggtttca	1711
ALDH1	11	intron3+863	gcaagtatggttaatcaaag G/A accatttattactcaaatat	1712
ALDH1	12	intron3+1757	agatgacaagatttcttcta T/A ttcaaaaattccctagcaca	1713
ALDH1	13	intron5+90	ttctctaaaacagatggatg C/A ttatgtatttgttaaatgtg	1714
ALDH1	14	intron6+213	caggaagccaaacacaaagg T/C ttggtgtcaaacagtcaact	1715
ALDH1	15	intron6+1323	ttttgaattaaattcttata C/T tgtaacttttaaacttttta	1716
ALDH1	16	intron7+638	gcaaaagaaagtggtggaag C/A atactgtaccatgcaaaaaa	1717
ALDH1	17	intron9+(1462-1463)	aatggaattctatgttttttt (T) gttgtgattatttatctatc	1718
ALDH1	17	intron9+(1462-1463)	aatggaattctatgttttttt　　gttgtgattatttatctatc	1719
ALDH1	18	intron9+1757	tgatctagaatttagtttct A/G taaatgaatagaatccagtg	1720
ALDH1	19	intron12-1383	aatcccacttattactctcc T/G gagagcttcaagtgcctata	1721
ALDH1	20	3'flanking+40	ttttaagtacaagttttggt T/C acagtgatttcttcttgtca	1722
ALDH2	1	intron3+1766	aaattggtggctcatcctgc C/Δ tggccccctcctcctcctc	1723
ALDH2	2	intron8+52	gaaggtagcccctggccacct G/C tgttgtggctccagccgatc	1724
ALDH2	3	intron8+69	cctgtgttgtggctccagcc G/A atcctgtcgccccccagtg	1725
ALDH2	4	intron9+5197	gctttcttatgaccttggtc C/A atttcccagttgtcttgttg	1726
ALDH2	5	intron11+114	gagctgggctcagtttctcc T/C gggtcagggtgtgatgtcga	1727
ALDH2	6	3'flanking+411	ggatatgatttctgcccctc T/C tctgctgtgggtaaacagct	1728
ALDH2	7	3'flanking+(432-433)	tctgctgtgggtaaacagct TC/Δ tgtttcatgcatttacttttt	1729
ALDH2	8	3'flanking+488	ccaataagaatgtgcttgaa G/T gtttcatgcatttaatttgt	1730
ALDH7	1	5'flanking-1455	ctgcctgtccaccacccacag C/T agcttgcacatcatcccccac	1731
ALDH7	2	intron1+464	catgaatgactctgggaaag A/G atcattcttagcaatggact	1732
ALDH7	3	intron1+2269	aaatggaatccaaacagcaa G/C agacctcccctcaccggtca	1733
ALDH7	4	intron2+1349	actgagcttctgccaccggc C/T gcctgccggccttcatgaga	1734

遺伝子名	No.	存在位置	配　　列	配列番号
ALDH7	5	intron2+1820	tccgtgtggaaggcaccttc C/G cccagcctcagtggctagga	1735
ALDH7	6	intron2+2046	aacctcaggcgctgcctcag C/G cagggagccagcctggcccc	1736
ALDH7	7	intron2+2939	aagcacgcactgaacatgga G/A tgagtgagtgaacgaatgaa	1737
ALDH7	8	intron3+7	tgcccaagaacctggtgagc C/T ggccgggctgaggcgggcag	1738
ALDH7	9	intron4+36	gcccctccggtcaccottc T/C cogctcgaggcctcagggcc	1739
ALDH7	10	intron6+(116-117)	attctcctctctctctct CT/Δ ggaccaggctgggagcagtc	1740
ALDH7	11	intron6+263	cagaccctcatacgtgaccc T/C gctgcccccaggctcttag	1741
ALDH7	12	intron6+1298	gtagacagagctggactcca T/G cctgggtgataagggatcc	1742
ALDH7	13	intron6+1411	gccagggtcacaagcagagg C/T gggaggagccaaggggtttg	1743
ALDH7	14	exon7+185	acctgcgtggcccccgacta C/T gtcctatgcagccctgagat	1744
ALDH7	15	exon7+339	tgcggcattgctgggctgc G/A gogtgtggccattgggggcc	1745
ALDH7	16	intron7+249	ccagggctccagggctcagc G/A tgctaagatgaactcccatc	1746
ALDH7	17	intron7+277	atgaactcccatcccaccac C/T ggctatcctgaaaggctgta	1747
ALDH7	18	intron7+498	gaccaaggtcgggggattct C/T tgtgtcccacaggcccgag	1748
ALDH7	19	intron8+14	cagccaggtgggggtgcggc C/T gggctgggcagggtcaggag	1749
ALDH7	20	intron8+49	caggagccgcagtgggcag C/T acaagtggtggcagcagggg	1750
ALDH7	21	intron8+111	tcaggactttgggatggtgg A/T cctcttggctctgtctctgc	1751
ALDH7	22	intron8+3219	atcctgatggggctcaaggc A/G gcctcacgcacatcctgttc	1752
ALDH7	23	exon9+33	gtgctgacccagaccagcag C/T gggggcttctgtgggaacga	1753
ALDH7	24	intron9+948	tcccaggcccccgagctgac C/A cttcttggtggccgtggccc	1754
ALDH7	25	intron9+1067	aggctccccaagcctgggtc C/T ctcttgccccacccactct	1755
ALDH7	26	exon10+137	ccgcaatcgccgcgccgcct G/A aggatgctgctggtggccat	1756
ALDH7	27	exon10+397	cgctcccaaccatgagagcc G/A aggtggaggcatgggaaac	1757
ALDH7	28	exon10+1198	ctcttccccatgctgctcat C/T ctcctgggccccatccactc	1758
ALDH7	29	exon10+1475	cagggggtggacctgagtttc G/A tctcctgtctctctggctga	1759
ALDH7	30	3'flanking+15	cctggcaatacttacatctc A/G gtgatttgctttctgtgcat	1760
ALDH7	31	3'flanking+60	caacaggactctggaccaag G/C cctggcgttgggtaacaat	1761
ALDH8	1	intron1+98	agggaaggggatgtgtgccc G/A tggccogtgggtcaggggcc	1762
ALDH8	2	intron1+157	atggctgcagggccatggg T/C acggggcttgctcaggagag	1763
ALDH8	3	intron1+354	totgtggcagacaaggatt C/G ggtcgggggcaccagggctg	1764
ALDH8	4	intron1+851	tatgacaggtccatcaggcc T/G cacottcctgtgtgtcttat	1765
ALDH8	5	intron1+894	ctcagcatctgccccccacag T/G gcttttgcacacgttggttc	1766
ALDH8	6	intron1-463	aaagaacoctccgagtccct C/G gtttagtcccagaagggagg	1767
ALDH8	7	exon2+61	gccttcaactgagggcgcac G/A cggccggccgagttccgggc	1768
ALDH8	8	intron2+8	ggacctgcataaggtgggcc A/G tggagagtgggccccggcag	1769
ALDH8	9	intron2+23	gggccgtggagagtgggccc G/C ggcaggggctggagcagcgt	1770
ALDH8	10	intron2+(180-181)	ttcactcctgaacactcaca (A) gccacoctgtgatgcaggct	1771
ALDH8	10	intron2+(180-181)	ttcactcctgaacactcaca gccacoctgtgatgcaggct	1772
ALDH8	11	exon3+72	gactacgctctcaagaacct T/G caggcctggatgaaggatga	1773
ALDH8	12	intron8+375	ctgcagcatcctaacctcac C/T gtcgcgactcaaggctgccg	1774
ALDH8	13	intron8+463	aatcaccccatggcacccc G/A accgtcactgagagggtgct	1775
ALDH8	14	exon9+33	atgctggagcggaccagcag C/A ggcagctttggaggcaatga	1776
ALDH8	15	exon10+428	aggtgtcctcactcaccoca C/T cctccccaattccagccctt	1777
ALDH9	1	exon1+121	actgtgtggggtatggcggg G/A tggtagggagaatgtggtgt	1778
ALDH9	2	intron1+67	cgcggatttcccggccagcc C/G ccgtttcctgtgttctgcag	1779
ALDH9	3	intron1+103	tgcagcgttgacttgagcac A/G agacagtgacagtggagagt	1780
ALDH9	4	intron1+1818	gaatttttgagaaaaaaaaa A/Δ tgttcctttagggttgcctt	1781
ALDH9	5	intron2+5891	tcaggaacaggaagtaaaga G/A gtttacatttctaaatttct	1782
ALDH9	6	intron2+6398	atcaaaaacacttgtctgat T/G atcgtgctctgaacctgcct	1783
ALDH9	7	intron2+9677	atgacgctgagtttggtgct A/G ttcttttgttttttcttgcct	1784
ALDH9	8	intron2+9991	gggcgaagtgagggacctac C/T cttggcttctaatctttcat	1785
ALDH9	9	intron2+10198	ttgtcagagacctctttgat A/G atccttacgtactatatcag	1786
ALDH9	10	intron2+10256	ttagtagataacttttttttt T/Δ gtaaggatggagaatastag	1787
ALDH9	11	intron2+11382	catattcaattcttttatgt T/C ctttagaccaaagaaaggca	1788
ALDH9	12	intron2+11455	taaacctttaagctcatcat C/T ggaccatctattgaatttct	1789
ALDH9	13	intron2+12044	atttaaagtgaaagctattt C/T tagttttaaaaattgagcag	1790
ALDH9	14	intron3+334	ctatttagcaaacttttttt T/Δ gacagtgtataaagttttca	1791
ALDH9	15	intron3+368	gttttcaacaattgatattg G/Δ aaggttggtagggcctagga	1792
ALDH9	16	intron4+191	ccctcaaggagcttatagtt T/A aggttgtacacaatcatgtc	1793
ALDH9	17	intron4+557	tagaaaaaattgtaatgtta A/G aaagcattactgttaggaca	1794

遺伝子名	No.	存在位置	配　　列	配列番号
ALDH9	18	intron5+830	agttcaagatgattttgtag G/C ttcagggcctagttgacttа	1795
ALDH9	19	intron5+838	atgattttgtaggttcaggg C/T ctagttgacttagcatgcaa	1796
ALDH9	20	intron6+120	agaaaagttgcacaaatagt A/C caaagaattcccatgtacct	1797
ALDH9	21	intron6+2569	attaaaatctgctttaaata T/C ttttttgggggagaggacac	1798
ALDH9	22	intron8+1414	ccgatcttcaaaaaattagc T/C gggggtggtggtgcacactg	1799
ALDH9	23	intron9+664	aaagttcacatttttttttt T/Δ ataacttcatggtcaagagc	1800
ALDH9	24	intron9+2170	taatgcacacatttttttttt T/Δ cttcatagggacatccaacg	1801
ALDH9	25	exon11+587	aaaacaaaaaacaaaaaaaa A/Δ ccttgttcctttataggttc	1802
ALDH10	1	intron1+39	gggtgtggggaaactggccc C/T cgccgcgcacttgtggactg	1803
ALDH10	2	intron3+2491	tgccgcgaagaaattggcac T/A gctgagttctacatgcagtt	1804
ALDH10	3	intron3+2595	ttctgtacatcaacttgtga T/A ggattgaggccagttctggt	1805
ALDH10	4	intron3+2775	taccgctttgcccctgacca G/A gggtaaattcttcaataact	1806
ALDH10	5	intron3+3424	aggcacttctgcacacaccc G/A cgtctcatgcattttccctg	1807
ALDH10	6	intron3+3676	atgttgaagagattgctgat G/A ttagacgttaggatttattt	1808
ALDH10	7	intron4+481	tagaaaataagaggtttcag G/T ttctctctgctaaatccggt	1809
ALDH10	8	intron4+769	atcctgctttatacctgaac G/A tcttgcaggcagagccaaaa	1810
ALDH10	9	intron4+796	aggcagagccaaaagccaca A/G ccaggagagtctgtaccgaa	1811
ALDH10	10	intron5+254	attagttgtggcatatactt T/G ttttaaaaaagttaaataat	1812
ALDH10	11	intron6+137	aatcctgctttctggtatac T/C gtacctgtagcttttgttat	1813
ALDH10	12	intron6+923	aggctaatgaatggtaagag G/A aaggggctatcctgattagc	1814
ALDH10	13	intron7+331	tgcttttctgatgttaatcc A/Δ cagggcattgctgaataaca	1815
ALDH10	14	intron8+643	tttagaacatgacctgcctg C/T ctctcccacatgtgagatga	1816
ALDH10	15	intron8+666	ctcccacatgtgagatgact G/A actcagcttttttatttctcc	1817
ALDH10	16	intron9+2129	tgttttcatttttaaaaaaa G/T gtttgactttggaattcatg	1818
ALDH10	17	exon10+(1894-1895)	ttggcttgtctactaatacа CA/Δ tctgcttcaaaatgaacata	1819
ALDH10	18	3'flanking+31	gtatttgtcaacttttttttt T/Δ ctcattttaaaattcttagc	1820
ALDH10	19	3'flanking+106	gtgtgttgggggtggtggtt G/A gtagctatagtaaataggtt	1821
ALDH10	20	3'flanking+1630	aaaagcacgtgggaaacaca A/G ttaatcatgtcttaccgtat	1822
ABCC7	1	5'flanking-834	gctaaaacactccaaagcct T/G ccttaaaaatgcgcactggg	1823
ABCC7	2	5'flanking-729	cctcctgcagattttttt T/Δ ctctttcagtacgtgtccta	1824
ABCC7	3	exon1+125	tagcagggaccccagcgccc G/C agagaccatgcagaggtcgc	1825
ABCC7	4	intron1+8200	ctatgtgagacgttaagaag G/A tagaggtggccaagaaggaa	1826
ABCC7	5	intron1+7538	agttctctttcttagcatgg C/A ctacagaggtgcaactacct	1827
ABCC7	6	intron1+13519	gaaacttaaatcttgagtca T/C acaattgtgtctacatactg	1828
ABCC7	7	intron1+14110	attacacagtatttttttttt T/Δ aattttggggaaagtcgatt	1829
ABCC7	8	intron1+14293	gccaggcagattcctgactc C/Δ tataacccagagcttatcag	1830
ABCC7	9	intron1+14316	taacccagagcttatcagag C/G atttatgtccccaaagagaa	1831
ABCC7	10	intron1+14433	cagaataacaatgatggctc G/A gaaaaatatgggtatttctg	1832
ABCC7	11	intron1+14824	acgttttgacagttgcacaa G/C tttctttctttaagctttaa	1833
ABCC7	12	intron1+23401	aatatttttgaaaatcacta C/G ggtatcctgcatagtgattt	1834
ABCC7	13	intron3+879	gaaaaatttcagttcatcca C/A ccccatgaaaaatacattta	1835
ABCC7	14	intron3+922	acttatcttaacaaagatga G/C tacacttaggcccagaatgt	1836
ABCC7	15	intron3+933	caaagatgagtacacttagg C/T ccagaatgttctctaatgct	1837
ABCC7	16	intron3+13704	tttttccaaataaaaaaaaa A/Δ tcaggtgatatctgtaaatg	1838
ABCC7	17	intron3+13758	tattaaagaacatgatgctt A/G aaacagattagggaaaacta	1839
ABCC7	18	intron4+240	ctctgttgtagttttttttt T/Δ ctcctaatcatgttatcatt	1840
ABCC7	19	intron4+376	ttatgttcagcaagaagagt A/G taatatatgattgttaatga	1841
ABCC7	20	intron4+586	tgtccagacaagagccaaa T/C tgccgaggcatcatttaggt	1842
ABCC7	21	intron4+1089	tttcaatctgaacattttac G/A taagtgaagactttgttaga	1843
ABCC7	22	intron4+1615	aaagttaggtggtattgtat C/T tgtcttcctttctcaatgtt	1844
ABCC7	23	intron4+1946	aatacaaacaaacttgagct T/C tgcctatacttttcaagaat	1845
ABCC7	24	intron6+783	tatctaagttttggagtcaa A/G tagcactttgtttgaatccc	1846
ABCC7	25	intron6+(1128-1131)	gattgattgattgattgatt GATT/Δ tacagagatcagagagctgg	1847
ABCC7	26	intron7+(731-732)	gtagcaatgagaccattttt (T) cttcagttgagctccatgtt	1848
ABCC7	26	intron7+(731-732)	gtagcaatgagaccattttt cttcagttgagctccatgtt	1849
ABCC7	27	intron7+1434	gaatgtttggttgtaacctg T/C ataatctggcatgaaattgt	1850
ABCC7	28	intron8+752	catgctctcttctcagtccc A/G ttccttcattatatcaccta	1851
ABCC7	29	intron8+1109	tatggccaagacttcagtat G/A cgtggacttaattcttcctt	1852
ABCC7	30	intron8+1312	atgaagacattcatttttit T/Δ ctccgtccaatgttggatta	1853
ABCC7	31	intron9+(6521-6522)	gtgtgtgtgtgtgtgtgtgt (GT) ttttttaacagggatttggg	1854

遺伝子名	No.	存在位置	配　　列	配列番号
ABCC7	31	intron9+(6521-6522)	gtgtgtgtgtgtgtgtgtgt　　ttttttaacagggatttggg	1855
ABCC7	32	intron10+2119	gaacactttatagtttttttt T/G ggccaaaagatctagctaaa	1856
ABCC7	33	intron11+3867	ttttttcttcaagaaattaga A/Δ gaggggagaaattggtttaa	1857
ABCC7	34	intron11+11844	tgaatcaaaatcatctaaaa A/Δ gctttcagaaaccagacttt	1858
ABCC7	35	intron11+12144	atatttaaacagagttacata T/C acttacaacttcatacatat	1859
ABCC7	36	intron11+20975	gtgtggatagtaaatgccag G/A gtaaatcacatagcatctaa	1860
ABCC7	37	intron11+27057	atggaagagaagttttagta G/A aggggaggaaggaggaggtg	1861
ABCC7	38	intron11+27131	gagagagacttttttttttt T/Δ aaggcgagagtttactacct	1862
ABCC7	39	intron13+152	gtattaactcaaatctgatc T/A gccctactgggccaggattc	1863
ABCC7	40	intron13+287	tttgcagtatcattgccttg T/C gatatatattacttttaatta	1864
ABCC7	41	intron15+(85-86)	atacatatatatgcacacac AT/Δ aaatatgtatatatacacat	1865
ABCC7	42	intron15+106	taaatatgtatatatacaca T/A gtatacatgtataagtatgc	1866
ABCC7	43	intron15+3341	ggaagtataaatttgtaaat A/C actgagacccaaacttacaa	1867
ABCC7	44	intron15+5556	tgctattgactaatagtaat A/T attttagggcagctttatga	1868
ABCC7	45	intron15+5919	tggtagttctatgtggaaac C/A gtgaggaaataattttatat	1869
ABCC7	46	intron17+2479	caaaaaggtatggaagtcag A/C ggagaaggagaccccctatgt	1870
ABCC7	47	intron18-81	aagtatgcaaaaaaaaaaaa A/Δ gaaataaatcactgacacac	1871
ABCC7	48	intron19+751	cattaataaaataacaaatc A/G tatctattcaaagaatggca	1872
ABCC7	49	intron19+820	tgacatttgtgatatgatta T/C tctaatttagtctttttcag	1873
ABCC7	50	intron21+1532	ttacctttaactttttttttt T/Δ agtttgatcaagctctcttta	1874
ABCC7	51	intron21+1607	atgottttggagttgggtct C/T ataaatgtatagaaatgttt	1875
ABCC7	52	intron21+11260	atgtggaacaatcatgacta T/C atgccttttacttictctat	1876
ABCC7	53	intron22+(130-131)	agaatcaatattaaacacac AT/Δ gttttattatatggagtcat	1877
ABCC7	54	intron23+1828	ctgtcctaaagtttaaaaag A/Δ aaaaaaaaaggaagaaggaa	1878
ABCC7	55	intron24+(7100-7112)	cctttacaaactcttagaca (T)12-14 agtttaacatgttacaaaac	1879
ABCC7	56	intron25+237	actcttccccttgtcaaca C/T atgatgaagcttttaaatac	1880
ABCC7	57	exon27+115	gggtgaagctctttccccac C/T ggaactcaagcaagtgcaag	1881
ABCC7	58	exon27+334	ggatgaattaagttttttttt T/Δ aaaaaagaaacatttggtaa	1882
ABCC8	1	5'flanking-1099	aaaggggctgaaggggtctt T/C cttttgtgttccccctgactg	1883
ABCC8	2	5'flanking-(424-422)	caccccaccaccaccaccac CAC/Δ aaggtaacgttctgccccac	1884
ABCC8	3	intron1+1212	agcctgggcaacatagtgag A/G ccccccccgcccttttctaca	1885
ABCC8	4	intron2+1003	aggaggactgtgaatcccag C/A ctgcatgtttgggtcggatt	1886
ABCC8	5	intron2+1253	catctcactaaggaagaatc C/T agtaaccagcaaggatgaga	1887
ABCC8	6	intron2+1382	cccagactgcactcctgcag T/C gctgcctggctcctgtagtt	1888
ABCC8	7	intron2+2371	tttcagagctgtctggaaat T/A tagggggcaggtgggcgggg	1889
ABCC8	8	intron3+1957	ccctacccctagcccagggg C/T ccccacatgagtatgaatgg	1890
ABCC8	9	intron3+(2088-2089)	agagaaccottcattaacca (CCA) gggcgtggctgaccagtgtc	1891
ABCC8	9	intron3+(2088-2089)	agagaaccottcattaacca　　gggcgtggctgaccagtgtc	1892
ABCC8	10	intron3+2204	taaagcacaagttatcaccc G/A tggatggatttgtccttttc	1893
ABCC8	11	intron3+2286	ttatctcccottgaaaggac A/G ctccacagagccagaaattc	1894
ABCC8	12	intron3+2312	cagagccagaaattctagaa C/G agggaaaagtggaggggagg	1895
ABCC8	13	intron3+2356	ctgtgaactgcagggacaga A/G ggaaatgggtattgggagaa	1896
ABCC8	14	intron3+2359	tgaactgcagggacagaagg A/C aatgggtattgggagaatgg	1897
ABCC8	15	intron3+2370	gacagaaggaaatgggtatt G/A ggagaatggccagccctcca	1898
ABCC8	16	intron3+2382	tgggtattgggagaatggcc A/G gccctccaaggggctgatgt	1899
ABCC8	17	intron3+4910	ggggacagccttcagctgtg G/A aattoctocagtcctagaga	1900
ABCC8	18	intron3+4969	cattcttccagtcctgaggc A/G tgagagcagaaggccgatgc	1901
ABCC8	19	intron3+5003	ccgatgcttctgccctccat C/G ctaatgtcctcctgcaggga	1902
ABCC8	20	intron3+5019	ccatcctaatgtcctcctgc A/C gggacoccaggtggatggca	1903
ABCC8	21	intron4+14	ggtgaggtaagcaggccac C/T tgggccagggtgggtggga	1904
ABCC8	22	intron4+167	agacactgcatctggcccac G/A tgtgctctaccccagggtcc	1905
ABCC8	23	intron4+204	cacgtgtgctctaccccagg G/C tocagagggagagggggt	1906
ABCC8	24	intron4+254	gttcgctgaggttggcggat G/A actttccgtagaaagggaag	1907
ABCC8	25	intron4+357	tgtattcatatcgtcacgct G/C gtaaatgaatgagtaagtgt	1908
ABCC8	26	intron5+92	ggcattaggtcaaaatcctg G/A tgggacaaaaggggaaactg	1909
ABCC8	27	intron6+4205	tctgtagaaagtacatgggg G/A catgaagatcattggcttga	1910
ABCC8	28	intron6+5519	gattcccagggaatgttaaa A/C aggaccgggtcttcctaaac	1911
ABCC8	29	intron6+5575	tctgacccagtaccagccag G/C ggggcaagtttccatcccc	1912
ABCC8	30	intron6+6587	gttgccatctgagatcttgc C/T ggaagtacacaagagaccct	1913
ABCC8	31	intron6+6747	ttccactggcctttctgct C/T agtaattgctacattacagg	1914

遺伝子名	No.	存在位置	配　　列	配列番号
ABCC8	32	intron9+191	gaggaagctgcctcccggtg A/G ggacaggaagcgggcatggc	1915
ABCC8	33	intron10+1983	cccaggagtccaacctccct T/G tgtccagctagaccatggtg	1916
ABCC8	34	intron10+2724	cctgggacatgttttcttat A/G taaacagcatcaaaagatgt	1917
ABCC8	35	intron10+2938	gcccgcccaggactcctcac G/C tgtccaagtcacctagggag	1918
ABCC8	36	intron10+3094	tccgaggatgtgttttttttt T/Δ ccctccgttagtcagcagtg	1919
ABCC8	37	intron10+3368	tcctgctcatatgcggcacc A/G tcagacttctgggcaggcaa	1920
ABCC8	38	intron10+8897	ggtattgattaaaagcctca C/T gggcagagaaattcgccatc	1921
ABCC8	39	intron11+308	tgtgtattgtagaagtgatg G/A gaaatccagaacagaaagct	1922
ABCC8	40	intron11+1171	gccctctcatttcccttcca G/A tgctgagcgtttccagtgtg	1923
ABCC8	41	exon12+7	gcctctgtccacagactttc G/A tgggccacgtcagcttcttc	1924
ABCC8	42	intron12+356	accaagaatgaggccatccc G/T tcccccacgtggctgccccat	1925
ABCC8	43	intron12+934	tgggttcaaagatggaatgg G/T gcataactcagcaaaattat	1926
ABCC8	44	intron12+1370	gggagggaggctggacaggg C/G atgaaggcagagcctggtgg	1927
ABCC8	45	intron15+412	ggaggtgggacccaggatgg C/T gtttcttgggaccacaagga	1928
ABCC8	46	intron15+688	actccccccggccccactcac A/G tctgccaccttcctcctctg	1929
ABCC8	47	intron16+4464	actcattccaagtattgatc G/A agaagagaggtaggtactgg	1930
ABCC8	48	intron16+4574	ttgaagatcttaagttgttt T/C tggttcactcatttcgcaaa	1931
ABCC8	49	intron16+5011	agctaaaagcaaaacagcct C/T tgacctggcaagcattccca	1932
ABCC8	50	intron16+7608	tgtcctacttttctttttgac C/G cttataacttcctgacttcg	1933
ABCC8	51	intron16+7730	ccagctcctagtgggctgga G/A ggaaggacatgcggttgggg	1934
ABCC8	52	intron16+8369	ttgcaaactgagttagggcc T/C ggagagcttactgtgtgctg	1935
ABCC8	53	intron16+9708	tgcacttgccgcctacttat T/G ccagacccaatgattgggtc	1936
ABCC8	54	intron17+651	tatagattaatgaggctctg A/G gtcctcaaaaccttcccte	1937
ABCC8	55	intron17+692	cccttacctctccaaaaaac A/G cttgagataccctagaggtg	1938
ABCC8	56	intron17+1541	ctcaggatcttcctggagga C/T atggttcactcccatgagag	1939
ABCC8	57	intron18+580	actaagcagatttctaccaa C/T tgcacctccccatcccctg	1940
ABCC8	58	intron18+658	gaacaagccccctgagaatgc C/T ttccgcaccccctactcccgc	1941
ABCC8	59	intron18+660	acaagccccctgagaatgcct T/C ccgcaccccctactcccgcc	1942
ABCC8	60	intron19+93	gcccttccatcgatcaccca T/C acccagccatctcactcccc	1943
ABCC8	61	intron19+123	tctcactccccaggtgctta T/C ctgcactccagcctctccat	1944
ABCC8	62	intron19+219	cataggggagaggcaggaa C/T ggagggaagggagagagccc	1945
ABCC8	63	intron19+845	tagtatttaacctgcccaaa C/T gctgtgtgaagtgctgacct	1946
ABCC8	64	intron20+338	tcccctccacaagcttagac A/G aacaggattctcctgtgact	1947
ABCC8	65	exon21+10	tttggtgacagggcatcaac C/T tgtctggtggtcaacgccag	1948
ABCC8	66	intron21+192	caaggatagcacaaatgccc C/Δ attgcagacttcagatggag	1949
ABCC8	67	intron23+17	gaaggtgggtatatccaggg A/G tggccaagcagccaccccctg	1950
ABCC8	68	intron23+67	gttctgctagaacctgaact C/T ataaaggtcttcctgtcctt	1951
ABCC8	69	intron26+268	gtgagcgtctgcacatccaa G/C taaagattgttttctcctcc	1952
ABCC8	70	intron26+308	cgataagtgggtgtaatttg C/T ccatccccacccatgagttc	1953
ABCC8	71	intron26+348	cagctccctgccctcccctc A/G ctctctctcctcagccagc	1954
ABCC8	72	intron26+807	gacagctgctgagtcaggcc G/A agccggcagctgagaaaggc	1955
ABCC8	73	intron26+834	cagctgagaaaggcggcagt G/C gtcagatgggcttgagaaac	1956
ABCC8	74	intron28+(118-121)	cctccaaaaaataaaaacaa AAAA/Δ cagaaatgaaggaaatagaa	1957
ABCC8	75	intron28+1348	tggggtaagcggaagacggg G/A ttgaacgctttgagtttggt	1958
ABCC8	76	intron29+1253	ctcttagggatcttgtctaa G/T taaagaagagcggcgcaaag	1959
ABCC8	77	intron29+1589	cagatcccagcttcctgtaa A/G cagcctcagatcaggccaaa	1960
ABCC8	78	intron29+2322	gcgcctcacactcctataac G/A cgcacatgccctgatgcaca	1961
ABCC8	79	intron29+2348	atgccctgatgcacacacat T/C ttcaacacgcacttactcta	1962
ABCC8	80	intron29+2418	agacacgtcaccctcccaca C/T gtctccaccctgggggtgtg	1963
ABCC8	81	intron29+2494	tcagtcccctcagacacatg C/A cctctctccacgcagagaca	1964
ABCC8	82	intron29+2735	gcggccaaggagagtgatga C/T ggcagccaggttgatcaga	1965
ABCC8	83	intron30+386	gctcctggggctccagcctt C/T gcagccctgtgtgtgtctg	1966
ABCC8	84	intron33+93	ggcttcgcagtcacctcgtg G/T ccctccagggccgaggcctc	1967
ABCC8	85	intron33+358	agggacctgggggcagacag C/T gaggccaccccttgtattgag	1968
ABCC8	86	intron38+54	cccagggacaggactggcct G/C ttgtggcgtcatcagtgca	1969
ABCC8	87	intron38+466	aggacattctggccacatgc C/Δ tcatcctcctcctccaagcc	1970
ABCC8	88	intron38+529	tggccccccaccgcgggtggt A/G ttcccaccatcctgacccgc	1971
ABCC9	1	intron3+38	tgttgtttctccttaaagag C/A tatttgtttttccccccaaa	1972
ABCC9	2	intron3+305	gctggccttctggcttgcag T/A agttgtattttaagaatcag	1973
ABCC9	3	intron3+320	tgcagaagttgtattttaag A/G atcagagctcttgtgaggag	1974

遺伝子名	No.	存在位置	配　　列	配列番号
ABCC9	4	intron3+631	ttctgtggaaatcagaggct G/C tctaaaatattcctaatttt	1975
ABCC9	5	intron3+8644	tggacgcactcaacattttc A/G agttattactccttcaactc	1976
ABCC9	6	intron4+757	aggatatcatgaaacactga A/C tcttagtaaaaactatcttt	1977
ABCC9	7	intron4+1022	tactgtggaatttttcttgc A/C acagagatatgtatttttca	1978
ABCC9	8	intron5-1217	cagtggtagatgtgttttct A/G ttgccatcatctacaaatat	1979
ABCC9	9	intron6+(106-107)	tatgagttgttcaaataggc (T)7-9 cagagaattgaatgctttct	1980
ABCC9	10	intron6+1347	tcagtcgtattcctactaaa A/Δ caaaatttgtaagttatgt	1981
ABCC9	11	intron6+1618	ctttttatttgctgcttacc G/A ttttactaaggttggatata	1982
ABCC9	12	intron6+1835	cttttaataaatgcaaactg C/T acacctggtctataaaaaga	1983
ABCC9	13	intron7+407	cctatagaatttttctttttc T/G tttttctcaaaaaaattaaa	1984
ABCC9	14	intron7+423	tttctttttttctcaaaaaaa C/T taaatgtttgttatttattt	1985
ABCC9	15	intron8+743	ttctgtagatgaagcttaag A/T gctagatcttatttgaaaaa	1986
ABCC9	16	intron8+850	tttttaacttattgtttgcc T/G tttcatttttaatagaaaa	1987
ABCC9	17	intron9+585	cgaatttgctgcttttagag A/T aatctttgcaaataataaaa	1988
ABCC9	18	intron9+1394	atttttcttcttgtaagtat G/C agtgatagagctgactgcag	1989
ABCC9	19	intron12+1167	atttgtaagacttttaaaat G/A agataattgtgctggtgtct	1990
ABCC9	20	intron12+1195	tgtgctggtgtctatatctt A/G ctgagaaaactagaatttat	1991
ABCC9	21	intron12+2123	ataagtgctctcccagtgtt G/A attggacttagagcatttttc	1992
ABCC9	22	intron12+(2653-2656)	caaaacagaataatgaaaag TAAC/Δ tattatctaaaataataaaa	1993
ABCC9	23	intron13+(3043-3044)	aacatactctcctcctctct (CTCTTT) aagtcaaaatatattagtat	1994
ABCC9	23	intron13+(3043-3044)	aacatactctcctcctctct (CT) aagtcaaaatatattagtat	1995
ABCC9	23	intron13+(3043-3044)	aacatactctcctcctctct aagtcaaaatatattagtat	1996
ABCC9	24	intron14+85	ttctgtgaaagtgtcccaaa T/A tgtgcctttaaattgttttt	1997
ABCC9	25	intron14+275	agtgtcacatgtatttttttc T/C ggtattcctatgtttatcaa	1998
ABCC9	26	intron14+453	ctcatttcaaacttggctat T/C tggactctccccaggcattg	1999
ABCC9	27	intron14+3709	atcccctagtgatgtacact G/A agcttgcctccatctttcct	2000
ABCC9	28	intron14+3813	otgatttatatattagotga C/T tttccaagttcagacatcta	2001
ABCC9	29	intron14+4000	ttctttacttcaatgtagc A/Δ ccaaatcagaaggtgacatt	2002
ABCC9	30	intron16+1466	atcccactggatttaattac A/C ttgtgtagcttgtacaacca	2003
ABCC9	31	intron16+5357	attttggaaggagaaattata T/G aacottccacaactgaattt	2004
ABCC9	32	intron17+1368	aatcctggtgttttttttt T/Δ ctttttcatttttcagtagg	2005
ABCC9	33	intron20+98	aagtaactcaaggaaagatg G/A tttaacttgtgaaatcgtaa	2006
ABCC9	34	intron22+28	ctcatagttcagaagagttc A/C gagoccaattcagaagagtt	2007
ABCC9	35	intron22+194	tgaacctataaaattctaat G/Δ ccatctttggatgaggtgca	2008
ABCC9	36	intron22+1370	ccagggacaaaagaagatga C/T gtaaacttaaggattgggac	2009
ABCC9	37	intron22+1487	agcaagccaggaagaaagtc C/G atteagttgtatttagaaat	2010
ABCC9	38	intron23+(455-462)	atagccatgaaggataagaa AATTAGAA/Δ tgccatttgt tatgtttcag	2011
ABCC9	39	intron24+(460-465)	aactctttctcttcatctgc TTTAAAA/TTTTAA gcaagccttg aaggagagtg	2012
ABCC9	40	intron24+595	gcatgcaaaataatgaagaa A/G acaatcttgtctgacattga	2013
ABCC9	41	intron28-926	aaatatttcagaatttgggg G/A tgtagagcatttgccgtcat	2014
ABCC9	42	intron29+2692	cttgtaagtctttttttttt T/Δ aaagtaatgaaaatttctaa	2015
ABCC9	43	intron29+5464	agacaacactgcttttttgt G/A tgttcacaattcaacgacag	2016
ABCC9	44	intron29-1830	aactggctgaaaggaaaaaa A/T tcatattgctgtaaatattt	2017
ABCC9	45	intron31+102	tgcttttgctttccacttca G/A tatccagaaaactctctcat	2018
ABCC9	46	intron33+877	aacatggaactatagtaaat A/G tagtttttttggggttcaga	2019
ABCC9	47	intron36+1281	aatttacactttttttttttt T/Δ gcaggagaatatttttgcaaa	2020
ABCC9	48	3'flanking+197	aatggagctcatgcatgtgt T/G ttcaaatatatacatgcaaa	2021
CES1	1	5'flanking-983	tatttccttagccagcggta T/C cacagtgtgtttagtgaatt	2022
CES1	2	5'flanking-814	tcacattgccttgacatcac A/C cctactgctcctccaccota	2023
CES1	3	5'flanking-248	agtcctgcaagggtgacacc G/Δ ttatgccacaagcagttggg	2024
CES1	4	intron1+22	tgagtccttctgaagtcaaa T/Δ atgcggggcacttttgaaa	2025
CES1	5	intron1+30	tctgaagtcaaatatgcggg G/T cacttttgaaatccttgtt	2026
CES1	6	intron1+1652	aagggaatccctgagctgag C/A atgaccagcccagtggtttc	2027
CES1	7	intron1+1726	cctcoctgaagtcctcagca A/C tcttagctggttcctcgccc	2028
CES1	8	intron1+2716	tgottccaaggaagttcatc T/G cagtattatttgtaattagc	2029
CES1	9	intron1+(2747-2749)	tgtaattagcaacaacaaca AAA/Δ gaaaagaagctaaatattga	2030
CES1	10	intron1+3288	ttatttgtccattaaagaaa A/Δ ctcaagcgcttagcctggca	2031
CES1	11	intron1+3691	gagaatatgggacacccctt T/G ttcatcctctcatccagcat	2032

遺伝子名	No.	存在位置	配　　列	配列番号
CES1	12	intron1+3819	tccttcttgcatttatttttt A/G gctggatgtttttatgcctc	2033
CES1	13	intron1+3880	aaccagctcaatgggttagg G/A aggacattgatcgtcatccc	2034
CES1	14	intron2+74	gagtcaaggcagtccccctga T/C gggctgatcctttgctctgg	2035
CES1	15	intron2+552	atggaaggtgtgtccattca C/A cctggccaagctgggaagaa	2036
CES1	16	intron2+885	cagtattttagatggtaaag T/C attatgatgtaatatattgt	2037
CES1	17	intron2+2001	ttggcatgtcagggctgcaa G/A actcatgtagaaatcactcc	2038
CES1	18	intron3+2119	cgctgagtgcatgaatagtc T/C aggcttgagggtgatgggag	2039
CES1	19	intron4+127	taaggcatccaagccccttc G/A taattggcacctacctaccc	2040
CES1	20	intron4+347	tctgtcatgacacttagcag T/G cagcccagcaggtgaaggtt	2041
CES1	21	intron4+(1984-1985)	tgtggtcctgaaggtcctgc (C) tgacatctctgctccccacc	2042
CES1	21	intron4+(1984-1985)	tgtggtcctgaaggtcctgc　　tgacatctctgctccccacc	2043
CES1	22	intron5+766	gaggtgggcagagggtcagc T/C cactactggattcctcagtc	2044
CES1	23	intron5+825	ggagtagatctagcctggaa T/G agcgagtgagtcactgaccc	2045
CES1	24	intron5+828	gtagatctagcctggaatag C/T gagtgagtcactgaccccac	2046
CES1	25	intron5+868	ctcctgagcatgaactctcc T/A cccctccactctgctgtcag	2047
CES1	26	intron7+68	acttcttcatttcagctgtc C/G tcttgcccagggacagtttc	2048
CES1	27	intron7+681	cctccaaaatcaacaatcca A/G ttatcgcctgtctgctagtt	2049
CES1	28	intron7+885	aggaactatccaaagagaaa T/C acattcatatacttcgcagg	2050
CES1	29	intron7+2151	gtcgtgtaaactgaaaatct C/G aggagttgatggcttcaggc	2051
CES1	30	intron7+2470	atatagatatacgaattcac G/A gagtgatgcgggaagaacct	2052
CES1	31	intron8+128	cgtgtttgtttctgaggccc A/C gagaggggtagtgactcacc	2053
CES1	32	intron8+2618	cctgatggcaacacatgagt T/C gggctctctctaatctgtga	2054
CES1	33	intron8+2665	aaaaattattcatcaaaggt G/A aaacctaaaattaagacatg	2055
CES1	34	intron8+3785	ccatggcgcatggccatgcc G/A gtctatggtactggtctcac	2056
CES1	35	intron8+3791	cgcatggccatgccggtcta T/C ggtactggtctcaccctcag	2057
CES1	36	intron10+222	gtgggctggagaagctgcat C/T gctcacccggggctggtggt	2058
CES1	37	intron10+230	gagaagctgcatcgctcacc A/C ggggctggtggtcacttttt	2059
CES1	38	intron11+1177	ctagcaggtgccctgacaca C/G ctttgcacaggaaggggcag	2060
CES1	39	intron11+1311	gccctatgctctgcgtctga A/G ctatatatagagttcccatc	2061
CES1	40	intron11+2025	ttctcatttgggatgctaag A/G ttaaaaattagcataacact	2062
CES1	41	intron11+2029	catttgggatgctaagatta A/C aaattagcataacacttcca	2063
CES1	42	intron11+2317	cattcacaaaagctctttct T/C ctatggttggctctgagttt	2064
CES1	43	intron11+3887	caaatatttggctctaattc C/T gcttccacctcagcagcgta	2065
CES1	44	intron12+2311	gcgcctctgggcatctcact G/A tgcatgcttaggcgccttgc	2066
CES1	45	intron12+2331	gtgcatgcttaggcgccttg C/G ggctctgttgtttttcagaa	2067
CES1	46	3'flanking+71	aacggtgatgaaagaggcga T/C gtgagaaggaaggtggcttt	2068
CES1	47	3'flanking+362	ttgcatggcacttactgacc G/A ttgcacaggcctgcaacacc	2069
CES1	48	3'flanking+581	atttctggattctgttagta C/T gtagaaagctctaaagcatg	2070
CES1	49	3'flanking+1348	aaatctgctgctgggagaga G/C agcaaagcatgcagatcaac	2071
ABCB4	33	intron22+767	acagtgggctgatgcataga A/Δ cctgtagcaatccaccagca	2072
AADA	23	intron2+46	tgtcactgaggtagttcgca A/G acattttactaagtcttcag	2073
AADA	24	3'flanking+208	aatgctaaaaaaaaaaaaaa A/Δ tcactgtggtactttgggga	2074
ABCA4	1	5'flanking - 1005	tgccatcataagcagaaact A/C tctctctcttcttggaagct	2075
ABCA4	2	5'flanking - 819	gtctagagtctttcaaagag A/T acacattctgagatttgagg	2076
ABCA4	3	5'flanking - 680	agcaccacccccattgcaggg C/A tggaatgacagtaatgggcc	2077
ABCA4	4	intron1 + 208	tgccccttcccaggaagatgt G/A tttctctgtcctcagccaca	2078
ABCA4	5	intron1 + 234	ctgtcctcagccacatgaaa A/G tcttttgcctaccgtgcctg	2079
ABCA4	6	intron1 + 510	agctcacgatcaagtcacag T/C ttaactggacacattatttt	2080
ABCA4	7	intron1 + 1527	gcttaacaaccagcataaaa G/A agagcgcgatgggacacgct	2081
ABCA4	8	intron1 + 2077	caggactgtagctgctggcc T/C aaaatgagcccattcctgtg	2082
ABCA4	9	intron1 + 2174	ccctctcaatctggccttta G/C ctggcatgggtgggcgactc	2083
ABCA4	10	intron1 + 2246	gctcccagggagatggagcc A/G ctcgggctgagggccttggc	2084
ABCA4	11	intron1 + 2364	ttctgtctggcacgcctccc G/A atggctcccacctgctacc	2085
ABCA4	12	intron1 + 4243	ctccctggggtatgcctgta C/G gcagttaagcgtcaaggaca	2086
ABCA4	13	intron1 + 4287	atgccgctctgggagaggga A/C gctgagcatgattttggaag	2087
ABCA4	14	intron1 + 4309	ctgagcatgattttggaagc C/T ggcagaagaggctattgtga	2088
ABCA4	15	intron1 + 4416	tgcagcaacgcccccgccc C/T ccgccaaaaacaaacacact	2089
ABCA4	16	intron1 + 4996	tttaccccctggaacaggcag G/A ccaagctggctggtcccctc	2090
ABCA4	17	intron1 + 5007	aacaggcaggccaagctggc T/C ggtcccctccctgatacaca	2091
ABCA4	18	intron1 + 5080	gtgtgtggctggtttcttag C/G aagcaccatggttccaagtt	2092

遺伝子名	No.	存在位置	配　　列	配列番号
ABCA4	19	intron1 + 5152	gggagatgaacgtaagtgga G/A ggcaggcctacaaggttgca	2093
ABCA4	20	intron1 + 7110	ccactggatctgcttttgga A/G tcaagagtccttaagctcca	2094
ABCA4	21	intron1 + 7290	gatttttgttggctttgcaa T/A ggatcacagtcatttattca	2095
ABCA4	22	intron1 + 7483	tctgagcctctttccttaac T/C gcagagtgagtggctacaga	2096
ABCA4	23	intron1 + 7497	cttaactgcagagtgagtgg C/T tacagagaaatctttactac	2097
ABCA4	24	intron2 + 1067	tcaagcagcagcagcaactg C/A gtggagtcttcttgaactaa	2098
ABCA4	25	intron2 + 1108	aacactcctatgcccctctc G/A gcacaaaatgacgtgtcccc	2099
ABCA4	26	intron2 + 1119	cccctctcggcacaaaatgac G/A tgtccccccttgcttccccct	2100
ABCA4	27	intron2 + 1243	cacccagcacagggactggc A/T cacatgagatgctcctgctt	2101
ABCA4	28	intron3 + 26	tgttgagatccctaccatgc A/G ggggaggaagttgcacaccc	2102
ABCA4	29	intron3 + 101	agcatggagcactgagtgtt C/T ttgtggctttgctgagcccc	2103
ABCA4	30	intron3 + 330	tgcttgggtggagtgaatca T/C tgtaggagaaaaactcagtt	2104
ABCA4	31	intron3 + 470	tgaagtcaggtttacaaagt C/G aagtttacttcttgggagaa	2105
ABCA4	32	intron3 + 634	tgaaaaccaatgaccccctct T/C ccaagaaaaatggccacata	2106
ABCA4	33	intron3 + 1016	ccttgggggagctcagtatg A/G ttcttccaggagaagcctgc	2107
ABCA4	34	intron3 + 1554	gaaagttgggtttcatgttt T/C gcactcacattatgagtgaa	2108
ABCA4	35	intron3 + 1686	ctagacattctcacagagcc A/G agggcagcaaggcggggctc	2109
ABCA4	36	intron3 + 1823	ttcacctctctccatggacc A/G gtctccctgctcctcaatg	2110
ABCA4	37	intron3 + 1938	caaattcctgggaacaaatc G/A ggttgacccagctttattct	2111
ABCA4	38	intron3 + 1951	acaaatcgggttgacccagc T/G ttattctccctgtcccatca	2112
ABCA4	39	intron3 + 2063	ggctgtcagagcctacctgc G/T tgaatgggtggaagggcagg	2113
ABCA4	40	intron3 + 2079	ctgcgtgaatgggtggaagg G/A caggtctcagagaattgggt	2114
ABCA4	41	intron3 + 2186	agacacacagagcatgggac C/T gagaggcgagcagaccctgc	2115
ABCA4	42	intron3 + 2214	gagcagaccctgcaaaaact G/A ggagactgaatagatcgctc	2116
ABCA4	43	intron4 + 2717	cgtgcttctgcacagccacc T/C gggaaggtatgccgatggtt	2117
ABCA4	44	intron4 + 2802	attctcagcagggaggatta A/G tggtaaaagcccaggaatgg	2118
ABCA4	45	intron4 + 3182	cccccagagccacagcagcc C/G tgtctcctgggtggtcttgt	2119
ABCA4	46	intron4 + 3515	agtataataaaagcaggagc C/T atagcccccaactctcaaga	2120
ABCA4	47	intron4 + 3907	aggggagtgacagtgggcac C/A actctcagggaacccattac	2121
ABCA4	48	intron4 + 3923	gcaccactctcagggaaccc A/G ttactgtgagagaagccact	2122
ABCA4	49	intron4 + 3952	agagaagcccctgtgccact G/C tgtggtcgaacttcaagacc	2123
ABCA4	50	intron4 + 4125	ggctgtccagcacacagggg C/A aggcctcttggccactgggg	2124
ABCA4	51	intron4 + 4637	aatcacttgccccaaggtca C/T cttaactgttaggtgttctt	2125
ABCA4	52	intron4 + 5319	acctctagggctcccagag A/G ccccaagaacagaaccttcc	2126
ABCA4	53	intron6 + 2266	caccettgcagacctcagac G/A ggtcctgggggcttgctttc	2127
ABCA4	54	intron6 + 2857	ccagaggagaaagctctgcc G/A tagtcggcctcagttaacca	2128
ABCA4	55	intron6 + 2861	aggagaaagctctgccgtag T/C cggcctcagttaaccacgga	2129
ABCA4	56	intron6 + 3078	gcaggcattaaaatgggact T/G tgcctttattgctcctgggc	2130
ABCA4	57	intron6 + 3375	ttaaatgccaaatgagttct C/G attaacaaagaaagagggaa	2131
ABCA4	58	intron6 + 3412	ggaaaatctcagtaaaccac C/T gtgacggcatctacccactt	2132
ABCA4	59	intron6 + 4635	ctttcgggtggatattgcta C/T gtcaagtgtctgggaaagcc	2133
ABCA4	60	intron6 + 5576	ccactaatatgcattcttta G/C taagcggtctcaatatacac	2134
ABCA4	61	intron6 + 5925	aaaaagcattttgctcttat A/G aaagcacagcctcttttgag	2135
ABCA4	62	intron6 + 6916	cccagacaacccaagcagag A/G cctcttagggccggaatcat	2136
ABCA4	63	intron6 + 6993	agcacaggatcaaggcctaa A/G ggccccttagactgacctca	2137
ABCA4	64	intron6 + 7242	ttgccattttgatctgtgac T/C ttttttttccagaaatagttt	2138
ABCA4	65	intron6 + 7454	atggagggctccctcgggac T/C aggcagtattcagagatgta	2139
ABCA4	66	intron6 - 264	aaacagcaattagaatcact T/C tgaaatagtgatagtattta	2140
ABCA4	67	intron6 - 86	aggaggggggagttttcaa A/G catataggagatcagactgt	2141
ABCA4	68	intron6 - 32	tatacctacaaacatatata T/C atttaaaaaattgttttact	2142
ABCA4	69	intron7 + 828	gatgtgggaaagttagagaa G/C agcccattgtactaatgctc	2143
ABCA4	70	intron7 + 1019	aggcttcttgactgtctaga T/C agcaagtctaatcatttgtg	2144
ABCA4	71	intron8 + 374	gtaaacacggctgtgggatg C/T ttttacaaacacaatatcgt	2145
ABCA4	72	intron8 + 874	tgatgagcttgttattggtg G/A ggtacagcctattaatttag	2146
ABCA4	73	intron9 + 605	tcgtgtctctgtcttgatct C/T tgtctggttttaggccaact	2147
ABCA4	74	exon10 + 1268	aacttttgaagaactggaac G/A cgttaggaagttggtcaaag	2148
ABCA4	75	exon10 + 1269	actttgaagaactggaacg C/T gttaggaagttggtcaaagc	2149
ABCA4	76	intron11 + 5236	ggcctggcacagatgaaata C/T tattcagagttcacagtgta	2150
ABCA4	77	intron11 + 5270	cagtgtattttcatttcata A/G tatatttgattttcaggtct	2151
ABCA4	78	intron11 + 5687	atcatgtaatgtactttaga C/G tcagatatataaatatttgt	2152

遺伝子名	No.	存在位置	配　　列	配列番号
ABCA4	79	intron11 + 7136	gacttcccaacttaccttag T/C ggagctgtagtcacatagaa	2153
ABCA4	80	intron11 + 7180	acgctcataaatgcttctct G/A ggctgtaaaggttgaatttt	2154
ABCA4	81	intron11 + 7701	gttagacgcaggcattacct C/T gtggctttgccccagtgtga	2155
ABCA4	82	intron11 + 8073	gggatgtttgcccacatcca T/C tggcatttctcaaaaggaac	2156
ABCA4	83	intron11 + 8586	cagctgcctgcgctggagag G/A gctcaaacctottccgccag	2157
ABCA4	84	intron11 + 8893	agcaaagatgccctttgact C/T cttttcccactagtggtgct	2158
ABCA4	85	intron11 + 9257	gaatgaggtcacttgctgca T/A ggcaggtggcttcccatga	2159
ABCA4	86	intron11 + 11234	cccaaataattttgtttttc G/A ttttaggaattaaatttcag	2160
ABCA4	87	intron11 + 11641	aagaaacaaacatttattga C/G aacttttggtgtgtgacctg	2161
ABCA4	88	intron11 + 11808	tggtatttcttaaagaaata C/T caattccatttccttttaac	2162
ABCA4	89	intron11 + 11923	aagatcattattaatatctc A/G tcagcgtggtgtcacttaag	2163
ABCA4	90	intron11 + 12055	tgagaacattacatgggacc T/C gccccagggcatggaggct	2164
ABCA4	91	intron12 + 305	tcaccctgtggtcgggaggt G/A tgagtgagctatccaagccc	2165
ABCA4	92	intron13 + 1461	ttgggtttcagtgtcagcat G/A tagctgtctactcagatccc	2166
ABCA4	93	intron14 + 1237	aagggcaccaaagttctaag A/G gatgaggggaggagctgagc	2167
ABCA4	94	intron14 + 1268	ggagctgagccccttgtcct T/C atctaggtttcccttgttct	2168
ABCA4	95	intron14 + 1309	ttcccatccctcagtctgct T/C cttttcccagtaccaacatg	2169
ABCA4	96	intron14 + 2979	tcacctgtgtgggtagcaaa C/T ctcagaaaatcaagtataga	2170
ABCA4	97	intron17 + 23	gagtcctttaaaacacaaat C/G ttaatgtttgaaatcaactc	2171
ABCA4	98	intron17 + 204	tgctgggccctgtgtgatca T/G gaatggctgatcatggatga	2172
ABCA4	99	intron17 + 715	gggactcccctagagctgaa G/A tactctcccatctgtttgtt	2173
ABCA4	100	intron18 + 1282	ggaagatgaagaacctaagc C/T gottccagaaattcatgagg	2174
ABCA4	101	intron18 + 1531	gtctaccccttaggaccatt G/A taagagtacattgaggtaat	2175
ABCA4	102	intron19 + 1802	actgctcacccaggcggcaa C/A gcctcgagtcatgcacccgaa	2176
ABCA4	103	intron20 － 195	acagattattccattgtatg C/A atgaactatgtaagccatcc	2177
ABCA4	104	intron23 + 755	ctggctgcgctgggtttc C/T tatgtccatccacggggagg	2178
ABCA4	105	intron26 + 497	ctgagttaggtctagatggg G/A acactttggatgaatgagga	2179
ABCA4	106	intron26 + 702	tatcaaatacaactcagacg T/G cagtctcctggcccctttga	2180
ABCA4	107	intron27 + 156	cctgctttccaaaccottat C/T ttgattcttggtaacatgaa	2181
ABCA4	108	intron27 + 385	tttaaagaacagtgagtcac G/A tgacttgctctttgaaatgc	2182
ABCA4	109	intron28 + 299	gacatgccatcagaccactg C/T gagtgttcaggcagcctacc	2183
ABCA4	110	intron29 + 168	ctccttccacacttgtgtgc A/G gggacattcactacctccta	2184
ABCA4	111	intron29 + 497	gctgtcaataaggaccaaaa C/T agactaatttcaaattcctc	2185
ABCA4	112	intron29 + 567	agctgctaggaataaaaagg G/A agacaaaacgatccacaagc	2186
ABCA4	113	intron29 + 577	aataaaaagggagacaaaac G/A atccacaagctagagatggt	2187
ABCA4	114	intron30 － 2494	aatcacagctcatctgctgc A/G tcatagggatcccaaaagaa	2188
ABCA4	115	intron30 － 2169	aatgtaacagccaaagtcct A/G gaaaaaggcaagccagttcc	2189
ABCA4	116	intron31 + 535	ctaactgtgaattatcatct T/G tgatcactgccctttgagat	2190
ABCA4	117	intron31 + 957	gagttctcagcagcaaatct C/A cagtatgaaattttggattt	2191
ABCA4	118	intron32 + 445	tccagaggtttagaacctca C/T caagtgggactctaggagcc	2192
ABCA4	119	intron33 + 48	aggatttttgacttgcttaa C/T taccatgaatgagaaactct	2193
ABCA4	120	intron35 + 129	tgtttagtcaggcacatatg A/C acatccgactttcaaataag	2194
ABCA4	121	intron35 + 209	tctcccaacatttatgtgg C/A aagtaagtttacatttggtt	2195
ABCA4	122	intron36 + 3209	ttgaggcctccacaccccac G/A gcaggttgccccctgaggaa	2196
ABCA4	123	intron36 + 3542	cttggcagggaggtagggca T/C ggggtggggtaggaggacta	2197
ABCA4	124	intron37 + 304	ctgggggcagccattcccca A/G cccctcacccagctctgact	2198
ABCA4	125	intron37 + 525	taaatttgaatgagtaattc A/G tccatctcggcctcagtttc	2199
ABCA4	126	intron37 + 766	tgttgcaggctggagaaccc T/G cctatgaattgtacagggct	2200
ABCA4	127	intron37 + 856	aaaaccccatgaagtggtca A/G ggcaggcatcattatctcca	2201
ABCA4	128	intron38 + 62	tagtagagtatgtgttggtc G/A agcagagccaggggcaagca	2202
ABCA4	129	intron38 + 761	tccttgggcaagttaatctt G/A atgaagagactgggtgttct	2203
ABCA4	130	intron38 + 1315	cagagtcagactctggaaag G/T cgggggggataagaacacagc	2204
ABCA4	131	intron38 + 1316	agagtcagactctggaaagg C/A gggggggataagaacacagcc	2205
ABCA4	132	intron38 + 1526	ccaacatttgctaagcaccc G/A octtcaaaaacctggtattt	2206
ABCA4	133	intron38 + 1561	gtattttcatgtaaattatc C/A gatacccagctgctatggaa	2207
ABCA4	134	intron38 + 1562	tattttcatgtaaattatcc G/A atacacagctgctatggaaa	2208
ABCA4	135	intron38 + 1674	ccagctgaacaccacgtgcc G/A ggtgtgtgctgatataaaca	2209
ABCA4	136	intron38 + 2867	tgcctggctagacaaagggg A/C agctcccgcccactagaaac	2210
ABCA4	137	intron38 + 2874	ctagacaaaggggaagctcc C/T gcccactagaaacttgcagg	2211
ABCA4	138	intron39 + 123	gaggggaccttgttgggctg G/A aggtgtcctgccagctggag	2212

遺伝子名	No.	存在位置	配　　列	配列番号
ABCA4	139	intron40 + 1904	gacactgtacagccagccca A/C tcctgaccccttttcttcat	2213
ABCA4	140	exon41 + 5814	ggaaatacaaactgacatctt A/G aggctacatgaactaaccaa	2214
ABCA4	141	intron41 + 122	atttggttcccagttttatg T/G agggtcatcatccctgtgtt	2215
ABCA4	142	intron41 + 287	tctgcagagcatgggtcagc C/T tcgagatgtctcagtactca	2216
ABCA4	143	intron41 + 411	cctcttcccctccttgctct C/A accctgtctcagttctcagt	2217
ABCA4	144	intron41 + 443	gttctcagtccggtttcttc G/A tatcttgcagatttatccag	2218
ABCA4	145	exon42 + 5844	cgtatcttgcagatttatcc A/G ggcacctccagcccagcagt	2219
ABCA4	146	intron43 + 328	tttgtagcctattcctataa A/G aatgcaccattgcttcccat	2220
ABCA4	147	intron43 + 345	taaaaatgcaccattgcttc C/G cattacctcccctccacacat	2221
ABCA4	148	intron43 + 370	acctcccctccacacattttt A/G caaaacgtttcagggagttt	2222
ABCA4	149	intron43 + 376	ctccacacatttttacaaaa C/T gtttcagggagtttactgag	2223
ABCA4	150	intron43 + 670	ttaaacagactggtcccctа T/C gggcaggacagagaggatga	2224
ABCA4	151	intron43 + 701	gagaggatgagctctcactc A/G tctgcctctttcctggctgc	2225
ABCA4	152	intron43 + 822	gttaggtgctgctgacatct G/A tccagcatctgcttgactgg	2226
ABCA4	153	intron43 + 915	ggcaggacgagtcctgagca C/T gcttcactggctcagacagg	2227
ABCA4	154	intron43 + 1242	actgagctggacgctagaaa G/T aaactataggcttaagacac	2228
ABCA4	155	intron43 + 1671	tagagaagtttacttccatc G/A ggacacatgcatctttttcta	2229
ABCA4	156	intron43 + 2036	ttgaaggatactcagtaatt G/A ctttttttcttgcagtattt	2230
ABCA4	157	intron45 + 176	gtgtttggttcacacagctc C/T ggagaaaaacaagtcacggc	2231
ABCA4	158	intron45 + 193	ctccggagaaaaacaagtca C/T ggcacagccttgacttggga	2232
ABCA4	159	intron47 + 238	cccaagtctctggatggggc A/G tctgatcaggatgcatgcag	2233
ABCA4	160	intron47 + 269	atgcatgcagagcctggctg G/A gatgagggagggctgctacc	2234
ABCA4	161	intron47 + 326	accacttatctcaacagatc C/G gggacctgtggcctatttac	2235
ABCA4	162	intron47 + 715	aagtcactaagctggtggt G/A ggaggaacagcacataaccc	2236
ABCA4	163	intron47 + 734	tgggaggaacagcacataac C/T caccttatctatgctgaggt	2237
ABCA4	164	intron47 + 931	ggacactgcatagatatcta T/C agaaatagcagcatgtcagg	2238
ABCA4	165	intron47 + 1260	acactctctggtggaccatc A/C ctcatccaagagagggtaac	2239
ABCA4	166	intron48 + 1663	tctcgctcttctcttacctc T/C aggtgttgtaaattttgct	2240
ABCA4	167	intron49 + 127	agagagccccacccacacca C/T ggtccctaccaagtccccac	2241
ABCA4	168	intron49 − 1545	gcagttaattccaaacttttt C/A tcccttattggatgagatca	2242
ABCA4	169	5'flanking −(1441−1400)	gtaaatctcagttgaatcag (TCA)14−16 atttttcagtctggttcctg	2243
ABCA4	170	intron1 + (4712−4720)	gaggggcggggactataggc (A)8−10 cagcctaattcaaggatgag	2244
ABCA4	171	intron1 + (7295−7304)	ttgttggctttgcaatggat CACAGTCAT/Δ ttattcactc attcattcac	2245
ABCA4	172	intron2 + (951−952)	cctgtccatcagactcttct TT/Δacctctcccggaggagccca	2246
ABCA4	173	intron3 + (2642−2653)	cctgggtgacagagcgagat (A)10−12 tagcatgagatattattact	2247
ABCA4	174	intron4 + 5202	cacaaagcatctgacacccc C/Δ atccagcctggctaacttt	2248
ABCA4	175	intron6 + (3029−3044)	cactaaaaacaaaaatttac (A)16−18 cctgaaagaaattgcaggca	2249
ABCA4	176	intron6 + (5138−5139)	ttcatgacagatcagatgtt (G) cttttatggatttacaaaga	2250
ABCA4	176	intron6 + (5138−5139)	ttcatgacagatcagatgtt cttttatggatttacaaaga	2251
ABCA4	177	intron6 + 5985	tttccttcttcaaaccccccc C/Δagactaggagaaggtctgtc	2252
ABCA4	178	intron6 + 6094	gggacggacagaaaaagacc T/Δagtttctgttgagccaaaga	2253
ABCA4	179	intron6 − 161	tatttttttcaattaaataaa A/Δ gagttttttgtttctaaaag	2254
ABCA4	180	intron7 + (809−810)	gggccgagtatgcacactga (TG) tgtgggaaagttagagaaga	2255
ABCA4	180	intron7 + (809−810)	gggccgagtatgcacactga tgtgggaaagttagagaaga	2256
ABCA4	181	intron8 + (472−484)	atcttccccaccttttcacta (T)10−13 ggtcttctatgggtaaagg	2257
ABCA4	182	intron9 + (48−71)	gtaccctggacctcccagaa (GT)11−13 gagagagatgtgccttcctg	2258
ABCA4	183	intron9 + 554	atagggggcagaaaagacaca A/Δ ccaaaagttctctctcacctt	2259
ABCA4	184	intron10 + 11	catgatcagagtaaggggggg G/Δ ttggaggatggggagggggag	2260
ABCA4	185	intron11 + 4242	ggagaggaaatgatgttagt G/Δ cctcctgtaaatggcccag	2261
ABCA4	186	intron11 + (13743−13753)	tgctcttttgtgggtaatgg (T)9−11 cctcttccaggagaagaaaa	2262
ABCA4	187	intron13 + (636−637)	cggggtggagggttgggagg (G) ctcatttgtcattatagatg	2263
ABCA4	187	intron13 + (636−637)	cggggtggagggttgggagg ctcatttgtcattatagatg	2264
ABCA4	188	intron18 + (569−570)	tgctgccctcatcttctctc TT/Δ aaactagttctgtatttctc	2265
ABCA4	189	intron20 − (304−297)	tataacctgacttttttttc (A)7−9 ggattgctttttaaacata	2266
ABCA4	190	intron22 + (1236−1246)	gctgaattagttcccttggg (T)9−11 agttaactcctgatttttgc	2267
ABCA4	191	intron26 + (4626−4635)	gataatcaatgctgtaaggg (A)9−10 tggcattagagatccagacc	2268
ABCA4	192	intron33 + (115−116)	taaaaccgtcttgtttgttt GT/Δ ttacatggtttttagggccc	2269
ABCA4	193	intron36 + 1078	taagcagctatcacttaaca A/Δ tacaaaaccagagattatca	2270
ABCA4	194	intron37 + (290−291)	ccttgaccaaagcctggggg (T) cagccattcccccaacccctc	2271

遺伝子名	No.	存在位置	配　　列	配列番号
ABCA4	194	intron37 + (290-291)	ccttgaccaaagcctgggag　cagccatttcccaaccctc	2272
ABCA4	195	intron38 + 898	atagaaagaggggtaaaaaa A/Δ gaaggcagtcgctgcagggc	2273
ABCA4	196	intron38 + (1209-1210)	gtggaccccctgagactgact CT/Δ ttccagatcttgttagggtt	2274
ABCA4	197	intron38 + 1322	actctgggaaggctgggag G/Δ atagaacacagccccagca	2275
ABCA4	198	intron38 + 3107	gggccccacctgctgaagag A/Δ ggggggtgggttgccccc	2276
ABCA4	199	intron40 + 152	ttttctccaatcatacaagt A/Δ gaggatcgggttaaaatagg	2277
ABCA4	200	intron43 + 330	tgtagcctatttcctataaaa A/Δ tgcaccattgcttcccatta	2278
ABCA4	201	intron43 + 1354	tttaattggcccagcccatgc C/Δ tttggtggctttgtcattg	2279
ABCA4	202	intron47 + (1305-1308)	catcctgctgaagagaaag AAAG/Δ caccaatggcccaagcccta	2280
ABCA7	1	5'flanking - 1598	agaatgttggcccctcccc C/T tcctgcatcctctgcaggag	2281
ABCA7	2	5'flanking - 1594	aatgttggcccctccccct C/T ctgcatcctctgcaggagcc	2282
ABCA7	3	5'flanking - 1180	ggccagtgagtgacgggcag G/A tcgcccaaatagcagcgtgc	2283
ABCA7	4	5'flanking - 480	agaggctgggtcgtgcctcc A/G gctgggcaactgcctgtctc	2284
ABCA7	5	5'untranslated - 9	ctctgtcccgtcccctgccc A/G gtctcaccatgggccttctgg	2285
ABCA7	6	intron5 + 91	ccccgggccaaggacctccc G/A ttccaggcatccaggctgtc	2286
ABCA7	7	exon6 + 583	cagctgttgggagccgctg A/G ggacctggcccaggaggtac	2287
ABCA7	8	intron8 + 103	gccggaggtcacggaaact A/G tttgaagaagtaggagttag	2288
ABCA7	9	intron8 + 166	tgcggaggatcagaggcaca C/T gcaggagcaaggcaggaggg	2289
ABCA7	10	exon9 + 955	accggacctttcgaggagctc A/G cctgctgaggggtgtccgg	2290
ABCA7	11	intron9 + 421	ttttttttttttttttttt T/A taagagatggagtctcactc	2291
ABCA7	12	intron9 + 463	gttgcccaggctggactgca G/A tggcgagatcttggctcact	2292
ABCA7	13	intron9 + 467	cccaggctggactgcagtgg C/T gagatcttggctcactgcaa	2293
ABCA7	14	intron9 + 488	gagatcttggctcactgcaa C/T ctccgcctcctgggttcaag	2294
ABCA7	15	exon10 + 1184	cgcgcacagctgtgtgtgggc A/G cctggtgggcacagctgggcc	2295
ABCA7	16	intron10 + 10	gagtgacgggagtgagggcc T/C gtccacctgccgggtctgtt	2296
ABCA7	17	exon11 + 1388	cctgggcccccggcccagggtgc G/A catcaaaatccgcatggaca	2297
ABCA7	18	intron12 + 115	caggctgcgaacttttgcacc T/G ttcacccactccacagtgacc	2298
ABCA7	19	exon13 + 1824	ccctttcctgctcagcgccgc A/G ctgctgtttctggtgctcaa	2299
ABCA7	20	intron13 + 55	gctgcgctgggagggtgcag A/G cagggacagccccacgtggg	2300
ABCA7	21	intron13 + 78	gggcgggccccacgtgggtg C/A gcgcccccagggccaatccag	2301
ABCA7	22	exon14 + 1851	cgttgcctctcacagctggg A/G gacatcctcccctacagcca	2302
ABCA7	23	exon15 + 2153	cgcgggcgcgcagtgccaca A/C cgtgggcaccccggcctccgg	2303
ABCA7	24	intron15 + 34	ggcgggcgctccgggccggct C/G gcaacctgctttgccgggagc	2304
ABCA7	25	intron16 + 8	ctgaaccccaaagggtgaggc A/C ctacgaggcttaatagctgg	2305
ABCA7	26	intron16 + 161	tcccgcagcttttataggcc C/T cggcccagcaggtcccggat	2306
ABCA7	27	exon17 + 2385	caccccatctctgcagtgct G/A gtagaagaggcaccgcccgg	2307
ABCA7	28	exon17 + 2421	cccggcctgagtcctgggt C/A tccgttgcagcctggagaa	2308
ABCA7	29	intron20 + 166	cgagacagtaagagttgggg A/G tagacagagttcccctgga	2309
ABCA7	30	exon21 + 3027	ctgctgggagaccgtgtggc C/T gtggtggcaggtggccgctt	2310
ABCA7	31	intron22 + 1386	gggtgggcgtgagccgggg C/T tcoctgaagcaccccttttgt	2311
ABCA7	32	exon23 + 3417	gggatctccgacaccagcct C/G gaggaggtgtgaggcctggg	2312
ABCA7	33	intron23 + 147	gggcgtctgtggtgctcagat G/A tccctttgggaaggcctgggg	2313
ABCA7	34	exon25 + 3528	gctggcctagacgtaaccct A/G cggctcaagatgccgccaca	2314
ABCA7	35	exon29 + 4046	cccagcctgccagtgtagcc G/A gcccgtgcccggcgcctgc	2315
ABCA7	36	intron30 + 81	cccccctgggagctctcccgg C/A cccccggccctcagctccc	2316
ABCA7	37	exon31 + 4239	ctgcctgcatggccccacag A/G tacggaggcttctcgctggg	2317
ABCA7	38	intron32 + 1	caaggagcagctgtctgagg G/C tgcactgtgagtcccttccac	2318
ABCA7	39	intron33 + 54	ccactgcttgccactgccct G/A tctggccccttgtaggcagg	2319
ABCA7	40	intron34 + 245	cagtacttttgggaggccgag G/A caggggcactgcttgtggcc	2320
ABCA7	41	exon36 + 5057	ggtgagccgggatcttgaaac A/G ggtcttcctttatcttcccca	2321
ABCA7	42	intron38 + 85	ggcccactcaccttttctgaa A/G gacctgcactctcccaggta	2322
ABCA7	43	intron40 + 154	ctctacctcccacacgcggga C/G caggcctgagacacccctg	2323
ABCA7	44	intron40 + 277	ctgagccccgggcgcccca T/C cccgcgctggcccgggaac	2324
ABCA7	45	exon41 + 5592	gtggcccgggaacccgctgc T/C gcgcacctcagcatgggata	2325
ABCA7	46	intron41 + 286	ctccttgactctgcctttctg T/C ggcctgcccacttgctcct	2326
ABCA7	47	intron41 + 389	tggccgttcccagtttgcag C/T cgtttcactgcctcttccat	2327
ABCA7	48	intron41 + 991	cacactatggcctgcccca C/T acccatcccagctccaccca	2328
ABCA7	49	intron41 + 994	actatggcctgccccacac C/T catcccagctccacccacac	2329
ABCA7	50	intron41 + 998	tggccctgccccacacccat C/G ccagctccacccacaccatg	2330
ABCA7	51	intron41 + 1001	ccctgccccacacccatccc A/G gctccacccacaccatggcc	2331

遺伝子名	No.	存在位置	配　　列	配列番号
ABCA7	52	intron41 + 1051	actcatgctggctccaccca C/T accatggccccgccccatac	2332
ABCA7	53	intron41 + 1131	tgccctgccccatgcccatt A/G tgcccctgctccacactcaa	2333
ABCA7	54	exon44 + 5985	gaagcgctctgctcgcgcct G/A gccatcatggtgaatgggcg	2334
ABCA7	55	intron44 + 201	ggcgcaggaccaggaggcgt G/C agccgggggctctgggtgga	2335
ABCA7	56	intron44 + 233	ctgggtggatttagaagaca C/T aatcaggtgtgcgttggagt	2336
ABCA7	57	intron44 + 313	agttaggggagggcctggtt A/G gtgggcgggggccataggaaa	2337
ABCA7	58	intron44 + 337	ggcgggggccataggaaagtg G/C ggcgggggtatttattgtgt	2338
ABCA7	59	exon45 + 6133	tggcggccgagttccctggg G/T cggagctgcgcgaggcacat	2339
ABCA7	60	exon45 + 6159	ctgcgcgaggcacatggagg C/T cgcctgcgcttccagctgcc	2340
ABCA7	61	intron45 + 27	acggcgccgggggtcgggctg G/C gggaggcagggctgggggcca	2341
ABCA7	62	3'untranslated + 6580	aaggctggagagaagccgtg G/C tggtgaaaccgtgtgcatgt	2342
ABCA7	63	3'flanking + 108	caagctgagtgtgcacatac G/A ggccaagtggcgattcatag	2343
ABCA7	64	3'flanking + 376	cttacaggagcccggtgtcc C/T ggagcacaggccagggccgg	2344
ABCA7	65	3'flanking + 687	cagcagggagacttggggag G/A ggggagagagttcaaactgc	2345
ABCA7	66	3'flanking + 688	agcagggagacttggggagg G/A gggagagagttcacactgcg	2346
ABCA7	67	3'flanking + 1169	cctcgacctgacccacttca C/T gggggctgcagggcgggtgat	2347
ABCA7	68	intron9 + (398-422)	cgtgaactaccacgtcctgc (T)22-26 aagagatggagtctcactct	2348
ABCA7	69	intron12 + (175-184)	ggggactctgagggtctggt (G)8-10 actctgagggtctgggggcc	2349
ABCA7	70	intron30 + (81-87)	cccccctgggagctctcccgg (C)6-7 ggccctcagctcccctccc	2350
ABCA7	71	intron34 + (349-361)	agaaagagaaagagagaaag (A)12-14 cagaaatgtgctttgggtga	2351
ABCG1	1	5'flanking - 1772	cctgggcttcagcaggggcc T/C cacacctgcaatgggtgcct	2352
ABCG1	2	5'flanking - 1754	cctcacacctgcaatgggtg C/T ctggggagagggtgcagatg	2353
ABCG1	3	5'flanking - 1450	tccaaagcccagatttggtg T/C ttttggggctcttttggaat	2354
ABCG1	4	intron1 + 4	ctggtggaggaagaaaggta G/A ggagggcggctgctttgtgt	2355
ABCG1	5	intron1 + 576	agctcaggaggtgtctggaa C/T gccacacagtgcaggagttt	2356
ABCG1	6	intron1 + 1426	aattctccttctcaaacttaa A/G gaaatattttatagaaaaat	2357
ABCG1	7	intron1 + 2342	agagcctgcaatgggccgcc G/A agggacctgcccatgactca	2358
ABCG1	8	intron1 + 2399	gaggggttgacagacaggat A/G tgtctgctgtgttccagctg	2359
ABCG1	9	intron1 + 2406	tgacagacaggatatgtctg C/G tgtgttccagctgctggttt	2360
ABCG1	10	intron1 + 2911	cccctctctgtgcccactgtt G/C tcccaacaccagcctgttct	2361
ABCG1	11	intron1 + 4363	tataatagattcctagcaga A/G aacataattgtgagaggaac	2362
ABCG1	12	intron1 + 4752	gctttcagagcccattcaca C/T aagggtctcattttattagg	2363
ABCG1	13	intron1 + 5026	ccaggtctgtgggatttcag G/A ccaaaaaggagcgtagcaag	2364
ABCG1	14	intron1 + 5532	gggttaaatattccgggcag C/T gccaagtcagattatctgta	2365
ABCG1	15	intron1 + 5681	gctaaagtgcatggaaggca T/C catgaataactcctttcagg	2366
ABCG1	16	intron1 + 6290	tcacagcagattcatgagag T/A tgaatgtttagccgccatgt	2367
ABCG1	17	intron1 + 6386	agatgctcccctccagccag C/T acattttctccctgtgagca	2368
ABCG1	18	intron1 + 6758	acctgcatggtgggtgcccc C/G ctgccttcctctactgcctt	2369
ABCG1	19	intron1 + 7029	tgggtcagattaaatatatc C/T tgaaggactaaaccgtaaaa	2370
ABCG1	20	intron1 + 7176	ttgctcacattgtgaaaaaa C/G gcaaaaagatgggttttcag	2371
ABCG1	21	intron1 + 9243	gcctgcgagcgctggcagta G/A gaagggtcgccagtgtggac	2372
ABCG1	22	intron1 + 11224	tctggtttagagaggaaaat G/A ggcagcatcattttgtcacc	2373
ABCG1	23	intron1 + 11371	gggctctcttggagcccttt T/G tctctcccagccctgcgtct	2374
ABCG1	24	intron1 + 12420	gggatttcgaatctcaacac T/C ctgagctctgtgctttcccc	2375
ABCG1	25	intron1 + 12484	gagttgtcctccaagagaat C/T tttgtatggttccttttctg	2376
ABCG1	26	intron1 + 12955	ctggggttggtgggagccac A/G gtctcacacctattggcagg	2377
ABCG1	27	intron1 + 12985	ctattggcaggtcgtgaaca T/C tgttcttggatttgcaaata	2378
ABCG1	28	intron1 + 20041	acatggccggcttcccttct T/C cctcggaatggcctggaatt	2379
ABCG1	29	intron1 + 20046	gccggcttcccttcttcctc G/A gaatggcctggaattcgatc	2380
ABCG1	30	intron1 + 21058	acaagacttagaatttgacc G/A tgattttaaaactattctaa	2381
ABCG1	31	intron1 + 26189	ttcttggatgtggccatgca C/T gggggcaaggattttgatgag	2382
ABCG1	32	intron1 + 27453	atcatgtggtttgggggaaa G/C ctgggaccccacttggtaca	2383
ABCG1	33	intron1 + 28098	caggaaggagacagctgctg G/C tgctgcttagagttaggcgc	2384
ABCG1	34	intron1 + 29670	ccttcagttgtaataggcag A/G aggagcgcacgaggaggctg	2385
ABCG1	35	intron1 + 29810	attgtttctcctgtgttttgt T/C tgtgttgactttccctttaa	2386
ABCG1	36	intron1 + 36220	cagatcccttggttgctggg C/T aggtagtaggagaggttttt	2387
ABCG1	37	intron1 + 36341	aaacagggcttgagtcctcc G/A taagggacaggagaccttcc	2388
ABCG1	38	intron1 + 36370	aggagaccttcccacatcct G/A gcaagaattcttctttttttc	2389
ABCG1	39	intron1 + 36662	cagactaaatgccacaattct G/A gattgagctgactgtattga	2390
ABCG1	40	intron1 + 36914	tgtaaaagatggagaagaac A/G cagtagtcgcttgctgtgag	2391

遺伝子名	No.	存在位置	配　　列	配列番号
ABCG1	41	intron1 + 37029	tgtgactcatggcctctgcc A/G ggggactgggctggccctgc	2392
ABCG1	42	intron4 + 1196	tgaaaagaaaatggatgagt G/A gaaaccaaaagagagaaaat	2393
ABCG1	43	intron4 + 1200	aagaaaatggatgagtggaa A/C ccaaaagagagaaaatgtgg	2394
ABCG1	44	intron4 + 2041	aagcagaggcttttccaccc G/A gagactcaagaagctgctcc	2395
ABCG1	45	intron4 + 2490	gtggtgaagtagagctgagc A/T cacgggggagccctccatcc	2396
ABCG1	46	intron4 + 2552	atggccttgggccactgcct G/A ctgtgccccgagccgagctt	2397
ABCG1	47	intron4 + 2822	cagcaggctccgtgctgaag T/C cacagcaagccaggccottg	2398
ABCG1	48	intron4 + 2850	agccaggccottggcctgcc G/A gagctggaagacccagaaca	2399
ABCG1	49	intron4 + 2919	gcctcccaggagtagctaca C/T gggaccccgaaggcagatggc	2400
ABCG1	50	intron4 + 3506	ggcagcctgggctgccgaga T/C cctccctggagcgcccgccg	2401
ABCG1	51	intron4 + 3538	cgcccgccgggaaagccccag G/A ggggctggagctacaagtgg	2402
ABCG1	52	intron4 + 3554	ccaggggggctggagctaca A/G gtggccttgcaggttttttg	2403
ABCG1	53	intron4 + 3721	ccagctcatgggcaggggtg C/T ggagggaaaggcacccacag	2404
ABCG1	54	intron4 + 3852	caccagagccactcagtogg C/T caagagcgtcgcccagtggt	2405
ABCG1	55	intron4 + 3921	gaagaccagcagtcgatgcc A/G gctgggaagagggctctgcc	2406
ABCG1	56	intron4 + 3979	acccaccagccttttccaga C/T agccttccagaagctgttic	2407
ABCG1	57	intron4 + 4291	gagcogctggagtagggtcc G/A cttgctatggctcccagggg	2408
ABCG1	58	intron4 + 4922	gaaaccaccagaaattgtgc A/G tcctctcatgtgtccattca	2409
ABCG1	59	intron4 + 4968	tattgactggacaccttctc C/T gtatggggcactgggctagg	2410
ABCG1	60	intron7 + 672	atcagtaacgggtcactaac G/A gatgotgotgagtggggcag	2411
ABCG1	61	intron7 + 840	atttcatttcctcaatgtcg T/C ctgaccagagagcgggaggt	2412
ABCG1	62	intron7 + 891	tggcccactgttgagggtgt G/A ggtgaccagaggggcctgga	2413
ABCG1	63	intron7 + 997	tgtgtcctgtttgtggctt C/G atctaggaggtgtggtggcc	2414
ABCG1	64	intron9 + 1616	ctggaggagaagacaggata A/C agtctaagacgtgctgtcac	2415
ABCG1	65	intron9 + 1630	aggataaagtctaagacgtg C/T tgtcacagagttcagggtcc	2416
ABCG1	66	intron9 + 1674	gcttccaaaggccgcatccg G/T gttgttctctgagccgagga	2417
ABCG1	67	intron9 + 1689	atccgggttgttctctgagc C/T gaggacggctttgcgaaagc	2418
ABCG1	68	intron10 + 446	tggctgacagtgaacacagc G/A gctgcttctccagaacttta	2419
ABCG1	69	intron10 + 581	atgcagagtttcagaagagg C/G agactcaggaagagtaaggc	2420
ABCG1	70	intron13 + 243	acccggagagccatggcagg A/C ccaagtgttctggacgttgc	2421
ABCG1	71	3'untranslated + 2370	gcctctcagctgatggctgc A/G cagtcagatgtctggtggca	2422
ABCG1	72	3'flanking + 1124	ctcagaactacatcgagtga G/A gtcagtgttgaaaacgccca	2423
ABCG1	73	3'flanking + 1252	atgggcccacagcccctgcc T/C cagaagcagctttggtctcg	2424
ABCG1	74	3'flanking + 1433	gggggaagagcttgggaacc A/G tgagggctgttaggctgcaa	2425
ABCG1	75	3'flanking + 1513	tgaagggtgaactggagtag G/C tgaggattctgcagttgacg	2426
ABCG1	76	intron1 + (19909–19944)	cogatgaggagggatgggg (CACCAGGCAGCAGACTCTGA TGAGGAGGGGAGGGGG)caccaggcagcagactctga	2427
ABCG1	77	intron1 + (19909–19944)	ccgatgaggaggggatgggg ca ccaggcagcagactctga	2428
ABCG1	78	intron1 + (25136–25137)	catgaacttgcctgaccata (G) cctgtgaggagctagggct	2429
ABCG1	79	intron1 + (25136–25137)	catgaacttgcctgaccata ccctgtgaggagctagggct	2430
ABCG2	1	intron1 + 152	tcatttgaaagtgggtatgc G/A gtttaaaactgacagttcaa	2431
ABCG2	2	intron1 + 614	agctagtcataaataaatac G/A ccagagtagtaaggaagaga	2432
ABCG2	3	intron1 + 10002	cctcatgaatggtatacatg T/A cccaacatatctctttcgat	2433
ABCG2	4	intron1 + 10123	aoagtggtoocttgggtgc G/A tataccaaatccctgcata	2434
ABCG2	5	intron1 + 10768	ataggaataattgagaacag G/A gtctgaagaactctgcagga	2435
ABCG2	6	intron1 + 10791	ctgaagaactctgcaggaaa T/C gaaaatagttcoctgctttt	2436
ABCG2	7	intron1 + 10792	tgaagaactctgcaggaaat G/A aaaatagttcoctgctttta	2437
ABCG2	8	intron1 + 14183	tcacttaaggctttgcaggg T/G gtctaggacacagaaagaga	2438
ABCG2	9	intron1 + 14934	aaagtgtctttaaaatttcc A/G tcttgagtcagtgagctatt	2439
ABCG2	10	intron1 + 14955	tcttgagtcagtgagctatt G/T aaattcaagcaataagttat	2440
ABCG2	11	intron1 + 17251	ctgtttgggaacagcaactc A/C atcataggcagagagaaagt	2441
ABCG2	12	intron1 + 17347	atttcaaacctgtttcacaa G/A ttgttaagctcatcttaagg	2442
ABCG2	13	intron1 + 17626	gaaggtgcataacaacttcc T/G acataaagtctggagctata	2443
ABCG2	14	intron1 + 18271	aaatgaagctgctcattgcc A/G cacatttaaaaatggacttg	2444
ABCG2	15	intron1 + 18369	ctattgcttttctgtctgca G/T aaagataaaaactctccaga	2445
ABCG2	16	exon2 + 34	atgtcgaagttttatccca G/A tgtcacaaggaaacaccaat	2446
ABCG2	17	intron2 + 36	tgtaaaaagacagcttttta A/G tttacctacagtgaacctca	2447
ABCG2	18	intron2 + 4230	caaccctaaattggagggcc C/T gggcgtggtgattgagaaag	2448
ABCG2	19	intron2 + 4518	gttgacagactttatagtg A/C gggacactgacctgcatgca	2449

遺伝子名	No.	存在位置	配　　列	配列番号
ABCG2	20	intron2 + 6278	atgtatgtaccacgtcttca T/C attcttaaaggatgacccta	2450
ABCG2	21	intron3 + 10	ggcaaatcttcgtgagtata A/G gagagtataagtaagcgttt	2451
ABCG2	22	exon5 + 421	tgacggtgagagaaaactta C/A agttctcagcagctcttcgg	2452
ABCG2	23	intron6 + 3158	actattctagttgattctag A/G ttgtcaatacaacacactga	2453
ABCG2	24	intron6 + 3203	tcctattctgttttaataaa A/G gcattgaatttaggtttgct	2454
ABCG2	25	intron6 + 3287	gtcaggctgaactagagcaa A/G caatctaaaggcaagaatag	2455
ABCG2	26	intron7 + 179	ttcatttttgtagcaccagc T/C tgttatttaggtatctttct	2456
ABCG2	27	intron9 + 5877	gcacttggactttgctttgc T/C acatacttgcattgctctgc	2457
ABCG2	28	intron9 + 5974	tatactaataaatggtgtgt A/T taagttttatctctaattg	2458
ABCG2	29	intron10 + 1908	gacgcttatgtgcagcctat G/T ttgatgtctggaaaggctga	2459
ABCG2	30	intron10 + 2094	ccctgagggctgaggtatct G/A gattatttccagacttgcta	2460
ABCG2	31	intron11 + 20	tgtgagtaggtctttgttct A/G ggaacggggctgtccagcag	2461
ABCG2	32	intron11 + 1447	tgttcttcaaggaaagcccc C/T gtcaaagaaggaaaagaagc	2462
ABCG2	33	intron12 + 49	atgtctttagtcttgcctat G/T ggtgaagtcagttgcacctt	2463
ABCG2	34	intron12 + 1566	tatgcagttacatggacaga C/T acaacattggagaccgaggg	2464
ABCG2	35	intron13 + 40	gctctgataaggaattgttt C/T tttcattcatttcttcctgc	2465
ABCG2	36	intron13 + 1823	ttactcaagcaggcctgact C/T ttagtatttgcttttttgtag	2466
ABCG2	37	intron14 + 497	ctaatgaaaacaaacaagaa T/C gaaagattgtcactgtaaat	2467
ABCG2	38	intron14 + 815	taactctttggaaacttctt A/G aaatttaaaactgtttacct	2468
ABCG2	39	intron15 + 110	ccaggggcactgaatttttc C/T gagcctacgttttctcatcc	2469
ABCG2	40	intron15 + 566	gccgcatagtcatgtgttgt T/A gtttttaaattaacttggaa	2470
ABCG2	41	intron15 + 639	aacaagaaacacttgaataa G/A ttgagaaaaaacccogtttt	2471
ABCG2	42	intron15 + 1197	tgagtagctgggattacagg C/T gcccaccacccacctggct	2472
ABCG2	43	intron16 + 520	catcaattcaggtcaagaaa T/C agaagattgtagcacacaaa	2473
ABCG2	44	5'flanking - (998-995)	gttgggatggctacactcac TCAC/△ aaagcctgatggcccgtttc	2474
ABCG2	45	intron13 + 405	ctgctagtttatttttttt T/△ aacatttttaatttatgttt	2475
ABCG2	46	intron13 + (692-702)	tcaatatgtttctgcttatc (T)9-11 aatggttacttaatcctaat	2476
ABCG2	47	intron15 + (645-650)	aaacacttgaataagttgag (A)7-8 ccccgttttcacataatgtt	2477
ABCG4	1	intron1 + 84	ggcctgggtgtcccatgttc G/A gaaagtcctgcaccagtggg	2478
ABCG4	2	intron2 + 77	gaacacagaaggtattctga A/G agggcattgaccccatcct	2479
ABCG4	3	exon6 + 679	tggtgtcctcatgaagtcc C/T tggcacaggggggccgtacc	2480
ABCG4	4	intron7 + 95	ggcctcctaggggtagagat C/T tcaccgtcgcctgccttccc	2481
ABCG4	5	intron7 + 158	cttgcccttgggaagtgagt G/A tgaatctaaactgagctctc	2482
ABCG4	6	intron8 + 106	ccccagaggcattgcaacca A/G tgggtgctaggaagaaccta	2483
ABCG4	7	intron8 + 1089	aggtacacaacttaatggta C/G aagattctctgtagacctgg	2484
ABCG4	8	intron11 + 1113	acgtgagacgagataagtga T/C ggtcatatggccagggagga	2485
ABCG4	9	intron11 + 1120	acgagataagtgatggtcat A/G tggccagggaggaaggggac	2486
ABCG4	10	intron11 + 1173	gggggacagcttgaacaaga A/G tgtggaggcaggatggacac	2487
ABCG4	11	3'untranslated + 2758	gagtgacaggcacatacatg A/C gaacaggccatctcagcccc	2488
ABCE1	1	5'flanking - 158	aactcagattctcggcacct C/T cagcagctggcttcgccaac	2489
ABCE1	2	intron9 + 237	ctgaaattatatgcaaattc C/T gtagctttataggaagcaga	2490
ABCE1	3	intron9 + 4203	ttgtgtaggaagctgataca T/G taatttgacatatgagatgt	2491
ABCE1	4	intron10 + 1811	ccaagaaacttcagctttct C/T ttcacttaaatataggaaac	2492
ABCE1	5	intron17 + 2301	atatccagaaacagatggta T/C gtgcagaacaggttgtacag	2493
ABCE1	6	3'untranslated + 1810	tggatgattagactgactct G/C agaatattgataagccattt	2494
ABCE1	7	intron1 + (5349-5363)	tttgtctgggttggttgggg (T)13-16 gagactgggtctgactctca	2495
ABCE1	8	intron1 + (5845-5854)	tacatttgtcaaaatttata (T)9-10 gcagataatcatttcatctc	2496
ABCE1	9	intron5 + (836-851)	taaattcacatgattctgta (T)14-16 aggatcctcctgactggcag	2497
ABCE1	10	intron8 + (1153-1169)	tctttcaaacttatatttgc (T)13-17 catagtttcatgtttgatga	2498
ABCE1	11	intron9 + (1023-1024)	ttgctctgtttcaaatctct (T) attcatgggccagcagctcg	2499
ABCE1	11	intron9 + (1023-1024)	ttgctctgtttcaaatctct attcatgggccagcagctcg	2500
ABCE1	12	intron9 + (2338-2346)	agtgtagatggacctcgggg (A)8-9 ctagttaaggaaaagtaata	2501
ABCE1	13	intron9 + (3213-3221)	ttccaattttccattgttac (T)8-9 cttgccagattactcctgaa	2502
ABCE1	14	intron10 + (284-299)	tcctctgcattttggcttct GCAGTATTACTGTAGT/△ atttg tcatttttcaaattaa	2503
ABCE1	15	intron10 + (840-853)	ttttttggtttctttctttc (T)13-14 aatcttggaggaatcttttt	2504
ABCE1	16	intron16 + (1163-1172)	gattagaaatccaggttaaa (T)9-10 gttttgcacaaaaatattac	2505
ABCE1	17	intron16 + (1372-1382)	taaaatttaatcaaaattga (T)10-11 ctcttagtcctcaaaccctt	2506
CHST1	1	intron1 + 2475	taaatggagaaaataacacc G/A acctgatagcattgttgtga	2507
CHST1	2	intron1 + 2612	aaactccccaagcatgotca C/A ctagatcottaccctaggtc	2508

遺伝子名	No.	存在位置	配　　列	配列番号
CHST1	3	intron1 + 3900	gccctgccccccactcccaga C/G ttgcggccctccagcccctt	2509
CHST1	4	intron1 + 6520	cctcccccagaggagctggg C/T acactggggccttgtgttgt	2510
CHST1	5	intron1 + 7534	attgtgtgttggcatactgc T/C cacatggaaggatgctctag	2511
CHST1	6	intron1 + 7911	ttttccttaggaagaaaaaac G/A ccttgctgttttatgcattt	2512
CHST1	7	intron1 + 7963	aaaacattcatgggggatta G/C tgctggctacgtcagagtca	2513
CHST1	8	intron1 + 9173	gcgctgccacagatcaggcc G/A aggtgggggacagaaatgcc	2514
CHST1	9	intron1 + 9701	cccagaattctgaatacagc A/G gcgatgacgggactacgagg	2515
CHST1	10	intron1 + 12132	aacagatccacaggaccaga C/A agcaaagggaggaacatgc	2516
CHST1	11	intron1 + 12465	atgcagggaaggggcttggc G/A caaaactgtcaactgagata	2517
CHST1	12	intron1 + 12561	atgctccctggtccactttc G/A ctttgagtttcaggtagctg	2518
CHST1	13	intron3 + 529	ccatggtctgcaggggtcct T/G catgctcagggattggggt	2519
CHST1	14	intron3 + 617	agaggacagaggaaagagga C/A cacctggagaactgggcgcc	2520
CHST1	15	intron3 + 796	aagaggcttccgcagctgtc C/T gcaggttaaatcctggggtg	2521
CHST1	16	intron3 + 818	caggttaaatcctggggtgc A/G aggaatgtttgttcagctcc	2522
CHST1	17	3'flanking + 762	ataactggtacaggtttact G/C gtgtctacactggcagagaa	2523
CHST1	18	intron1 + 7874	gttttccccttgccttgcct T/△ cattttcatcacctcatttt	2524
CHST1	19	3'flanking + (335-349)	cacactgccacacctggcta (T)12-15 ggattttagtagagacgggg	2525
CHST3	1	5'untranslated - 294	tccagcgtgccgaccggccc C/G gcagcgcctccatcgctccg	2526
CHST3	2	intron1 + 96	gcgtccaggcgcgcgcgcca G/A actttggagggagaagggag	2527
CHST3	3	intron1 + 4467	agagaagaatggggcagagc C/G ggagcagccaggggaggtga	2528
CHST3	4	intron1 + 4853	ggatgagcactgcccagctg A/G tcgctgcccaccttccacag	2529
CHST3	5	intron1 + 4965	tccactgcagaggggacaca G/C tgaccaggacggaagttggg	2530
CHST3	6	intron1 + 5046	gggctgtccatctttgtacc C/T ctggttccatcccagtgcct	2531
CHST3	7	intron1 + 5300	ccttttcttctctaaggcct A/G aagagatgacagaatgctgc	2532
CHST3	8	intron1 + 5354	agcgcgtggactccacagcg G/A ggtgtggggtggccccctggc	2533
CHST3	9	intron1 + 5428	gacacgcttcagccctctgt C/G tctattgccccaaatctggc	2534
CHST3	10	intron1 + 5621	ctgtggcttccctgggcccct A/G ggaaatttatcaotgaggtt	2535
CHST3	11	intron1 + 6555	gagtggggcactgctggaag G/C ttctggttcctgctttgttc	2536
CHST3	12	intron1 + 6990	aaacacactgggccacccccc G/A tcccccactgtgactacac	2537
CHST3	13	intron1 + 7133	ctgagggcctgtcctgcagg T/G ttgatgtgtctgaagaggcc	2538
CHST3	14	intron1 + 7161	gtctgaagaggccccgagaa T/C agaaatctagaacctgccag	2539
CHST3	15	intron1 + 7199	cagtcacgaagcagtgtcac C/T caccagaggatgaagaactg	2540
CHST3	16	intron1 + 7316	cttgcatctggtgtaggtgc C/T tgggggtagcgtgcccagga	2541
CHST3	17	intron1 + 7967	gacaggaaccccaccccgag T/G gatgtctggccctgtgacct	2542
CHST3	18	intron1 + 11412	gcttgcacttctgattcatt C/T tgcagtcactggctctttgt	2543
CHST3	19	intron1 + 11591	ccctggaagggcctcactgc G/A gtgactcattacccagcatg	2544
CHST3	20	intron1 + 12541	acccacacagcatgaatggg G/C ccagcccccagcctgcccgct	2545
CHST3	21	intron1 + 12672	gtagccacagctgcggctgt G/C gggtccgggcatggcaaggg	2546
CHST3	22	intron1 + 14809	ggatgtgtagggtttgggct C/T ggccttaagggatgggtgga	2547
CHST3	23	intron1 + 16161	gatgctggtcaggcattgtc G/A ttgggatctttaacaccacc	2548
CHST3	24	intron1 + 16385	tatttagcatgtgggtttca A/C ctttctgttttttcaaaggg	2549
CHST3	25	intron1 + 33638	gacttgggccacgtccttgg G/C catgaatcttggtctatgtc	2550
CHST3	26	intron1 + 33878	agcaagaaagtgtgctcccc C/T acagcccccactcaggcataa	2551
CHST3	27	intron1 + 34690	agcacacatggagctttccc G/A cagtgggtttcagcgctccc	2552
CHST3	28	intron1 + 35145	agggaagccgaagcctcact T/C gctgggacttgcctgggcctc	2553
CHST3	29	intron1 + 35340	tgtgaagttttgcccacagt T/C ggtggccatggttcgcaccg	2554
CHST3	30	intron1 + 35436	gccactcatgtatgggagcaa T/C tgccttttttttcttcctctt	2555
CHST3	31	intron1 + 36150	ccatagaagaggctgggcct G/T aggaagccagggaagcagga	2556
CHST3	32	intron1 + 36194	ggtgtggggaggccagcagg G/A gtgtgggcctcagcgggggag	2557
CHST3	33	intron1 + 36561	ctctggtgtttgctgtcaat A/G tgcagagtgctggacaaaac	2558
CHST3	34	intron1 + 37602	ctggaacagcaacttaaaaa A/T agaaatagtccctggaaggg	2559
CHST3	35	intron1 + 37725	gggtagccagggcagctccc C/T gacccgcacctgcctttt	2560
CHST3	36	intron1 + 37734	gcagctccccgacccgca C/G ctgccttttcacccctctcc	2561
CHST3	37	intron1 + 38208	gccattctagatgcgagtcc C/T gactttggggtgcttgca	2562
CHST3	38	intron1 + 38219	cgagtcccgacttttgggg T/C gcttgcattctgggaaggga	2563
CHST3	39	intron2 + 255	ctacagctgtgaaaggttag A/G caagatacttaacatttctg	2564
CHST3	40	3'untranslated + 2202	acacctcagaggagcctgtg C/A ttaacatttgtaggattatt	2565
CHST3	41	3'untranslated + 2569	aggcctcatctgggtagggg C/G caagaggaaagtacagagtg	2566
CHST3	42	3'untranslated + 2717	ctggaatlcctccttagggc C/T ctgggaagagtattgcttaa	2567
CHST3	43	3'untranslated + 2753	cttaacgcaggatgtgctgg G/A tgttttgtttcgggcttttta	2568

遺伝子名	No.	存在位置	配　　列	配列番号
CHST3	44	3'untranslated + 2800	gcttggtgtctttcttgttt C/T atggctgtgtttttgctttt	2569
CHST3	45	3'untranslated + 3283	ccgagggctgcccagctctg C/T ttctggtttcctggacaatt	2570
CHST3	46	3'untranslated + 3327	ctgtcagatacggcccattg T/C aaacccagagggctgcattt	2571
CHST3	47	3'untranslated + 3787	gttccccatgtggaggtcgg A/G ggggctgggactgggagggg	2572
CHST3	48	3'untranslated + 3860	ggccctgctaatgtggacag T/C agactttatccctccttctt	2573
CHST3	49	3'untranslated + 4915	ccagatgtgcatagaagcca G/A tctctgtcacatacaccgca	2574
CHST3	50	3'untranslated + 4993	taaagcaaatttggctttt G/A tccttctgcaatacatgcac	2575
CHST3	51	3'untranslated + 5223	ggaaggagcttcagcaggag G/A tcottcccagaaggttgatt	2576
CHST3	52	3'untranslated + 5370	tcatacctgtaatcccagca G/T ttggggaggccaaggtggga	2577
CHST3	53	3'untranslated + 5545	ccattcccaaagtcagaaag T/C gaagccagatctcaagggct	2578
CHST3	54	3'untranslated + 5859	caaaagcacaaagcagaatt G/C gcaacttcacttgtctca	2579
CHST3	55	3'untranslated + 5870	cagaattggcaacttcac T/A tgtctcaagagctccaagat	2580
CHST3	56	3'untranslated + 5971	ttccaaggctacagacatgg C/T gccatcctcacaggcctagc	2581
CHST3	57	3'untranslated + 6208	atttcatgtctgcatggtac G/A agcacacccttcacggca	2582
CHST3	58	3'untranslated + 6223	tacgagacacccccttcac G/A gcatacactgccatggtatg	2583
CHST3	59	3'flanking + 281	agacaggagtgttgggccag C/T ggtcaggggcctggggatg	2584
CHST3	60	3'flanking + 997	acctcttaaagtatttgagc C/T ggtgcctgtcatcccaacct	2585
CHST3	61	intron1 + 22595	cgggagcaggaaaaaaaaaa A/Δ gaataagaagaaaagaggct	2586
CHST3	62	intron1 + (35423-35424)	gctcatgctcacagccactc AT/Δ gtatggagcaattgccttttt	2587
NDUFV1	1	intron3 + 670	ctgggtggagtggggtggca T/C ggagttgaagaccccagtcct	2588
NDUFV1	2	intron6 + 160	tgtgccggccccagccctga C/G catgcatcccctttgggggacc	2589
NDUFV1	3	intron9 + 27	accaccccttctgcgtagcac G/A gagggtgggtggcatcaagg	2590
NDUFV1	4	3'flanking + 1111	tgtaggctgaggtcagcccc A/G atccagtccaaagcccaccc	2591
NDUFV1	5	3'flanking + 1658	gaatgcggaagtgctctgtg G/A gcacccaccatgctccgggc	2592
NDUFV1	6	3'flanking + 1713	gatctgggggcggagggtaca C/T ggggctggcgctgggtgaag	2593
NDUFV1	7	intron4 + 214	tggtgtaaatttttttttt T/Δ gcttcaaaaatatagtattt	2594
NDUFV1	8	3'flanking + (772-774)	tgaactcgggttcagggtc TTC/Δ ctgtgaacactggttttgaa	2595
NDUFV2	1	intron1 + 526	ggaaatgctggctaaataaa C /T ggtatcaaactaactctgaa	2596
NDUFV2	2	intron1 + 6689	tcgttggatggtagtattgt T/G tgaacaacagaagaaattca	2597
NDUFV2	3	intron1 + 14767	ccaaatgcatgccagcagcg C/T gtggcaggaaggtacacaag	2598
NDUFV2	4	exon2 + 86	aaggaatttgcataagacag T/C tatgcaaaatggagctggag	2599
NDUFV2	5	intron2 - 29	cagaagatcttactctctaa T/G gaagctggataacacttttt	2600
NDUFV2	6	intron2 - 168	tttactttggtaatcatact T/G atcaaatgtgtgtttagaca	2601
NDUFV2	7	intron4 + 677	aaaccacatactatttgatt C/A tgatgagaatcacataacca	2602
NDUFV2	8	intron4 + 2295	tatgattcaacttcaaaag A/T gtattgtgatatgaaataga	2603
NDUFV2	9	intron5 + 102	caacttctgccatcttattg G/A atctgtacttacctagtaat	2604
NDUFV2	10	intron7 + 5466	tggtaagaggctttaagata A/C caaatgctcagctttcagga	2605
NDUFV2	11	intron1 + (13562-13563)	tactcttaaaattaatcctt (CTT) ttattataagtatacagtct	2606
NDUFV2	11	intron1 + (13562-13563)	tactcttaaaattaatcctt　　ttattataagtatacagtct	2607
NDUFV3	1	5'flanking - 606	aattacgactaacgttgggg A/G cgaactctttgctaaataaa	2608
NDUFV3	2	5'flanking - 222	cgccgcgccccccgccacagc G/A cccaggcgcccgcagggcac	2609
NDUFV3	3	5'flanking - 111	tggccccaagggaggcactt A/G gccctactggggatgcgcgc	2610
NDUFV3	4	intron1 + 137	ttgggccgctgaccccgctc C/T ctgggcccaggactgaccgc	2611
NDUFV3	5	intron2 + 152	tatacaagacacaagatcta T/C aacagatttagaccaaaca	2612
NDUFV3	6	intron2 + 6304	ttcacagatgaaggggttcc G/A aaatttttgtcaagaaagac	2613
NDUFV3	7	intron2 + 6433	tcgccttcgtcttcatcctc T/G tccagctcctctgattctga	2614
NDUFV3	8	intron2 + 6563	cctttgaaaacagagcccccc C/T gagttacagtatcagcaaaa	2615
NDUFV3	9	intron2 + 9819	actatcttctgtgcgcatgc G/A cagagcccaccttgcagagc	2616
NDUFV3	10	intron2 + 9858	aggatgccagctctttaaat G/A agacatcgtttttgcttaac	2617
NDUFV3	11	intron2 + 11673	cttggtaggtaagcgcctgt A/G tgtgagccaagtcattcata	2618
NDUFA10	1	5'flanking - 1734	tgcaccttgaactgtttact T/C tcctgtaaccatttaccctt	2619
NDUFA10	2	5'flanking - 1492	aaaacatccacgcaaacagg T/C tgtgcgaagttacgtctgcg	2620
NDUFA10	3	intron3 + 370	aagactgtgcatgtgccatg C/A agacagagatgtggatgcca	2621
NDUFA10	4	intron3 + 2485	ttgttattttctttttctctg G/A aatgcagtgatcagttgaca	2622
NDUFA10	5	intron4 + 236	ctgtgaaagcagattggagc C/T ctggacctcaaacacacgca	2623
NDUFA10	6	intron4 + 1742	tgtcggcatctgctgagtgt C/T tgctgaagtctgaggactgg	2624
NDUFA10	7	intron4 + 2090	ggctgggggaaagcagatca T/C gttggctaaaggacaggtgg	2625
NDUFA10	8	intron4 + 3054	cagctgattatactactgaa A/C cgggataaatgcagcttgat	2626
NDUFA10	9	intron4 + 3066	ctactgaaacgggataaatg C/T agcttgatgattttcagctg	2627
NDUFA10	10	intron4 + 3377	gtcacagtttaaatgctgct G/A ttttactctgtgtaaglagc	2628

遺伝子名	No.	存在位置	配　　列	配列番号
NDUFA10	11	intron5 + 46	aagcatctctattttgaatg T/C agatcagcactaaaagccct	2629
NDUFA10	12	intron8 + 1465	gcaacgcccagttcctggta C/T aggcctcatatccagcgtgc	2630
NDUFA10	13	intron8 + 1809	cctggaggcacaaggatggc C/A ggggcactcaacttccctct	2631
NDUFA10	14	intron8 + 11226	gttgtgtgactgtgtggggc A/G tctcacctctcgggctgcag	2632
NDUFA10	15	intron8 + 11319	atcttgccttccctcctgcc G/A tctgttcaggcttgaatcct	2633
NDUFA10	16	intron8 + 11386	ccataatcctagcttgaacc C/T tccttttccctgctgaccc	2634
NDUFA10	17	intron8 + 12301	acataattattgtaaacatg C/T cgcttaccagtgacattcat	2635
NDUFA10	18	intron8 + 13361	ccaggccactgattgctttc G/A cattttctagcattttctta	2636
NDUFA10	19	intron9 + 183	tttctgtgtggaaagctgat G/A aagtcctcagatgacagccc	2637
NDUFA10	20	intron9 + 6669	aataataatgaccatttctg G/T aaattcatagaattcctttt	2638
NDUFA10	21	intron9 + 8028	gaggacattccacagaacgt G/A tgactattagagcagaaggt	2639
NDUFA10	22	intron9 + 10742	ctggaggagaggggtggagc C/G agttcagccagcactggggt	2640
NDUFA10	23	intron9 + 10985	agaaagggttacacaggagc A/G cacttctcagggagtggtgt	2641
NDUFA10	24	intron9 + 10989	agggttacacaggagcacac T/C tctcagggagtggtgtgacg	2642
NDUFA10	25	intron9 + 12601	ctgtgaatcctctcacctgc G/A tgaaggggctggctgcctct	2643
NDUFA10	26	intron9 + 13908	cacattgttatgtaaccaag C/T ctggaattgcagtgtgaaga	2644
NDUFA10	27	intron9 + 13911	attgttatgtaaccaagcct G/T gaattgcagtgtgaagaact	2645
NDUFA10	28	intron9 + 14064	tcttgactattagaaaccct A/G tcagataaattttaaaacag	2646
NDUFA10	29	intron9 + 14184	tggctttggttgggaacagc G/A agagatacagaaccgacggt	2647
NDUFA10	30	intron9 + 16487	cttgaagctgatcgttccct C/A cttgaagctgatcgttccct	2648
NDUFA10	31	intron9 + 16779	gccagacgtgactgctttag G/A ttcctcatgacattcagacc	2649
NDUFA10	32	intron9 + 17663	ttccaaatcaccccagaact T/G tgcagtattttgaagctcct	2650
NDUFA10	33	5'flanking - (1668-1659)	gtaaaattgttttaactaga (C)9-11 ttcctaaaccaaggtataaa	2651
NDUFA10	34	5'flanking - (1355-1334)	ctgtatccattggaaggcac (A)15-21 tgcaaaggaaacaaggcaaa	2652
NDUFA10	35	intron1 + (46-61)	tggcggggtggcagggtggc GGGGTGGCGGGGTGGG/Δ gag cagttccacatctcccc	2653
NDUFA10	36	intron4 + 2486	ctcactggaacttttttttt T/Δ aatttaatttttaaaatttt	2654
NDUFA10	37	intron7 + (1600-1601)	cacttccattctgactgtta (A) cggtgtgattcttcctgcca	2655
NDUFA10	37	intron7 + (1600-1601)	cacttccattctgactgtta cggtgtgattcttcctgcca	2656
NDUFA10	38	intron9 + 1054	gcgcgtgctgtttctcccctt A/Δ tctgtccttgtacacgtgtg	2657
NDUFA10	39	intron9 + (8161-8172)	tttctcgctttctgggagac (T)10-12 aatgttgaaaatatgtgttt	2658
NDUFA10	40	intron9 + (8646-8647	aattccccccattgcttctct (TT) ctgtagacattttaaacctg	2659
NDUFA10	40	intron9 + (8646-8647)	aattccccccattgcttctct ctgtagacattttaaacctg	2660
NDUFA10	41	intron9 + (16503-16523)	ccctccttgaagctgatcgt TCCCTCCTTG AAGCTGATCGT/Δ gtccaagatagttgctagga	2661
NDUFA10	42	intron9 + (17905-17936)	caaatatatgtatacatgta (CA)12-18 tccttcatgaaaactctttc	2662
MGST1	37	5'flanking - 1376	ttaataaatgtttattcaat T/G aaaccaactgctaatattct	2663
MGST1	38	intron1A + 147	cctggagattttaactttct G/A cgaagtttttaaaaacaact	2664
MGST1	39	intron1B + 36	ggagaaggggaccgcatgca A/G agggtggcaggcagggaggg	2665
MGST1	40	intron1C + 456	cccctttgggacggttctcac C/T tgtgccccacttccccagtc	2666
MGST1	41	intron1C + 719	gcccgcaagcattgctgtat A/G gcacccaggcctccagtgag	2667
MGST1	42	intron1C + 985	cgagtaaaatttttctaccg C/G tttgttttagagtggtgtct	2668
MGST1	43	intron2 + 3083	aaaaaatttgtagatatggg T/G actccctatgttgcccaggc	2669
MGST1	44	intron2 + 3106	tccctatgttgcccaggctg A/G tcttgaattcttgggctcaa	2670
MGST1	45	intron3 + 1703	ttctcttctaagaagaagtc T/C gtgcagatacttagcacaaa	2671
MGST1	46	intron3 + 2557	tccagcatcttccctttcca T/C ttttaagttagacttttttt	2672
MGST1	47	intron3 + 3032	agagacatttagaatatatt C/A cctttaaaggtagagaataa	2673
MGST1	48	intron3 + 3045	atatattccctttaaaggta G/C agaataacccttcactgaga	2674
MGST1	49	intron3 + 3289	ggtttatagtgttccccccc T/A ccccgccccccaaaagaccca	2675
MGST1	50	intron3 + 3885	gaagctgccgctccaggaag G/C agtctgtcgttggagaagag	2676
MGST1	51	intron3 + 3976	ggaaagctggggaactgttt G/T cctggaacagagtctcaaaa	2677
MGST1	52	intron3 + 4298	tgtcaactgcgtaacacagg G/T gtagaagtggcattgtttt	2678
MGST1	53	intron3 + 4519	tttaatagaaaatggtattc G/T tgtcttttctttcccatctc	2679
MGST1	54	3'untranslated + 603	gggtaaacccatttttgaata T/C tagcattgccaatatcctgt	2680
MGST1	55	3'flanking + 147	tatttgctttccttctctct C/T tgttttctttttctctgaaa	2681
MGST1	56	3'flanking + 237	cagcacgtttttcctatgaa C/T aagacattctccaaataact	2682
MGST1	57	3'flanking + 1318	tggctctgtgtgcatgaaca T/C gcacgcgtgcacgcgcacac	2683
MGST1	58	3'flanking + 1331	atgaacatgcacgcgtgcac G/A cgcacacacacacacacaca	2684
MGST1	59	intron1C + (904-923)	tgcgattatcttttggtaatt (A)18-20 ggcaaatcagtccaaatttg	2685
MGST1	60	intron1C + (3433-3434)	ccccttcaatactagaacaa (AA) gcagacacattaaatgttac	2686

遺伝子名	No.	存在位置	配　　列	配列番号
MGST1	61	intron1C + (3433-3434)	cccctteaatactagaacaa　　gcagacacattaaatgttac	2687
MGST1	62	intron1C + 5145	actatttcaattttttttt T/△ ggaggggagacagagtctc	2688
MGST1	63	intron2 + (552-563)	cccagcattataagaatgac (T)9-13 aagtgcagatgtggggaggg	2689
MGST1	64	exon3 + (172-173)	tagcatttggcaaaggagaa AA/△ tgccaagaagtatcttcgaa	2690
MGST1	65	intron3 + (152-158)	agaaaactggatgtctgaaa TTGACA/GTCCAATAT cactg cacttgtatgtgttg	2691
MGST1	66	intron3 + (2198-2200)	ggattttagattcctcccta CTA/△ ttctttccgaccttccaccc	2692
MGST1	67	intron3 + (2571-2580)	tttccatttttaagttagac (T)9-10 cacctctctcgttacttcag	2693
MGST1	68	intron3 + (4682-4683)	tcctcttcatgtctctatgt (GAGATGTTG TGGCTCACAT) agtcatcctctttgtgagac	2694
MGST1	69	intron3 + (4682-4683)	tcctcttcatgtctctatgt　　agtcatcctctttgtgagac	2695
MGST1	70	3'flank + (1359-1360)	acacacacacacacacacac CC/△ tgctctggagttgggcaact	2696
MGST1	71	3'flank + (1889-1891)	ttagaatagtttctaactat ACT/△ tttactcccaagagaagctt	2697
HMGI7L1	1	3'untranslated + 864	ctttctgatttttgatagtc G/C gttgaagaagggagtttgaa	2698
UGT2A1	1	5'flanking - 1602	ataacatcttctgcagagaa A/C cttcaatggeaatacactca	2699
UGT2A1	2	5'flanking - 1480	tacagattatctttggtgat G/C ggagagcttagaagagacat	2700
UGT2A1	3	5'flanking - 1406	atttcagaagatttattaac A/T tgaaaaggatcactctgctt	2701
UGT2A1	4	5'flanking - 1388	acatgaaaaggatcactctg C/T ttattcacagacatatgcat	2702
UGT2A1	5	5'flanking - 935	aaattattcaatctctttgg G/A cagtggtttctttttctttg	2703
UGT2A1	6	5'flanking - 287	cctgaatgtagagttgagat G/A tacagaagctttatccaatt	2704
UGT2A1	7	5'flanking - 128	gagaagtaagacacattacc C/T ataaatctgtaaatatcctc	2705
UGT2A1	8	intron1 + 535	cattgatcagggtgatttat C/T catgctaagcttatttaatt	2706
UGT2A1	9	intron1 + 642	tatattgatcatgttgatac A/C tttatacacatatttgtcta	2707
UGT2A1	10	intron1 + 1221	ttttaatctaataagcaatt C/G aggaccatctaaagggaaat	2708
UGT2A1	11	intron1 + 1448	aggtgcttacaggcaacatc C/T acatagcagtctgtggctgg	2709
UGT2A1	12	intron1 + 2000	gacacattagcttcttttct A/G cagatctctgttctaaaaca	2710
UGT2A1	13	intron1 + 3118	cttaaaattctttaatgaaa T/G cattgcaacaaatttatatc	2711
UGT2A1	14	intron1 + 3191	ataaatagaacaactcccta A/T gtttacttctctgcagtgga	2712
UGT2A1	15	intron1 + 3770	atcaccagataatttactat C/T cattaaggagtaggtcatca	2713
UGT2A1	16	intron1 + 4584	tgattggttagaatctttga A/C aaatcttctagtatcattcc	2714
UGT2A1	17	intron1 + 4854	tactctgtgcattgttaata G/A cctatcacttgtggtctgcc	2715
UGT2A1	18	intron1 - 19146	ctgtttaaattctcattcaa C/T ggccacatggttaaaataaa	2716
UGT2A1	19	intron1 - 18346	atggcaatatttttagaaat G/A ttaactcccaataatgaata	2717
UGT2A1	20	intron1 - 18218	tatatcattattttaacttа T/G agatagcactagccctaatt	2718
UGT2A1	21	intron1 - 17937	ctcctaataatttggactca C/T catacttattcagcactatc	2719
UGT2A1	22	intron1 - 12585	ttccacacagggacaagtca A/G cagaggaaatttttcttgct	2720
UGT2A1	23	intron1 - 11430	aacaaaggtttatttttctta C/G agttctgatggctagacgtc	2721
UGT2A1	24	intron1 - 10761	tttaaaatatgcatgtattt T/G ccacttttaaaaactatatc	2722
UGT2A1	25	intron1 - 381	aaatcctccctcttcctttc C/T tttcccaggccccaatctac	2723
UGT2A1	26	intron1 - 329	ttcccttttctcctttttctcc A/G tctctctctcttcctctcic	2724
UGT2A1	27	intron1 - 41	ttttctcctcagcaaacata T/A aagctaatttcctccatcca	2725
UGT2A1	28	intron2 + 263	caccttgatactggacttgg T/C gggacagaaaaccagatcat	2726
UGT2A1	29	intron2 + 454	agaaagcccattgaaataag G/C cagggttttaggttttaat	2727
UGT2A1	30	intron2 + 554	aaaaactttttgagttgac A/T atggtgagtttagtttctga	2728
UGT2A1	31	intron2 + 1113	ctgcaggcaagctctagtga A/T tgtttattatagaaataat	2729
UGT2A1	32	intron2 + 1304	gacaaatcagccatgttttа C/T aatagcagacattatgccat	2730
UGT2A1	33	intron2 + 1305	acaaatcagccatgttttac A/G atagcagacattatgccatt	2731
UGT2A1	34	intron2 + 1367	atcgatataggctttgggaa A/C tatgaataccaaccatgggt	2732
UGT2A1	35	intron2 + 2074	aaatttttttcttagacctat G/T aatcaaaggaggcatacagt	2733
UGT2A1	36	intron2 + 2164	attttattagatataactgg A/C atgctaacaattttaaaagc	2734
UGT2A1	37	intron2 + 2298	taacaatttcagttagcatg A/C gaagagttgtcccttattta	2735
UGT2A1	38	intron2 + 2346	tttctgtaatggttttgctt T/C catgcttggacttgtaatca	2736
UGT2A1	39	exon3 + 922	gtgttgtggtgttttctctg G/A gatcaatggtcaaaaacctt	2737
UGT2A1	40	intron3 - 217	aagcttagaagtgataaata T/C caaaacaataatactatact	2738
UGT2A1	41	intron3 - 194	aaacaataatactatactgg G/A tagactattagtacaagact	2739
UGT2A1	42	exon5 + 1171	acggagtccctatggtggga G/A ttcccatgtttgctgatcag	2740
UGT2A1	43	intron5 + 1546	tttttaaaattcagaaactc A/G gttatggtgtattcttacaa	2741
UGT2A1	44	intron5 + 1547	ttttaaaattcagaaactca G/A ttatggtgtattcttacaaa	2742
UGT2A1	45	intron5 + 2013	atcatattcattacccctccc G/T ctattattgtattttgaatc	2743
UGT2A1	46	intron5 + 2318	aatttagtgottttttcttaa C/T ggaagtaacctgcttaaaaa	2744

遺伝子名	No.	存在位置	配　　列	配列番号
UGT2A1	47	intron5 + 2505	taattgacttttattaatac G/A tacatgttgtataagtcata	2745
UGT2A1	48	intron5 + 2639	tagactattacaaagttgtt A/G gttgctgacaatttttgttca	2746
UGT2A1	49	intron5 + 4009	gaatccaggctggaacttttt C/A ttccagacacaaaccaaaat	2747
UGT2A1	50	intron5 + 4311	atacagacactgtccttttc G/A tcacaaacatacagatgtgt	2748
UGT2A1	51	intron5 + 4545	agctcacacagtatcaaaat T/C atttttggaaaaattatgct	2749
UGT2A1	52	intron5 + 4616	actttttatgtctacattt G/C atcatactgtgttaagcata	2750
UGT2A1	53	intron5 + 4717	tgcaagaattatatttctc C/A acgtaactatggccttaaac	2751
UGT2A1	54	exon6 + 1524	gctatatttttggtcataca A/G tgttgtttgttttcctgtca	2752
UGT2A1	55	3'untranslated + 1683	aaggagtttaacaaaaacac G/A tctcccatcctgtttccaaa	2753
UGT2A1	56	3'flanking + 685	aatctagaaaataattatca T/C ttttataaaattttagtca	2754
UGT2A1	57	intron1 - (18967-18965)	ctcccaattagattgattag TAT/Δ gagttcctggggttactggt	2755
UGT2A1	58	intron1 - (18862-18803)	aatacattcttccccccttca (AC)14-17 atgcttactggcctatttat	2756
UGT2A1	59	intron1 - (17463-17447)	aaacttagaaacctctattc (A)16-27 gtaaagaaaatggcagagaa	2757
UGT2A1	60	intron1 - 10860	attcaatgcaacttttttt T/Δ gtaatggcagaattagaaca	2758
UGT2A1	61	intron2 + (528-538)	ctgttagggaaacaattggtt (A)8-10 ctttttgagttgacaatgg	2759
UGT2A1	62	intron2 + (1514-1533)	ttgtgtgtatgtgtatgttt (GT)9-11 tattttaatgaattaatatc	2760
UGT2A1	63	intron5 + (916-917)	gcttagtatattatatatat AA/Δ gtctatatatatagcttagt	2761
UGT2A1	64	intron5 + 1163	caatatttatgtcatttttt T/Δ ctcacatttactctgtttcc	2762
UGT2A1	65	intron5 + (3819-3838)	agacagacagacacacaaac (AC)8-12 tcaacacatgtaaactactc	2763
UGT2A1	66	intron5 + 4785	tatcttcaatgaaaataaaa A/Δ caaaaattgtctaatttctg	2764
OATP1	1	5'flanking - 916	acagagtagatgttcaataa G/A tatttgttgtatctgtgaga	2765
OATP1	2	5'flanking - 843	tagtgcagcgactatgcctt G/A atgtgtgtgtgtttgggatt	2766
OATP1	3	5'flanking - 526	aaatgtgtgcctgtatgtta T/C acatctgtacatatatttcc	2767
OATP1	4	5'flanking - 172	acaaacacaactcaaagtat G/A tgtgttattaaaagtagcta	2768
OATP1	5	intron1 + 206	ttgattcaggcaagttagtc C/G taaatggctttgagagactt	2769
OATP1	6	intron1 + 454	caacataacaataatttcct G/A taagaaaaatggccattttg	2770
OATP1	7	intron1 + 999	gtttagcaaggttagatatt A/G atgtggatgttaagacaaaa	2771
OATP1	8	intron1 + 1223	ttgctagaagctagtaggac C/T agctttataaatacagagat	2772
OATP1	9	intron1 + 1326	aactagttaggcaacccatg T/C gttttaggggaaaagcaatg	2773
OATP1	10	intron1 + 1336	gcaacccatgtgttttaggg G/A aaaagcaatgaggtcatgat	2774
OATP1	11	intron1 + 1498	atagttgctcttaagaata C/T actctgagaaggtttatagt	2775
OATP1	12	intron1 + 5041	ttatgctcccgaggagttag C/T tctctaaatgcataaggaga	2776
OATP1	13	intron1 + 9532	aaagactgggagcacttccc A/G atgacaaatactagactaga	2777
OATP1	14	intron2 + 198	ttacctcatattaacaccta A/C atattgccacatatcctacc	2778
OATP1	15	intron2 + 961	aaaaagttatatagaaatat A/G agtgtcactccttttctagtt	2779
OATP1	16	intron2 + 1110	gtctactagtgttcaactcc T/C ttagatcttagcctgtatca	2780
OATP1	17	intron2 + 1419	aaagcctaagaaggatgcag T/C gcaatagcctatgtgagaag	2781
OATP1	18	intron2 + 3339	tatggtttgcaaaaaactta T/C tcgtatatttgttttttca	2782
OATP1	19	intron3 + 66	caggaaatgaagttgcactt T/C cctctctaggagcaatgctt	2783
OATP1	20	intron3 + 205	tcagttttgtcaatttacac A/G atggggatttgggaccttit	2784
OATP1	21	intron3 + 6377	aatgaatagactttgagtta C/T tggatttttagtggataaat	2785
OATP1	22	intron3 + 7238	tgaatgtcacatttttttaaa G/A tttgtgttccttatctcata	2786
OATP1	23	intron4 + 1016	ttttattctggattcatgtt T/C gtggaaattgcagtagtcca	2787
OATP1	24	intron5 + 110	tccacaatgatgagtagagt A/G tcttggcacagttggccttc	2788
OATP1	25	intron6 + 496	agtgtctgaattataagcca A/G ttttatagttggttgggacc	2789
OATP1	26	intron7 + 1934	aaagtgaaaggaaattaaaa G/C tgagaacttgagcctgaatg	2790
OATP1	27	intron7 + 2140	tagaatgtaccaaatgaatc A/G gcatctctgaggatgggacc	2791
OATP1	28	intron7 + 2365	tgaaatcttctttatcaact C/T gattttcctccagactttac	2792
OATP1	29	intron8 + 88	gcaaactcctaagttgaagt G/C ttttaggatatttttttgact	2793
OATP1	30	intron9 + 534	tcatattttgtatttttaaag G/A ttatctgggttttactgaaa	2794
OATP1	31	intron9 + 1286	tattcttctgagataaatca T/C tgaaggagtggctatgtggt	2795
OATP1	32	intron11 + 215	ttcactcctattcctcgcta C/T ttttcttcctatttcttag	2796
OATP1	33	intron11 + 663	ttcttcttctttttggagctc T/A aaagtagagttcagttaatc	2797
OATP1	34	intron11 + 999	atcatcactgcatgagagtt A/G gaattatctaactttgtgat	2798
OATP1	35	intron11 + 16727	ttttcttttatttacaaactt A/G tttacttttcaggtgtatga	2799
OATP1	36	intron12 + 48	ctatcagaacaatattatta T/G tattatttttttattacactt	2800
OATP1	37	intron12 + 686	tatgttttgataaactttgc C/A gtacaaataaagaaaattga	2801
OATP1	38	intron12 + 708	tacaaataaagaaaattgaa A/G tatttccaaataaatcaagt	2802
OATP1	39	intron13 + 418	tctctggtctccaaaatcat A/G tattttctcctctttacat	2803
OATP1	40	intron13 + 436	atatattttctccctctttta C/A attttgctgaaacaatcttc	2804

遺伝子名	No.	存在位置	配　　列	配列番号
OATP1	41	3'untranslated + 2130	gtctttaagaacctaaaaaa C/A ctcttaactcaaaataataa	2805
OATP1	42	3'flanking + 57	agtgactaaagttttctta C/A aaacaagtgtctgaatcaaa	2806
OATP1	43	3'flanking + 572	aatacactatggttatttat G/A tgtactataaatggagtgag	2807
OATP1	44	3'flanking + 788	atttcctaaatgatcagatg C/T atcatatgaaaaaagaaagc	2808
OATP1	45	3'flanking + 1356	aggtgactgacataaatggg G/A gcagaggacataatgaggtt	2809
OATP1	46	5'untrnslated - (189-188)	attttctaatctgtattaaa (A) gcgttccaggtatttttgta	2810
OATP1	47	5'untrnslated - (189-188)	attttctaatctgtattaaa gcgttccaggtatttttgta	2811
OATP1	48	intron4 + (725-726)	tgatctttaatagcgggaaa AA/△ caggcaagtacgctatagtt	2812
OATP1	49	intron4 + (1082-1083)	attgagtcaggaaaccaaaa CA/△ gtttcaaaaatttgaaaaat	2813
OATP1	50	intron4 + 2301	aatgtcatgtctttttttt T/△ catgcagcgtgtacaaagga	2814
OATP1	51	intron9 + (241-246)	attgtatgtgcatgtgggtg TGTGTG/△ catgattgtctttgtgatat	2815
OATP2	1	5'flanking - 2574	ggataaggcaacccctatgt A/G tcactgctgcaggagcgggga	2816
OATP2	2	5'flanking - 2366	aacataggaatgtgcagagc C/T ctgtggggattagagaagag	2817
OATP2	3	5'flanking - 2244	tgatgatgccagagctttga T/G cattggtgggtatagaaaca	2818
OATP2	4	5'flanking - 1723	tctttcagacttcaaaggcc A/G tgatatttcatcagagctgt	2819
OATP2	5	5'flanking - 1180	tgcttatttaacaggcataa T/G ctttggtctcctgagccaga	2820
OATP2	6	5'flanking - 811	tatgtgcatatgtgtatata G/A gtaaaagtgtgtatatatgt	2821
OATP2	7	intron1 + 7188	aatcatttgaaatttaagaa A/G aaaatatgttcagagaaaaa	2822
OATP2	8	intron1 + 7331	gtgaaatgaggaacaaagtg T/C ccacctttttttcctgaata	2823
OATP2	9	intron1 + 7391	agagagatgtgaaatagtat T/G tttctgggggagtagggaa	2824
OATP2	10	intron1 + 7886	ttgttagtagaaagaaaatc G/A aagcctaaaactaaaggaag	2825
OATP2	11	intron1 + 7958	ttgctattatataattttttt T/A aaaaaaagatttcctaatat	2826
OATP2	12	intron1 + 7959	tgctattatataattttttt A/T aaaaaagatttcctaatatt	2827
OATP2	13	intron1 + 8036	ggaaaaaatggggtgaaatt A/T atcaaagggcagcttattac	2828
OATP2	14	intron1 + 9164	acattatattctatataaaa G/T agtcagttgaagtaaaaagt	2829
OATP2	15	intron1 + 10123	tctgtctttcctacttttgt T/G tccagcattgacctagcaga	2830
OATP2	16	intron2 + 193	tgattaagtatttctttggc G/A aaatttttgatgcttaatag	2831
OATP2	17	intron2 + 1020	ttgagtaacatttaggccaa G/A tggcagtcataaggaaaaag	2832
OATP2	18	intron2 + 14865	agaggaattaatcataagag G/T tttatttggctaaagtgaca	2833
OATP2	19	intron2 + 14931	gttagttaataacagaaaaa A/T tatcagaaattttaaaaaat	2834
OATP2	20	intron2 + 15417	ttctaaaataagtaagctaa A/T tattctatattatactacta	2835
OATP2	21	intron2 + 20823	ttgtataagagatacaaaac A/C aattcctactagggaaata	2836
OATP2	22	intron2 + 20852	ctagggaaataaagcttca G/C taaggaggtggcattaagct	2837
OATP2	23	intron2 + 20930	atggagagaagcagcagtgt A/G ccacagataaatgaagtgag	2838
OATP2	24	intron2 + 21360	ttcaaaagctgtatttctca T/C tagtgctttttgtgaataaa	2839
OATP2	25	intron2 + 21467	tatatacacaatacctgtcc A/G gaagatgtggtataagccaa	2840
OATP2	26	intron2 + 21621	tatcaatacttatgaagaga A/G ctaactattctaactaggga	2841
OATP2	27	intron2 + 22760	ttccccacctcctgttggtt C/G tcctcttaaacttctccttg	2842
OATP2	28	intron2 + 23199	cctatctgcacataacatta C/T aaacttatggcaattataaa	2843
OATP2	29	intron2 + 23218	acaaacttatggcaattata A/G aactcaatacatattatact	2844
OATP2	30	intron2 + 23330	gcccttgttcctgttcctct G/A tacctgcctcaactacatag	2845
OATP2	31	intron2 + 23673	ctggagacggtagctcaaac T/C gaggatgaaaatagacattt	2846
OATP2	32	intron3 + 89	ggttatcaactggggtaaat T/G tatctctcaoaggcaattttg	2847
OATP2	33	intron3 + 224	tgctaaatattctataatgc A/G caaagaatgatgtaactgaa	2848
OATP2	34	intron4 + 97	ccctttaaataggcagttac C/A ttttgagaagatacccacta	2849
OATP2	35	intron4 + 568	ttcatgatccaaattgtggc A/G acgtatttccaggcaacaag	2850
OATP2	36	intron4 + 599	aggcaacaagatagaagaag A/G aaagaataagaagcaacaaa	2851
OATP2	37	intron4 + 753	aaaatagacattattccaag T/A taccaagttcccggttaaaa	2852
OATP2	38	intron4 + 781	ttcccggttaaaaatcccaa G/C tataattactgtggaaggaa	2853
OATP2	39	intron4 + 1196	aaggaccacaatctagatca G/T cattgctctaaatatgccat	2854
OATP2	40	intron4 + 1229	tatgccataatatgtgacac T/C tttgcaootggtatttctac	2855
OATP2	41	intron4 + 1623	catctagttgaaatggatta G/C attttatttttactacattt	2856
OATP2	42	exon5 + 388	attctaaagaaactaatatc A/G attcatcagaaaattcaaca	2857
OATP2	43	exon5 + 452	taatcaaattttatcactca A/G tagagcatcacctgagatag	2858
OATP2	44	intron5 + 165	ttaatatacacagttcgccc A/T ttaacaacacaggtttaaac	2859
OATP2	45	intron5 + 189	acaacacaggtttaaactac G/A ggttttcacttctatgcaaa	2860
OATP2	46	intron5 + 191	aacacaggtttaaactacgc G/A ttttcacttctatgcaaatt	2861
OATP2	47	intron5 + 507	atataactttgctttcattg C/T aaaaggcaaactgttatatc	2862
OATP2	48	intron5 + 520	ttcattgcaaaaggcaaact A/G ttatatcatttaaagacttt	2863
OATP2	49	intron5 + 856	agtcatgataaacctaatag A/G ataaaacaacaaaaaagaaa	2864

遺伝子名	No.	存在位置	配　　列	配列番号
OATP2	50	intron5 + 1157	acagataatttttacttgtt T/C gtgcttttctgtatgatatg	2865
OATP2	51	intron5 + 1226	ccttgattgtaataatctcc A/C catgccaagagtggggccag	2866
OATP2	52	intron5 + 1228	ttgattgtaataatctccac A/C tgccaagagtggggccaggt	2867
OATP2	53	intron5 + 1304	actgttctcgtggtaatgaa G/T aagtctcacaagatctgatg	2868
OATP2	54	intron5 + 1348	ttataaatgagagttcccct G/A caaaagctctcttgcctgcc	2869
OATP2	55	intron5 + 1407	ttgctcttccttcatcttcc G/A ccatgattgtgaggcccccc	2870
OATP2	56	exon6 + 521	gtcatacatgtggatatatg T/C gttcatgggtaatatgcttc	2871
OATP2	57	exon6 + 571	gggagactcccatagtacca T/C tggggctttcttacattgat	2872
OATP2	58	exon6 + 597	ctttcttacattgatgattt C/T gctaaagaaggacattcttc	2873
OATP2	59	intron7 + 33	agaacaaggtaccatgataa C/T gtctttctaagcacacatgc	2874
OATP2	60	intron7 + 267	caaaataaccaaatgtaaaa T/A gtctccctcccaaactgact	2875
OATP2	61	intron7 + 1260	gtaatctcacatttctctgc A/G tttacacttggtaaaacttt	2876
OATP2	62	intron7 + 1386	agtctcaaattaatagccaa G/A agcatgcctttattgtaacc	2877
OATP2	63	intron7 + 1472	ctttccacatgacagaatg G/A catgttcttagcaaataata	2878
OATP2	64	intron7 + 1697	tttacatgttcaattttaga C/A atatgccttagagtagctac	2879
OATP2	65	intron7 + 2273	ttctcacgtcctatctagcg C/T gattatgacccttagttact	2880
OATP2	66	intron8 + 207	gtggaagagaattaggtttg T/C actttttagcagggagaaac	2881
OATP2	67	intron8 + 546	tcggagaagtttctccctc T/C gtaattgagtaatatttat	2882
OATP2	68	intron8 + 565	atgtaattagagtaatattt A/C ttttggtaattatctatcta	2883
OATP2	69	intron8 + 668	taagtaatgtaaattaggat G/T catcagcatttgacagtgcc	2884
OATP2	70	intron8 + 739	tggagaaccattgagagtca A/G taaacaaagagaatgacttg	2885
OATP2	71	intron8 + 2193	tgatcacagatccaaatgac A/G taatttctaccatgaacaga	2886
OATP2	72	intron9 + 112	attttagtaatacaggataa G/C tataattttcttgtattctt	2887
OATP2	73	intron9 + 266	ttagaggtagtatctgtata A/G ttggatcttataatttagtg	2888
OATP2	74	intron9 + 305	tgctaagatctgagacaaac C/G cttttgtaattataatcatt	2889
OATP2	75	intron9 + 888	aggttctgtatgttttttaa T/C aaatgacaaagatatattaa	2890
OATP2	76	intron11 + 10224	tacacttgttccataaaaaa T/C tcctctatattattcctagt	2891
OATP2	77	intron11 + 10359	attaatagattcaacgtgag G/C ttcccttaaacttttagccta	2892
OATP2	78	intron11 + 10916	cttatatagaaagaaatcca C/G aaaactettttaccttttat	2893
OATP2	79	intron11 + 10997	aatatattagtttgaacaag T/C gagacttcactaaatataat	2894
OATP2	80	intron11 + 11018	gagacttcactaaatataat G/A caatgtatttgcagcactgt	2895
OATP2	81	intron12 + 442	aacattccaaaactttaat C/T gactcacagcatgacttttta	2896
OATP2	82	intron12 + 445	attccaaaactttaatcga C/T tcacagcatgacttttataa	2897
OATP2	83	intron12 + 447	tccaaaactttaatcgact C/A acagcatgacttttataata	2898
OATP2	84	intron12 + 907	aatgaaaagaagotggcaga T/C tgaaacatactgaatgagag	2899
OATP2	85	intron13 + 65	tatatatatatatatatata C/T acacacacatacatatatta	2900
OATP2	86	intron13 + 870	aattctgagtatcctattto G/A atgtatccaatctgtggcac	2901
OATP2	87	intron13 + 1935	taaaaaaaaaaaaagtctgc T/C tttacagcaattgagccaag	2902
OATP2	88	intron13 + 2261	aacgaatcctccaaattttt G/C aactttatttaatcaaaat	2903
OATP2	89	intron14 + 248	tcaaggataataaccaactt G/A tcaaaaatcagagataatag	2904
OATP2	90	intron14 + 2463	atttgtttactaatatggaa C/G cttcttcaagacatattttt	2905
OATP2	91	intron14 + 2857	tcatcatgtatttccaggac A/T cctggcaagatgctcctcag	2906
OATP2	92	intron14 + 11458	atctccagaggtcctgctgt C/T tccccaaagtccactgaccc	2907
OATP2	93	3'untranslated + 2243	ataataaaacaaactgtagg T/C agaaaaaatgagagtactca	2908
OATP2	94	3'untranslated + 2404	tcttaataaaacaaatgagt A/G tcatacaggtagaggttaaa	2909
OATP2	95	3'untranslated + 2515	cagagtttgaactataatac T/G aaggcctgaagtctagcttg	2910
OATP2	96	3'untranslated + 2539	gcctgaagtctagcttggat A/G tatgctacaataatatctgt	2911
OATP2	97	intron1 + 457	taattggcaaacataaaaaa (A) caggtgtctcaaagtcacat	2912
OATP2	98	intron1 + 457	taattggcaaacataaaaaa caggtgtctcaaagtcacat	2913
OATP2	99	intron1 + (7537-7538)	gatcagcattacaaccaaga (G) atggagaatgacattcagga	2914
OATP2	100	intron1 + (7537-7538)	gatcagcattacaaccaaga atggagaatgacattcagga	2915
OATP2	101	intron1 + (10032-10035)	tgtgtgattctatattactt ACTT/Δ gtttcaaatttctctccaca	2916
OATP2	102	intron1 + (10058-10061)	ttcaaatttctctccacaaa TTTA/Δ tttttctattaaattgtaat	2917
OATP2	103	intron2 + (413-423)	acttatttaaaaattcttttt (A)11-13 caaaaaacaggatttaaaaa	2918
OATP2	104	intron3 + (1595-1603)	ttgccaagtaattcaagtgc (T)8-10 gtatttaaaacaacttttca	2919
OATP2	105	intron4 + (10-23)	ttcatgggatagtaagtgtt (A)12-14 cctctgtgccactatcagta	2920
OATP2	106	intron5 + (1567-1572)	gtgaatataaattacttgta CTTGTA/Δ aattaaaaaaaaataagtag	2921
OATP2	107	intron5 + (1577-1585)	attacttgtacttgtaaatt (A)9-10 taagtagaataattaagagt	2922
OATP2	108	intron8 + (1939-1941)	ttctctaactcctctactc CTT/Δ atttcaagcagatgcaactg	2923
OATP2	109	intron10 + (3077-3078)	aaattctttatctacttttt (CTT) ttccctctttctctgctttc	2924

遺伝子名	No.	存在位置	配　　列	配列番号
OATP2	110	intron10 + (3077-3078)	aaattctttatctacttttt　ttccctctttctctgctttc	2925
OATP2	111	intron11 + 11011	aacaagtgagacttcactaa A/△ tataatgcaatgtatttgca	2926
OATP2	112	intron12 + (1160-1169)	agcatgacatggtagagatg (A)9-11 gcattttaacatttgttaa	2927
OATP2	113	intron12 + (1310-1312)	tccatcttaatataaaatgt TGT/△ ctactcaaaaggagaagtct	2928
OATP2	114	intron13 + (9-34)	tacgagcactaggtatgatg (A)24-27 tatatatatatatatatata	2929
OATP2	115	intron13 + (35-64)	aaaaaaaaaaaaaaaaaaaa (TA)10-21 cacacacacatacatatatt	2930
OATP2	116	intron13 + (1379-1387)	aaaatttattcaccacaatac (A)8-10 caaagtaaagttatgaacac	2931
OATP2	117	intron13 + (1916-1928)	aattctcttaaaataatgtt (A)11-13 gtctgcttttacagcaattg	2932
OATP2	118	intron14 + (588-596)	caattatactttacctctttt (A)8-10 ctaatttcaaattcatatat	2933
OATP8	1	5'flanking - 1413	aataggggcttaataactct G/C aaacttatgatttctcatat	2934
OATP8	2	5'flanking - 1345	gaattttatcctacagatatg A/G ccacacagaaaatgacatat	2935
OATP8	3	intron1 + 38962	atgaaattagtttaaaaata G/A caaccttaactatactcctc	2936
OATP8	4	intron2 + 253	acagacttaccaacaaagaa T/G tatccttcccaaaatgtcta	2937
OATP8	5	intron2 + 329	actcatggtttgcaaattaa C/G tttttaggaaactttatctc	2938
OATP8	6	intron2 + 2568	ccattctggtgctttctttc G/A tgaaactatttttccatcagt	2939
OATP8	7	intron2 + 2679	ctcttattgctcttcttcca T/C gttttaatctaaataattta	2940
OATP8	8	intron2 + 2753	caggaaacttttccaaaagcc C/A ctaattaatttaagctcccc	2941
OATP8	9	intron2 + 3132	tggtttaatgtaggagagtt T/C accttcacagttaaattaca	2942
OATP8	10	intron2 + 3193	aatgtcttgggcatatttgc A/G ttcatttggggcattcagtt	2943
OATP8	11	intron2 + 3207	atttgcattcatttggggca T/C tcagttctactagatacaaa	2944
OATP8	12	exon3 + 334	gaactggaagtattttgaca T/G ctttaccacatttcttcatg	2945
OATP8	13	intron3 + 76	agaattttattttatactt G/A taagtgggcagttacctttt	2946
OATP8	14	intron4 + 2443	tcaatttcatgttgctctta C/T agttataggtattctaaaga	2947
OATP8	15	intron4 + 67	taatcacgtctataaagttt C/G tgatattctttaacaaaatt	2948
OATP8	16	intron4 + 91	tattctttaacaaaattgat T/A taagaacaaataggaagaac	2949
OATP8	17	intron4 + 197	ggtttgaactgcacctgttc G/A cttatatgcagcttttgtcc	2950
OATP8	18	intron4 + 813	tttaacagaataaaaaaaaa T/A attttgtaacgacaaaagaa	2951
OATP8	19	intron4 + 974	atatgcaccttaaaaataac C/G tggattttttaaatatgtaat	2952
OATP8	20	intron4 + 1003	taaatatgtaatgtacataa G/T gaatattatgcatatttttgt	2953
OATP8	21	intron6 + 155	cattaataatcagaataaaa A/G agaaatttagctcctattta	2954
OATP8	22	intron6 + 750	atccaactgggttttagatt T/G cctctttctgcctctcctcc	2955
OATP8	23	intron6 + 780	gcctctcctccatatgcacc C/T tctcttttcctcagcaaaca	2956
OATP8	24	intron6 + 1248	ctatgccctgtaatctcaca C/T ttccctttatttaaaattgg	2957
OATP8	25	intron6 + 1500	tcgtgtctgtgttagcatat A/G ataactcatcagggtttgtg	2958
OATP8	26	intron6 + 2008	ataacataaatgagtaaaga A/G tatcaagggcaggaaattag	2959
OATP8	27	intron6 + 2087	actactctccccatacacac T/C aaaactcatgtgctccccag	2960
OATP8	28	intron6 + 12305	tcatctatggaggactgcaa T/C cattatcattatttccccaga	2961
OATP8	29	intron7 + 363	taacaaatgatacccagccat C/G atactattctctggtaatag	2962
OATP8	30	intron7 + 411	cctttatttttgagaacct G/A gtggatgatattaagacgta	2963
OATP8	31	intron7 + 428	cctggtggatgatattaaga C/A gtatatagatcaatgtaata	2964
OATP8	32	intron7 + 634	aaaattatatatatacatat A/G taatcttacctaagtattca	2965
OATP8	33	intron7 + 1791	tgtttttttaagggtagtga T/C gtgaatagtaaagcgaattt	2966
OATP8	34	intron7 + 2000	agttgagcaaattgctctca G/A gtagcataatgtcacttgaa	2967
OATP8	35	intron7 + 2043	gtttattgatccatttttta A/G tggatcaacattgtagtgag	2968
OATP8	36	intron7 + 2171	atttatttgagcaaaggtc G/A cgactctcttagaaagcctc	2969
OATP8	37	intron7 + 2173	ttatttgagcaaaggtcgc G/A actctcttagaaagcctcac	2970
OATP8	38	intron7 + 2179	tgagcaaaggtcgcgactct C/T ttagaaagcctcacaaatca	2971
OATP8	39	intron7 + 2219	atttgtaactttaagtctta T/G ataacttatatttacaaaat	2972
OATP8	40	intron7 + 2261	cagatattaatatatatttt A/T ttattgaaatatgttatttt	2973
OATP8	41	intron8 + 150	acaaaatttctccatcttgt T/C atatcatcgttgttctgcat	2974
OATP8	42	intron8 + 154	aatttctccatcttgtaata A/T catcgttgttctgcatttga	2975
OATP8	43	intron8 + 1303	ttttttttgagatggagtct C/T gctctgttgcccaggctggg	2976
OATP8	44	intron8 + 1372	aagctccgcctcccaggttc T/G ccacccttctcttaaagaaa	2977
OATP8	45	exon9 + 1272	tccttcttgtttcaacttct A/G tatttccctctaatctgcga	2978
OATP8	46	intron10 + 63	tcacagatttgatttaataa A/T tacttatcaaatcttcctat	2979
OATP8	47	intron10 + 911	cttgcccaatatcctaccaa C/T gtattattaaacggcatgga	2980
OATP8	48	intron10 + 972	tcctagtttccttgaagata G/A gctacaactttagtaaactt	2981
OATP8	49	intron10 + 1101	tcccctggtcctgtgttgtcc A/T gtagtgaagacctgaaagag	2982
OATP8	50	intron10 + 1103	cctggtcctgtgttgtccag T/C agtgaagacctgaaagagag	2983
OATP8	51	intron10 + 2027	cccattttcatgagtggcta A/G gttttgtcccgtttcaaact	2984

遺伝子名	No.	存在位置	配　　列	配列番号
OATP8	52	intron10 + 2025	ccattttcatgagtggctaa G/A ttttgtcccgtttcaaacta	2985
OATP8	53	intron10 + 2148	gtattttggaaagaaaatgt A/G ggtggaagagaaatatttta	2986
OATP8	54	intron10 + 2214	atatacagaatttcatacac T/C aatttcttaaattcctaaat	2987
OATP8	55	intron10 + 2316	taaatattttagtttgagac T/G tctttaaatataatggaatg	2988
OATP8	56	intron10 + 2372	tgtatttggcaaatgtattt G/T ttaatatttcaaaaactatt	2989
OATP8	57	exon11 + 1557	cagaacagaaattactcagc A/G cacttgggtgaatgcccaag	2990
OATP8	58	intron11 + 147	tttcttagaattattttgat A/C tttcaataacatcattaata	2991
OATP8	59	intron11 + 10339	aaaaaactgcattttagtgg G/C ttagctagaaaagatttgtc	2992
OATP8	60	intron11 + 10358	ggttagctagaaaagatttg T/G ctcatatacacaataaatta	2993
OATP8	61	intron11 + 10538	caacagaggatcaatgtaaa T/G gaaatctcttaaattaaaca	2994
OATP8	62	intron12 + 55	ataaatattaatgttaaata C/T taaagactgaatgcaattaa	2995
OATP8	63	intron12 + 1802	taaaatgaatcggtaaaaca T/G tcatgtataaatcactgtca	2996
OATP8	64	intron12 + 2612	ataggcatataatactcttt C/A ttcctctgtatatagggag	2997
OATP8	65	exon13 + 1833	aacagctgtggagcacaagg G/A gcttgtaggatatataattc	2998
OATP8	66	5'flanking - (1590-1587)	atatacataacatatacctg TATC/△ tatgttatgtgtctgcttat	2999
OATP8	67	5'untranslated - (11-28)	agcatcagcaacaattaaaa ATATTCACT TGGTATCTG/△ tagtttaataatggaccaac	3000
OATP8	68	5'untranslated - (4-7)	tattcacttggtatctgtag TTTA/△ ataatggaccaacatcaaca	3001
OATP8	69	intron4 + (213-214)	cctgttcgcttatatgcagc (T) ttttgtccaaccaaacagaa	3002
OATP8	70	intron4 + (213-214)	cctgttcgcttatatgcagc　　ttttgtccaaccaaacagaa	3003
OATP8	71	intron4 + 505	tataacttttctctttataaa G/△ atgcaaaatgttatagcatt	3004
OATP8	72	intron4 + 616	aaaaataaatgaagtggagg A/△ aaaaaaatgatttcaagttt	3005
OATP8	73	intron4 + (804-812)	acatccatgtttaacagaat (A)9-11 tattttgtaacgacaaaaga	3006
OATP8	74	intron4 + 855	gagattgtttaaccaaatta G/△ gaaactattattcaacacac	3007
OATP8	75	intron7 + (619-628)	ttttatatatgaattaaaat (AT)4-5 catatataatcttacctaag	3008
OATP8	76	intron7 + (1773-1779)	attttctatattatgaactg (T)7-8 aagggtagtgatgtgaatag	3009
OATP8	78	intron8 + (1270-1290)	tagtgtgccacccttctctc (T)19-23 gagatggagtctcgctctgt	3010
OATP8	79	intron10 + 665	ttctttcttaactcaaaggc T/△ ttttttttccatgtgacac	3011
OATP8	80	intron11 + (247-250)	aaaaatcttaaggcacacac TGAT/△ tgacagttgccttgattgta	3012
OATP8	81	intron12 + (1622-1630)	aaataaattgttggcatcta (T)8-10 atttttctaagggtcgctgt	3013
OATP8	82	3'untranslated + (2464-2465)	gagaaaagcctgatgccttt A/△ aaaaaaaatgaaacactttg	3014
OAT1	1	5'untranslated - 127	gcagctcggactcagctccc G/A gagcaacccagctgcggagg	3015
OAT1	2	5'untranslated - 20	gaaggcctcagccccagcc A/G ctgggctgggcctggcccaa	3016
OAT1	3	intron3 + 150	caatagaacaaccttttctc G/A ggctcatgccgccctgaccc	3017
OAT1	4	intron4 + 211	ttctctggcttccccactc A/C gttctccagcctgcctgctc	3018
OAT1	5	intron5 + 33	gagacttcccatgataacct C/T ccagggcttcaccccccaaac	3019
OAT1	6	intron8 + 168	gaaccagatgccccccagcct C/T gactcagtcccagtctccac	3020
OAT1	7	intron1 + (58-71)	ggaagatgggggccttttgtt (A)13-15 gtacatggagaaattaactg	3021
OAT1	8	intron3 + (1306-1319)	aataggttgaggaggagcag (A)12-15 tcaagagtgtggaggggca	3022
OAT2	1	intron4 + 842	ttgacctccaaaagtgtttg G/A attacaggcatgggccattg	3023
OAT2	2	intron5 + 33	gtgtgtgtgagcatgcatat C/A tgtgtgtggtggggagtggg	3024
OAT2	3	intorn5 + 163	ccacatccatcattcgagac A/C aactcgtctcagctgccatg	3025
OAT2	4	intorn5 + 184	cacatccatcattcgagaca A/C actcgtctcagctgccatga	3026
OAT2	5	exon7 + 1269	actagactgctagtgtcctc C/T ggtgagcccagtcccatagg	3027
OAT2	6	3'untranslated + 1792	ataaatgtgtacatgagtgt A/G tgaacacaaatacataaggt	3028
OAT2	7	3'flanking + 1386	tgtagcagcccacatcgcca G/A tgttcacacctgagagagag	3029
OAT3	1	5'flanking - 580	ctgtgtcagagacacagcca C/G ggaggtcctggctgccccag	3030
OAT3	2	5'flanking - 463	ttcctgagaggcaaatcccc T/C tcccctactcgggaggtgcc	3031
OAT3	3	5'untranslated - 16	cctgcccacagctctggctc G/A tcttgccccagtgccatgac	3032
OAT3	4	exon2 + 153	cctgtccaccactgtcgccc G/A ccccacaatgcctccacagg	3033
OAT3	5	intron2 + 177	gcaccaagacccttggcttc T/C tcccactcgagtccaagca	3034
OAT3	6	intron2 + 6201	gctcatcctctctggtcctt T/G tgccccagcacaggttcctc	3035
OAT3	7	intron3 + 79	tctgctccacccgtgcaccc G/C caaagaggcaaagagctggg	3036
OAT3	8	exon5 + 723	tggcgttggctgcagttaac T/A gtgtccattcccttcttcgt	3037
OAT3	9	intron5 + 524	tcgaagtacaaaggaaagtt T/C aaagagaagcctgagcctgg	3038
OAT3	10	intron7 + 386	gaccaatgggttcagactc G/A aagacaaaaattatgtttat	3039
OAT3	11	intron7 + 754	gcccacgtcagacatgacca G/A tcaatcacagcactttctcc	3040
OAT3	12	intron9 + 81	attgtcctgtcctctaccca G/A gggagccatcctttatgaac	3041
OAT3	13	5'flanking - (661-660)	tacatttggtccccagggag (G) agcggctgatcaggagaaa	3042
OAT3	14	5'flanking - (661-660)	tacatttggtccccagggag　　agcggctgatcaggagaaa	3043

遺伝子名	No.	存在位置	配　　列	配列番号
OAT2	15	intron8 + (211-212)	tctgacttggactgggcaaa AA/Δ gtatgatttgtatctgtgcag	3044
ALDH1A2	1	5'flanking-716	cagggatcctcattctcaag C/G cgcgcgcgcgccactgcca	3045
ALDH1A2	2	intron1+314	cggccgcgctgccgcgcgg G/Δ aagccgtcggcaccgcttag	3046
ALDH1A2	3	intron1+(684-875)	tttgaactgaagaccttaa (T)11-13 atcacgaacgttgccatctt	3047
ALDH1A2	4	intron1+1370	gcatgcacctctgaggtttt A/G tttttgcgcgtctctctaacc	3048
ALDH1A2	5	intron1+1687	ggtacgttttcacgaattta A/Δ ttggaagctcttccagttc	3049
ALDH1A2	6	intron1+1934	tcagctcttttagtgaacctt C/G tcaatttctaagccaagca	3050
ALDH1A2	7	intron1+(1971-1980)	agcatagtggcaaagcagta (T)9-11 aaacgtcaagcgcgcgcgct	3051
ALDH1A2	8	intron1+2295	tactgtcagccaatatgttta T/C tgttttgtctttgctaaac	3052
ALDH1A2	9	intron1+2387	ttaggacccaccatgagtcca C/T tacttaaaatataatgaccag	3053
ALDH1A2	10	intron1+2641	agcaatgtgcttttttcaaag T/Δ gaatgggtgtagtcaaggag	3054
ALDH1A2	11	intron1+3035	gacttttatacttttgcata A/G ctgatgtttatgcaaatcaac	3055
ALDH1A2	12	intron1+3319	aaagagttatgtttttttt T/Δ atgcaatctgtatttatatgg	3056
ALDH1A2	13	intron1+3474	tgtgtcttttattttattcat T/D taaacttctgctttctgtgcc	3057
ALDH1A2	14	intron1+4186	cattcaaaatgtcagtcaaaact A/G catgttaaatagaggacttca	3058
ALDH1A2	15	intron1+4227	cgtaacttcagtttttttcagta T/Δ aaatacttttttcaatacctat	3059
ALDH1A2	16	intron1+4254	cgtaacttcagtttttttcaag T/A gtacctgcaggcgcgtgaa	3060
ALDH1A2	17	intron1+4367	tcattcaaaatgtcagtgggcct A/G tgttaccctgtggaattatc	3061
ALDH1A2	18	intron1+5835	caatccaagttgccaaatagct T/D gtttctgtgattttaagtag	3062
ALDH1A2	19	intron1+6206	tttgaaagccctctctgcca T/G ttctttaaattctttattga	3063
ALDH1A2	20	intron1+9559	tgatccattgatgaattatt C/T actctgtgtcctgctgtagat	3064
ALDH1A2	21	intron1+(9031-9039)	tacaacgtgtttctcaaaaga (AAGA) cattttttttgaataactct	3065
ALDH1A2	21	intron1+(9031-9032)	tacaacgtgtttctcaaaga cattttttttgaataactct	3066
ALDH1A2	22	intron1+12731	ctgaaatgtgaaccctttcag T/A gtacctgcaggcgcgtgaa	3067
ALDH1A2	23	intron1+13442	cagtgtcataagtgtccaag G/A gaaatccaaaatgttcatat	3068
ALDH1A2	24	intron1+(14173-14176)	tctaaaaaaaaaaaaaata AAAA/Δ gagaaattcaagtttaagat	3069
ALDH1A2	25	intron1+14588	actgattttattgttcaaag C/G cttcttcaagcttaggaiat	3070
ALDH1A2	26	intron1+14595	ttggttcaaagcttcttctca A/G cctaggaiatgcattgagg	3071
ALDH1A2	27	intron1+14711	gttgagacattaacttcta A/G ttcaaatgaagatgctagtt	3072
ALDH1A2	28	intron1+(15327-15337)	gaagagcacagtgagaagac (T)9-11 aacccagaaaaaaaaaaaaa	3073
ALDH1A2	29	intron1+17258	atcagtaccatgtgttgggg A/G tacaacacttaatttaaaat	3074
ALDH1A2	30	intron1+18277	taatacaaatcatttgaagc A/G tttactatttaaaaaacaaa	3075
ALDH1A2	31	intron1+18734	cttgagtaaaaatactgcatt T/A taagtctgtgaagatatag	3076
ALDH1A2	32	intron1+19081	ttaatcacctcaatctttaa C/T gaaattctgatttttctt	3077
ALDH1A2	33	intron1+21514	aatcaggatatgggggttc G/A ttctttatctgccacaaat	3078
ALDH1A2	34	intron1+21732	catttttaaaatagtgcttta A/G tggaacttggctgtttaaagt	3079
ALDH1A2	35	intron1+21865	tcgcatagtttaaaaatgt C/T tgtgtaggactctttcca	3080
ALDH1A2	36	intron1+26262	taaagaaggaaaaaaaaaa A/Δ ctaatctgagacttaacagg	3081
ALDH1A2	37	intron1+27805	gcatgtatttacccaaggaa T/G tgcacacttccagacagtag	3082
ALDH1A2	38	intron1+28204	tcaatccatttttttaactgt C/G cttctaaatgtgtgcttaa	3083
ALDH1A2	39	intron1+28521	tcttttgttaccattcttaaa T/C cgagatatcagatatcttc	3084
ALDH1A2	40	intron1+49478	gaattaaaagtatgaggcct C/T gatagacccatttttcacct	3085
ALDH1A2	41	intron1+49334	gcctctcaatttttctcatgt G/T tcatagaggaaaaccctgc	3086
ALDH1A2	42	intron1+50351	gactgactgtgttcttagtt C/G agaaatttcactatgtgct	3087
ALDH1A2	43	intron1+51181	tgttattacctatgtagttc C/T gtacctcattgtgccttgct	3088
ALDH1A2	44	intron3+654	ttaaacttcattgattaaaa G/A gaatccttcagaaccagag	3089
ALDH1A2	45	intron3+668	gtaaaaggaatcttcttcagaa C/T cagagtgggtgtgtacgtgac	3090
ALDH1A2	46	intron3+1712	cctgcacttctgctccgttt G/T cccgtgaatttctgtgagcca	3091
ALDH1A2	47	intron3+1273	tattcatactctgaaaaagg T/A gttcacgtgtgagaaattc	3092
ALDH1A2	48	intron3+1743	ccacacctaaatgagattca C/T gtttaaaacactctcaagct	3093
ALDH1A2	49	intron3+2891	tgcacaatatacdcattgt A/G gttttatctagaactgtac	3094
ALDH1A2	50	intron3+2919	ctagaactagaccaaatg G/A cagtactgtgaatctttttg	3095
ALDH1A2	51	intron4+290	cattgtgctgcattaggtgg T/C gaagtagatgtgaaggtgca	3096
ALDH1A2	52	intron4+389	ctccttgccctcctgaaaca T/G ctaagatctactctttgaaa	3097
ALDH1A2	53	intron4+461	gattatggctgttttcagt G/T tctttttaatattttttctct	3098
ALDH1A2	54	intron4+506	tctatatttctctgaaggcc G/A tgaatactttgaaaatgta	3099
ALDH1A2	55	intron4+1952	ttgctcccgctccaccattat C/G atttcattattaaaacaaca	3100
ALDH1A2	56	intron4+2079	ctctctttggcctcaggtta C/T cttgttttttctttiacttcc	3101
ALDH1A2	57	intron4+2519	ttggtccaaagagtcttct C/G cctggtgtctcaaacagatg	3102
ALDH1A2	58	intron4+(2840-2851)	ttttatctgcaacttgac (T)11-13 cacagtgaagtctggaatat	3103

遺伝子名	No.	存在位置	配　　列	配列番号
ALDH1A2	59	intron4+7231	aataggatacaaatacacaa A/T gatagtgattcagatcctaa	3104
ALDH1A2	60	intron4+7958	taaaatcgtttttattgtta C/T taggtatataaaatttgcta	3105
ALDH1A2	61	intron4+8090	tctgattttatcactgttta C/T agattgcttagtcatactca	3106
ALDH1A2	62	intron4+12823	tgttagcctgtagctaaatg C/T ttttcaaatatgtgaacggt	3107
ALDH1A2	63	intron4+12939	atgaggtccgactttaaga T/C ttttgtctacattttcttcc	3108
ALDH1A2	64	intron4+14935	tattgatggagttcttttta T/G aaatggacttttaccttctt	3109
ALDH1A2	65	intron4+15321	gcatttgggtgtctgagaga C/T atatccagaaatatgctatg	3110
ALDH1A2	66	intron4+15412	tttcaagtttatttctgttt T/G ttttttttttttttttttg	3111
ALDH1A2	67	intron5+1888	aatccaaacatctgtacttt G/T tagtggacaagatttatgtc	3112
ALDH1A2	68	intron7+9166	gaaaagctacttattcaaa G/A ataaaagtattttaagaaaa	3113
ALDH1A2	69	intron7+9914	aagctggagaaaatactagg C/T tttcctcaacagtgatttcc	3114
ALDH1A2	70	intron7+18942	tttggaggggaactaatccc G/A tgacttctaggttatctctt	3115
ALDH1A2	71	intron7+19820	ttcaccccticatttaggtt A/G ggggaggtggcttgctacag	3116
ALDH1A2	72	intron7+19826	cctcattttaggttagggga G/A gtggcttgctacagttttag	3117
ALDH1A2	73	intron7+19913	cgtgaatcattcagtatttt A/G tttaaaaatacccagtttgaa	3118
ALDH1A2	74	intron7+(20110-20111)	catgatttattctctaacta (ACTA) tgctaagtcaaagattctgc	3119
ALDH1A2	74	intron7+(20110-20111)	catgatttattctctaacta　　tgctaagtcaaagattctgc	3120
ALDH1A2	75	intron7+21857	acaatgaaaattaagaaagg A/T gaagagggaagaagcagaga	3121
ALDH1A2	76	intron7+21929	tacaagacacaggcatcttt A/G actagtttactgggatctct	3122
ALDH1A2	77	intron7+23308	ggctttgacttcggaaacct G/T tgggttataacaaagtactg	3123
ALDH1A2	78	intron7+23554	gacattggtgaaaacgaggg C/T tgtttaggagtgtcctgtcc	3124
ALDH1A2	79	intron7+(23701-23703)	catctgagatttgccttgtg GTG/Δ tttacgagttagtgggtgc	3125
ALDH1A2	80	intron7+26479	gatacatgaacaatttgttt T/C atcctcatgatatctttcaa	3126
ALDH1A2	81	intron7+26561	taaaggcccacaatgcagtga T/C tgaaatctccagttacattt	3127
ALDH1A2	82	intron7+26662	tttccttagtccttccatca C/T gaaactaaagctgtcttcca	3128
ALDH1A2	83	intron8+76	tttatatctcacacttttgat G/A ggacactagcaaaagatatt	3129
ALDH1A2	84	intron8+(700-711)	accatctcattcagtgattc (T)11-12 ccctccacttgttgccaggc	3130
ALDH1A2	85	intron8+724	ttttttttccctccacttgt T/C gccaggcagagctgctttcc	3131
ALDH1A2	86	intron8+800	cagattgcttgaatttcagc C/A ccagcttggaatttgccagag	3132
ALDH1A2	87	intron8+1251	gatttctgtgaaaattgagg G/A gatctggcaacctggggctc	3133
ALDH1A2	88	intron8+1627	ggcccctccccaggcaaagc G/A gtgagaacatggctgtttcc	3134
ALDH1A2	89	exon9+141	tggagcgggccaagaggcgc G/A tagtgggagtccctttgac	3135
ALDH1A2	90	intron9+778	aaccagtctggacagatccc T/C tgtagcttgtgaaagtgtag	3136
ALDH1A2	91	intron9+801	tagcttgtgaaagtgtagga A/G gtgaagggctggctcacttc	3137
ALDH1A2	92	intron9+868	tctgaaggcctcgtgtactt T/C agtggggtgggagaggccac	3138
ALDH1A2	93	intron9+1338	aatttttgcctctttttact A/G tcaatacaacttgctaagtt	3139
ALDH1A2	94	intron10+(227-229)	ctatgtgcttatgattatta TTA/Δ gccaacagaacaatcagaat	3140
ALDH1A2	95	intron10+316	ctaaatgtgggtcactggga T/C gttaaccaggagagagaatc	3141
ALDH1A2	96	intron10+368	ctttacatctgtgcaagaga G/A ggacaaggagcaaatcagcc	3142
ALDH1A2	97	intron10+660	gtaaacttgcattgaaatgt G/A gaaagcaggtaaaggaatga	3143
ALDH1A2	98	intron11+104	tggggaataccaaaagcaac C/T aaagttcaccagaaaagggg	3144
ALDH1A2	99	intron11+229	aaacttctaaaagaaatacc A/G tgccagtcagattatgtgct	3145
ALDH1A2	100	intron12+117	catacattcaacaaacattt C/T gtggagcacatgctactata	3146
ALDH1A2	101	intron12+691	gatagggaagatcactgtga A/G ctggaaaaatctgggaaacc	3147
ALDH1A2	102	intron12+1934	catcttgtctagattgcatg T/C ttgtttgtttgtttgtctct	3148
ALDH1A2	103	intron12+1973	ctacttaccccaaaaacatg T/A tttctctttcttaaatgacc	3149
ALDH1A2	104	intron12+2722	ccagagtgactccagtatac C/A tcactgcccaggacccacag	3150
ALDH1A2	105	intron12+3855	cacttgaaagcaaccataat T/C gtgaggtttctgatgctgta	3151
ALDH1A2	106	intron12+4185	ttgctttaagcgaaatgaac T/C atacggacaggagaacagcc	3152
ALDH1A2	107	intron12+4991	acaggaacacttagcatgc A/G acccactcccaccctccgtc	3153
ALDH1A2	108	intron12+(5018-5019)	cccaccctccgtcttgggggg (G) aggaaagcacactactgtcc	3154
ALDH1A2	108	intron12+(5018-5019)	cccaccctccgtcttgggggg　　aggaaagcacactactgtcc	3155
ALDH1A2	109	intron12+(5051-5052)	actgtcccaaagaactaata (A) ctgaaccagtgctgccttgt	3156
ALDH1A2	109	intron12+(5051-5052)	actgtcccaaagaactaata　　ctgaaccagtgctgccttgt	3157
ALDH1A2	110	intron12+(5300-5302)	ttaaagttttaaaaaaaactt CCT/Δ taaaaactactcatgagatg	3158
ALDH1A2	111	intron12+5405	catcccaggacttgctgttc G/C caggtgataaactgcacctc	3159
ALDH1A2	112	intron12+5435	aactgcacctcccccaggact C/A ccgctgcactcacatgcagc	3160
ALDH1A2	113	3'flanking+449	tttgggccgggaacaatttt T/C caaggttgtaaagccaaatt	3161
ALDH1A2	114	3'flanking+597	acctgggatattcctgaccc A/C atctggttttctttttaccca	3162
ALDH1A2	115	3'flanking+669	atagagactggaagtcatca T/C gtgcagttcaccgcttctga	3163

遺伝子名	No.	存在位置	配　　列	配列番号
ALDH1A2	116	3'flanking+1122	cgtgctccactgagctcctc T/G gtcacacccattcttgccc	3164
ALDH1A2	117	3'flanking+2214	tgcagctgtaaaaagaaatc T/C gtaaatggtgaccgtactac	3165
ALDH1A3	1	5'flanking-1425	cagtgttagccagccgatat C/T ggtcaaggctgcccccgctcg	3166
ALDH1A3	2	5'flanking-1379	ccattatcccctttcccccgg C/T ctcagctgtgcactccaggc	3167
ALDH1A3	3	5'flanking-1270	aacttaccccctctatccagc T/A ctatccagaaggacaccagg	3168
ALDH1A3	4	5'flanking-(1214-1213)	acggaggcctcaaaacagga (GGA) aaataaggagacccctcccc	3169
ALDH1A3	4	5'flanking-(1214-1213)	acggaggcctcaaaacagga aaataaggagacccctcccc	3170
ALDH1A3	5	5'flanking-1103	gcacagcttttgtcaggagt C/T cgtgcctccggtctttgttc	3171
ALDH1A3	6	intron1+986	gccttaactttccccaccttt T/G ggcttctcttgatttttgct	3172
ALDH1A3	7	intron1+1462	gtacaggatttcaaaatact G/A tatatagaaaccagacagta	3173
ALDH1A3	8	intron1+1661	cctgttgtcttggtgggtgc G/A caaccttgccagttaaagg	3174
ALDH1A3	9	intron1+2360	agaggatagaagtcccttct A/G atttagagggcctctttctt	3175
ALDH1A3	10	intron1+2516	tgaaaacatattcttttga G/A tttagctgagtggcctgttg	3176
ALDH1A3	11	intron1+2624	cctgagacaccttacagctc C/T gtcctgcttccatgtcattc	3177
ALDH1A3	12	intron1+3255	tttcatctttctacaaatgg G/C cccctcttcctggctgcact	3178
ALDH1A3	13	intron1+(3643-3656)	gcttcagaggtttttgtggg (T)12-14 aacattctatcaacttttaa	3179
ALDH1A3	14	intron1+4265	ccaaaagccctctcttttaa T/C atgacattaataagacaatt	3180
ALDH1A3	15	intron1+5187	caagatggataagacgtcac C/T taaggtcttagcatgttga	3181
ALDH1A3	16	intron2+43	ctctaagtaattcaattatg G/T atgaccaaaggctaaggaaa	3182
ALDH1A3	17	intron2+127	cagggcctgggctagctgcg T/C gaattggcatgtggttctca	3183
ALDH1A3	18	intron2+(285-300)	aggaaaggttttctttttttc (T)16-17 atcaattatttggacctgga	3184
ALDH1A3	19	intron2+776	cgtgtgcagagtaggcttgg A/G ttttatcttgcccatgagtt	3185
ALDH1A3	20	intron2+1216	actcggtagagtcactcctg A/C ctggtgtcccacatccactc	3186
ALDH1A3	21	intron3+81	accatggggtatgggaaaaa A/C gatcacggtcctggttttgt	3187
ALDH1A3	22	intron3+236	gctcagcttcttgaccaagt T/G gttgtctataggcagttgag	3188
ALDH1A3	23	intron3+1467	ggcccggttgtagggagaga G/T atctcctttctggcctttga	3189
ALDH1A3	24	intron3+1725	ccacatgttccccgggtgag A/G gtagctccctcccagggtaa	3190
ALDH1A3	25	intron3+3777	gccagaagtagatgcccccca A/G ttcagctgctgcattactgg	3191
ALDH1A3	26	intron3+3829	caagtcactgggccgttagc G/C tccgtgcctgcaccttgaag	3192
ALDH1A3	27	intron3+4299	tcactttccacagccacact G/A gccagcctggccgagaagga	3193
ALDH1A3	28	intron4+84	agagccccccctgactgttt C/G cctaaggcaccattcccaac	3194
ALDH1A3	29	intron4+126	ccactcctctccaaatggt A/G ctgccaattcttcttctaag	3195
ALDH1A3	30	intron6+(290-291)	tagagaattttcagggggg (G) tcaaccaagagggagccaaa	3196
ALDH1A3	30	intron6+(290-291)	tagagaattttcagggggg tcaaccaagagggagccaaa	3197
ALDH1A3	31	intron6+705	aacagctggtgatgagccaa T/G tttccactttccttggtga	3198
ALDH1A3	32	intron7+56	gggccgtgttatttgcacc C/T gtgagcttttcctttgacag	3199
ALDH1A3	33	intron7+1107	gatgctgttactctccttgg A/G gacagacactgcccctgtgga	3200
ALDH1A3	34	intron7+1610	aagagccacacagaaccacc C/G ccctactgggctgttggaat	3201
ALDH1A3	35	intron7+1820	cacctgtaagtggagcggct T/C agaccaaggatcccaggatg	3202
ALDH1A3	36	intron8+963	gagaaaggacaggaggagga C/T acaggctctcaggaaggaaa	3203
ALDH1A3	37	intron8+1824	accattcttatccactaagc G/A tgtccccccaagatcttattc	3204
ALDH1A3	38	intron8+2384	cgcctccctcgccccctcccc C/A tccagtggacttggcagtgg	3205
ALDH1A3	39	intron9+24	atccccctggtgtgtgtgaa A/C ccatggtgcttgtctagggg	3206
ALDH1A3	40	intron9+91	gcctacagggtcccctctccg T/C gaaaggaatgctgacctgtc	3207
ALDH1A3	41	intron9+219	actgaggcatgggaggaggg C/G gctattcccagggcagaagg	3208
ALDH1A3	42	intron9+435	ccagacggagagagcctggg G/A caggagaatgtatctccagg	3209
ALDH1A3	43	intron9+1472	ttgacttttgaggccagata C/T accgatttcttccaagagaa	3210
ALDH1A3	44	intron9+2038	taaacaatgtgttcctacgg G/A ctctccagggagtgtggagt	3211
ALDH1A3	45	intron9+2124	caaacagggtctgccagatg G/A cctatgcccagcagccaggg	3212
ALDH1A3	46	intron9+2154	agcagccagggaggcctgc G/C gttgggcgaagccccctgtgt	3213
ALDH1A3	47	intron9+2197	cttttggcccctcagggagg G/A gaagagcagctcagcagcat	3214
ALDH1A3	48	intron9+2466	ttcttagttcctcatgtttc C/T ctctagaatgttttcgtgtg	3215
ALDH1A3	49	intron9+3655	gattggtcaagtggcatgca C/T ggtttatgccctctctcctg	3216
ALDH1A3	50	intron9+3954	gggtgcgcttttgacaactg G/G tcagtagcgtgttcacaagc	3217
ALDH1A3	51	exon10+88	tggaatgcgggggctcagcc A/G tggaagacaaggggctcttc	3218
ALDH1A3	52	intron10+8	tgccaaagaggaggtacaag G/A gggctgtggcaaggctacga	3219
ALDH1A3	53	intron10+307	ctctctgattttctaacaca A/C ccggtcccgagtcagtcat	3220
ALDH1A3	54	intron10+378	gtgggttttgccaggaatca G/A ttcaagaacctgtggattca	3221
ALDH1A3	55	intron10+975	aatattgtgtcattccttcc C/G ctggtagttattatggaaac	3222
ALDH1A3	56	intron10+1088	cagtgccaggagccagggag C/T cttctccagatgactctgag	3223

遺伝子名	No.	存在位置	配　　列	配列番号
ALDH1A3	57	intron11+105	ttgtttacattgtatattat A/G taccaagccctgtctcagtg	3224
ALDH1A3	58	intron11+274	agggctccagtacctgtgcc T/G gtggccccctgtgctgtactg	3225
ALDH1A3	59	intron11+1088	cagtgccaggagccaggggg T/A cttctccagatgactctgag	3226
ALDH1A3	60	intron12+96	ctccaatctgctgacacccc G/A tccccccacaccgccgctc	3227
ALDH1A3	61	intron12+5642	tctgtgctaacgtctgcttc T/C ctcatgccccctaggctggc	3228
ALDH1A3	62	exon13+104	gggctccttcctcaaacatc G/C gacggcggaatgtggcagat	3229
ALDH1A3	63	exon13+281	ataggttgtctgtgaaatcg C/T agtcctgcctgggagggag	3230
ALDH1A3	64	3'flanking+743	gtgagcaggaaactgtagga G/A aaggatattttccctcattt	3231
ALDH1A3	65	3'flanking+1145	gcctcccagctacccaccc A/G cctcaggaggggtcattcca	3232
ALDH1A3	66	3'flanking+1185	aacctagggtgctgagaatc T/C gggtgggattaccagcaaaa	3233
ALDH1A3	67	3'flanking+1600	acaccacgccctgcaaattg T/C tgggaacttgtcggtggcaa	3234
ALDH1A3	68	3'flanking+1847	caggagccctgcggctgccc C/G ggttctgtgaaatggcagtg	3235
ALDH1L1	1	intron1+252	cgcagcgccaggactggccc G/C ccgaggatctggccggccgc	3236
ALDH1L1	2	intron1+544	ctcaggggctgcgctggagt C/T ccagctccagccactgcgct	3237
ALDH1L1	3	intron1-6596	cagatttttcttaaggtgca C/G tagccactgaggatattttt	3238
ALDH1L1	4	intron1-6513	caattatggtttatcttagg G/A acatgtttatagagatagta	3239
ALDH1L1	5	intron1-6478	atagtattcttacttagctt G/A cattctaaattttgttccct	3240
ALDH1L1	6	intron2+240	gtggcattagggtcctggag A/G agggctatagagaagcccag	3241
ALDH1L1	7	intron2+1326	gaggaggagaccggagagga G/C agccagtccagtcagggccc	3242
ALDH1L1	8	intron3+386	gtcctactctaacttccact G/A ccgctgctctgggcagcaca	3243
ALDH1L1	9	intron4+271	gggcccgttcaatagacaag G/C aaggctaaaggcagggactg	3244
ALDH1L1	10	intron4+356	taggattctatttctctctc C/T ttcactcgttgattctcctt	3245
ALDH1L1	11	intron4+608	gtgctctgataggctgtctc A/C gtcacatgcttcctgctggg	3246
ALDH1L1	12	intron4+664	ggtcacatggcctgagcggc A/G gggcggctcagtcacctggg	3247
ALDH1L1	13	intron4+785	gagggctgcttgcccctgcc C/G gaggacaggctggcagggac	3248
ALDH1L1	14	intron4+874	ccctgggagcccttgctgt T/G tgggcgcagcggaagagca	3249
ALDH1L1	15	intron4+1349	tccctcaggctcttgctcac G/A tgggcccagactccttggct	3250
ALDH1L1	16	intron4+1789	ctggggctgggaaggaggca G/A ggtcctattgctggggatag	3251
ALDH1L1	17	intron4+1815	ggcagggtcctattgctggg G/A atagcaacccactggatctc	3252
ALDH1L1	18	intron5+272	aaagcccacaggagataag A/G gtgggagttaggggcaaaa	3253
ALDH1L1	19	intron5+301	taggggcaaaacgtcagcc G/A tagtgcgagcagtcttcaag	3254
ALDH1L1	20	intron5+343	caaggtgtgagggacagtgc G/A ggtctctggagcaatagcca	3255
ALDH1L1	21	intron6+926	cctgcctgggctactggctt C/T ggaggcttcttctcacccac	3256
ALDH1L1	22	exon7+41	aacgctgaacacttcaggcc T/C ggtgcccgagggagcagctt	3257
ALDH1L1	23	intron7+305	cctagaatcagagagaagcc C/T tcccagggagcctgggttca	3258
ALDH1L1	24	intron7+837	gtccggacaaacccccatggg C/T gtggtacccccagccgtgtt	3259
ALDH1L1	25	intron7+866	cccagccgtgttgctgtgtc C/T ggcctaccagagtgaggcgt	3260
ALDH1L1	26	intron7+884	tccggcctaccagagtgagg C/T gtggcagtatggggcctggc	3261
ALDH1L1	27	intron7+1118	aatgttccagaaaatcatgc G/C aggcagtaagggcagaggaa	3262
ALDH1L1	28	intron7+1168	aaagtaaaggttcaggagaa G/A tctagcctggggctgctccc	3263
ALDH1L1	29	intron7+1451	cagggcacccacagcatctg T/C ccagagaccctgcaaagacag	3264
ALDH1L1	30	intron7+1489	caggaatgcaaagaaggcaa T/C taagtgtcttaagaggaagc	3265
ALDH1L1	31	intron7+1579	tcagggtgggaggggagtga G/A gagagaccagctgagcacac	3266
ALDH1L1	32	intron7+1691	ctggctgggctttagcttgc A/C gaaagctccagaacatcttt	3267
ALDH1L1	33	intron8+2627	aaagaggagagccgggggtg C/T ttgtgccagggttgggggga	3268
ALDH1L1	34	intron8+2646	gcttgtgccagggggttgggg G/A aactggttctgattgggcct	3269
ALDH1L1	35	intron8+2925	ctgctgccctccataggtcc C/G agactgaatccttcagagga	3270
ALDH1L1	36	exon9+4	caggtcttgctttgcagagt G/T tttggcagcggatcctcccc	3271
ALDH1L1	37	exon10+109	cagctgttagtgaggaagct G/T cgaggggacgctgaggaggg	3272
ALDH1L1	38	intron10+(671-672)	tggcattttcctctgtctga (AG) gtcctcttagcccaccctaa	3273
ALDH1L1	38	intron10+(671-672)	tggcattttcctctgtctga gtcctcttagcccaccctaa	3274
ALDH1L1	39	intron11+8	caccgatggaagtgtgagtg C/A aggcccagcacccccttctcc	3275
ALDH1L1	40	intron11+447	atgagccaaagcacgcctat G/A gtagatacacacgtgaacat	3276
ALDH1L1	41	intron11+601	ctcaaaatgagtcatttgag A/G ggagttaatgaaagctcct	3277
ALDH1L1	42	intron11+639	catctgcaaagggagaggga G/A ggggtagggacacagcagg	3278
ALDH1L1	43	intron12+684	tcctgggagaagagagggtg C/T ggccagatgagccgagaaca	3279
ALDH1L1	44	intron12+767	cgtctagggtgcgaagcca A/G gttatggcgtggtcccaaog	3280
ALDH1L1	45	intron12+1014	tcataggttccagtcccctt C/T gcaagcccctcaattctagg	3281
ALDH1L1	46	intron12+1359	ctggttctgcctcagctcag C/T acagcagaggctgggtctag	3282
ALDH1L1	47	intron12+1734	ggtggtccaggctgctggtg G/T tcagtagggccggccgagcc	3283

遺伝子名	No.	存在位置	配　　列	配列番号
ALDH1L1	48	intron12+1901	ttcagcagcctaactgaatt G/A acaatagaatagtcctgcaa	3284
ALDH1L1	49	intron12−470	gggatgggccacctctcca T/C ctctggagatgccaggctca	3285
ALDH1L1	50	intron12−334	aagggcagcctcttgggcca T/C gaccccttgctgtctgcag	3286
ALDH1L1	51	intron12−325	ctcttgggccatgacccctt T/C gctgtctgcagcaagtgggt	3287
ALDH1L1	52	intron12−221	gaaggaagcgagggaagatc G/C aggaaaggagagagggacag	3288
ALDH1L1	53	intron12−4	cccgcttcccctcaccctgg T/C caggttggcagatctcatgg	3289
ALDH1L1	54	intron13+34	tcccacccagtgtgagcaca T/C gcagactggcccagccatat	3290
ALDH1L1	55	intron13+58	gactggcccagccatatagg A/G gaactccaagggcagcacag	3291
ALDH1L1	56	intron13+125	ccacaactggtggcttggaa T/C gacacctgtttattagcttg	3292
ALDH1L1	57	intron13+126	cacaactggtggcttggaat G/A acacctgtttattagcttgt	3293
ALDH1L1	58	intron13+281	acctgcatccagacgagttc T/G ggtgttgacagagttcagtt	3294
ALDH1L1	59	intron13+299	tcgggtgttgacagagttca A/G ttccgtgtggatgcagggct	3295
ALDH1L1	60	intron14+121	catttatcaaacagccatcc A/G tgtgcttcttgagcacctgc	3296
ALDH1L1	61	intron14+167	gccaggcattgttgtaagga C/T ttgaggacaattgtatttaa	3297
ALDH1L1	62	intron14+205	taatctcccagtaacactgg A/G tcagtcaggtccaaggtggg	3298
ALDH1L1	63	intron14+219	cactggatcagtcaggtcca C/G ggtgggaaacaagagtaaac	3299
ALDH1L1	64	intron14+2275	tctcatctgtgatgcatccg T/C cagacctctgctcccagcct	3300
ALDH1L1	65	intron14+2431	agaatgactgagtgatcaga C/G ctagagagccccagcccccgg	3301
ALDH1L1	66	intron14+2660	agccaagcatttcttgggga C/T accaagaaaccttgcttggt	3302
ALDH1L1	67	intron14+2740	aactccaccctcaccgtcca T/C gcagctcccaggagcgtca	3303
ALDH1L1	68	intron14+2756	tccatgcagctcccaggag T/C gtcagagggcagaggagggg	3304
ALDH1L1	69	intron14+2805	ccgcacagcaggagaatggc T/C ccaagggagggagggacggg	3305
ALDH1L1	70	intron14+(3636−3637)	tctcctgggtgtgtgtgggg (G) tgtggggcagctcccctatc	3306
ALDH1L1	70	intron14+(3636−3637)	tctcctgggtgtgtgtgggg　tgtgggcagctcccctatc	3307
ALDH1L1	71	intron14+4347	tccaggacagaaacagcagg C/T gtgagctgcctctcagaggg	3308
ALDH1L1	72	intron15+380	atgtcccttatgtggcttcc A/G agaccagaagtcctggagag	3309
ALDH1L1	73	intron15+(1055−1056)	gccacaatctgcagctactc (C) tcccagcttgctgctgggct	3310
ALDH1L1	73	intron15+(1055−1056)	gccacaatctgcagctactc　tcccagcttgctgctgggct	3311
ALDH1L1	74	intron17+15	gaaaaagtgcgtggctgggg G/C tggagcagaggagggctgc	3312
ALDH1L1	75	intron17+44	aggaggggctgctgtgagtg C/T gcctgggacatggcagtgct	3313
ALDH1L1	76	intron17+51	gctgctgtgagtgcgcctgg G/A acatggcagtgctgtccaca	3314
ALDH1L1	77	intron17−(2224−2223)	ctggtgtcatctcccagact CT/△ gtcactaaaccacaatatga	3315
ALDH1L1	78	intron18+140	agcgtcatcacaagcatagc G/A tggcaggcagcaggcttagg	3316
ALDH1L1	79	intron19+(51−52)	tggttcactgggacagcagc GC/△ ctggctggagggggtggag	3317
ALDH1L1	80	intron19+399	tcaggtcagcctgggcctga C/A catggacaggggccctggag	3318
ALDH1L1	81	intron19+1794	gtcctgtctgggggtcttaa G/C ggagtcatgagacttccaca	3319
ALDH1L1	82	intron19+1969	tgatcgggggtgcggtttggg G/T ggacaggacaggagcagaga	3320
ALDH1L1	83	intron19+1972	tcggggtgcggtttgggggcg A/G caggacaggagcagagaata	3321
ALDH1L1	84	intron19+2083	tgagaagagcagaggggtgt G/T ccgggtgctcgagtcacacc	3322
ALDH1L1	85	intron19+2119	acacctgtgtctgattaggg C/T tgattaggggtgcagagttt	3323
ALDH1L1	86	intron20+1388	ttaccctcttcccactcccg C/T tggactgtgagttccatgag	3324
ALDH1L1	87	intron20+1564	cccaggaaccaggaacagtg G/A ggagccatcaccccgccctg	3325
ALDH1L1	88	intron20+1873	tcagtgttaaaacatcattt G/A tgtatgtatgaaaaatattg	3326
ALDH1L1	89	intron20+2427	actaggattggatggacttg G/C gatcaggtctcagctctgtc	3327
ALDH1L1	90	intron20+2458	cagctctgtcacctgccaac C/T ggcggcccctttccctcaa	3328
ALDH1L1	91	intron20+2544	ccaggtgggagagccatctg C/T agcgtggtgacacccatcac	3329
ALDH1L1	92	intron20+2573	gacccccatcacacgggtgc C/T gtgacccggtgcttatgtcg	3330
ALDH1L1	93	intron20+2574	acacccatcacacgggtgcc G/A tgacccggtgcttatgtcgg	3331
ALDH1L1	94	exon21+33	agccaactgttttcacagac G/A tggaagaccacatgttcata	3332
ALDH1L1	95	exon21+87	ccttcgggcctgtcatgatc A/G tctctcggtttgctgatggg	3333
ALDH1L1	96	intron21+323	ccatgcattaaaccacccccc C/G acactgagtgacttggaata	3334
ALDH1L1	97	intron21+361	ataatcagagatttatttta C/G tcacggtctaggttcaatga	3335
ALDH1L1	98	intron21+478	gtcttgcgggaggcttcctc C/A gcgtggcagcctcgggttg	3336
ALDH1L1	99	intron21+1086	caacccaatcttgccccccgg C/T gctgcagcccggcaacatttt	3337
ALDH1L1	100	intron22+235	gggcctggaggagacactcc A/C gccaggaggcactgggggcc	3338
ALDH1L1	101	intron22+313	atagcagggaggagttggcc G/A tgaagacccagggcccgtg	3339
ALDH1L1	102	intron22+1214	tgggcccacttatgaatcct G/C cccgagttccctcagctccc	3340
ALDH1L1	103	intron22+1226	tgaatcctccccgagttccc T/C cagctccctcctaaccctag	3341
ALDH1L1	104	intron22+1623	ggggcttcccactgtccaga C/G aaggcggtgggagctgggga	3342
ALDH1L1	105	intron22+1698	attctgggaagtcctggccc A/G ctatccactgccagggataa	3343

遺伝子名	No.	存在位置	配　　列	配列番号
ALDH1L1	106	3'flanking+145	gagagacaggaggaaatggg C/T gtgggtcatctcaggcccca	3344
ALDH1L1	107	3'flanking+239	tgggaaacaggtgggaagac G/A gggattgagctgggtgagcc	3345
ALDH1L1	108	3'flanking+288	ggaagcagctcagactcccct C/T agcagatgggggcgggccct	3346
ALDH1L1	109	3'flanking+1513	agggtcggctcagaccccgg A/C gtgctcctggcatgtccagc	3347
ALDH1L1	110	3'flanking+1707	cggtgggacttgccctagca C/T gtgccacttataccagaaca	3348
ALDH1L1	111	3'flanking+1709	gtgggacttgccctagcacg C/T gccacttataccagaacaga	3349
ALDH1L1	112	3'flanking+1745	acagatgagtccatgtcaac C/T gcttcctgagttccctttgt	3350
ALDH1L1	113	3'flanking+1843	ctgcctctcagcccacagcc G/A ggccgctcacactcctccca	3351
CYP3A4	1	intron2+(754-763)	cacaaaatgagtttgtgggg (T)9-11 acacaaaggcggaatcacat	3352
CYP3A4	2	intron7+258	accactaatcaactttctgc C/T tctatggatttgcctattct	3353
CYP3A4	3	intron7+894	tgctgatctcactgctgtag C/T ggtgctccttatgcatagac	3354
CYP3A4	4	exon9+(32-33)	ttccttcagctgatgattga (A) ctctcagaattcaaaagaaa	3355
CYP3A4	4	exon9+(32-33)	ttccttcagctgatgattga　　ctctcagaattcaaaagaaa	3356
CYP3A4	5	intron10+12	cccaataaggtgagtggatg G/A tacatggagaaggaggggagg	3357
CYP3A4	6	intron10+459	agacatgtgacttttttttt T/Δ gaaaggtaacaatcactttc	3358
CYP3A4	7	intron10+608	agccgtctcgaatgtctccc C/T acttcataactcctccacac	3359
CYP3A4	8	intron12+2467	ttttttgcccattactccat A/G gagatcagaatatcactctg	3360

【００３６】

表１において、「遺伝子名」の欄には薬物代謝酵素をコードする遺伝子名を記載した。「配列」の欄においてアルファベット大文字で示した塩基がSNP情報である。「/」を付した2つの塩基は、その塩基のホモ又はヘテロのSNPを示す。例えば、「A/G」と表示した場合は、アレルがA/A若しくはG/Gのホモ、又はA/Gのヘテロであることを意味する。表中の配列は、SNPの前後20塩基を示している。但し、括弧を付した塩基（例えばABCB4の第26番の（T））はインサートによる多型を、Δ（例えばNAT2の第10番目）は1塩基の欠失による多型を意味する。また、配列番号674に示す配列中、nはVNTRであり、$(cctgy)_X$（Xは１～50の整数）からなる繰り返し配列を表している。また、括弧に数字を付した塩基は、その括弧内の塩基がその数字の数だけ繰り返されていることを意味する。例えば、配列番号1552の配列（表１、ABCB11の第55番）において「(T)9-12」とあるのは、Tが９～12個の繰り返し配列であることを意味する。

【００３７】

「存在位置」は、SNPのゲノム上の位置を示す。5'フランキング（flanking）領域、イントロン（intron）領域、3'フランキング（flanking）領域のSNPsの存在位置は、エキソン/イントロン結合点（exon/intron junction）の最初のイントロンの塩基配列を1番として数えた。エキソン領域のSNPsの存在位置は、エキソン/イントロン結合点の最初のエキソンの塩基配列を1番として数えた。（+）表示又は無表示は3'下流方向に、（-）は5'上流方向に向かって数えた数字を示

した。「No.」の欄に記載された数字は、各遺伝子の遺伝子地図（図９～141）上のSNPの位置を示す番号と対応する。

【００３８】

４．オリゴヌクレオチドプローブ又はオリゴヌクレオチドプライマーの作製

本発明の検出方法においてプライマー及び/又はプローブとして使用されるオリゴヌクレオチドは、例えばSNPを検出するときは表1に示す塩基配列（配列番号１～3360）を基本とし、これらの配列自体を合成してもよく、これらの配列の一部を含むように設計し合成してもよい。但し、その塩基配列中には必ずSNP（表１の「配列」の欄にアルファベット大文字で表示した部分）が含まれるようにする。また、本発明においてはこれらの配列の相補鎖も含まれる。

【００３９】

SNPを例に説明すると、SNP部位は、プライマー又はプローブの塩基配列の3'若しくは5'端に存在するように設計し、あるいは、相補的な配列の3'若しくは5'端に存在するように設計し、又は前２者の3'若しくは5'端から４塩基内、好ましくは2塩基内に存在するように設計する。あるいは、オリゴヌクレオチドの塩基配列全長の中央にSNPが存在するように設計する。「中央」とは、SNPの塩基よりも5'端に向かう塩基の数と、3'端に向かう塩基の数とがほぼ同数となる中心部の領域をいい、オリゴヌクレオチドの塩基数が奇数の場合は、中心部の5塩基、好ましくは中心部の３塩基、さらに好ましくは最も中心部の1塩基をいう。例えば、41個の塩基数の場合は、第19番目～第23番目、好ましくは第20番目～第22番目、さらに好ましくは第21番目の塩基が「中央」となる。また、オリゴヌクレオチドの塩基数が偶数の場合は、中心部の４塩基、好ましくは中心部の２塩基をいう。例えば、40個の塩基数の場合は、第19番目～第22番目、好ましくは第20番目の塩基が「中央」となる。

【００４０】

多型部位が複数の塩基で構成される場合は、プローブ又はプライマーにその配列が含まれるように設計する。特に、プローブ又はプライマーのDNAと相補する5'末端側又は3'末端側の１～４塩基のいずれか（「対応塩基」と称する。好ましくは5'末端又は3'末端の塩基。）が、当該複数の塩基の最も端の塩基に対応

するように設計する。例えば、後述のインベーダー法において表１のNDUFA7の第12番（配列番号828）に示す遺伝子多型（CAGAGGCT）を検出するためにインベーダープローブ及びアレルプローブを作製する場合は、図4aに示すアレルプローブについては、対応塩基（図では塩基として「T」を例示してある）の位置が「CAGAGGCT」配列の最も左の「C」となるように設計し、インベーダープローブについては図4bに示す「N」の塩基が「CAGAGGCT」配列の最も左の「C」を「N」（A、T、CまたはGのいずれか）に置換して設計する。逆に、インベーダープローブの対応塩基の位置を「CAGAGGCT」配列の最も右の「T」として設計する場合には、その塩基を「N」として、アレルプローブの対応塩基を「T」に設計する。なお、インベーダープローブおよびアレルプローブの対応塩基を「CAGAGGCT」配列のいずれかに設定することも可能である。

【００４１】

塩基配列の長さは、少なくとも13塩基、好ましくは13塩基～60塩基、さらに好ましくは15～40塩基、最も好ましくは18～30塩基となるように設計する。このオリゴヌクレオチド配列は、被検遺伝子を検出するためのプローブとして使用することができ、また、フォワード（センス）プライマー及びリバース（アンチセンス）プライマーのどちらに使用してもよい。

【００４２】

また、オリゴヌクレオチドは、ゲノムDNAとハイブリダイズする領域とハイブリダイズしない領域とがタンデムに連結したものであってもよい。連結の順序はどちらが上流でも下流でもよい。このオリゴヌクレオチドのうちハイブリダイズする領域は、表1に記載のSNPを含む配列情報から設計し、ゲノムDNAとハイブリダイズする領域の最も5'側又は3'側の配列がSNPとなるように作製する。上記オリゴヌクレオチドのうちハイブリダイズしない領域は、表1に記載のSNPを含む配列とハイブリダイズしないように、ランダムに配列を設計する。このオリゴヌクレオチドは、主としてインベーダー法によるSNPの検出に、プローブとして使用することができる。

【００４３】

さらに、本発明において使用されるプライマーは、表1に示す塩基配列のうち

、そのSNPに起因する機能変化、有効／無効の判断、副作用の有無を調べる目的で、PCRにて増幅される配列の中にSNPを含むよう設計される。この場合の、プライマーの長さは、少なくとも15塩基、好ましくは15～30塩基、さらに好ましくは18～24塩基の長さを有するように設計する。このときのプライマー配列は、増幅断片が500bp以下、好ましくは100～300bp、さらに好ましくは100～150bpとなるように鋳型DNAの領域から適宜選択する。

【００４４】

以上のように設計されたオリゴヌクレオチドプライマー又はオリゴヌクレオチドプローブは、公知の手法により化学合成することができるが、通常は、市販の化学合成装置を使用して合成される。

なお、プローブには、予め蛍光標識（例えばFAM, VIC, Cy3等）を付加して作業の自動化を図ることも可能である。

【００４５】

上記オリゴヌクレオチドは、ポリメラーゼ（例えばTaqポリメラーゼ）、緩衝液（例えばTris緩衝液）、dNTP、蛍光色素（VIC、FAM等）などと共に、遺伝子多型検出用キットに含めることができる。

【００４６】

５．検出

上記のようにして調製されたオリゴヌクレオチドをプライマーとし、DNAポリメラーゼを用いて薬物代謝酵素をコードする遺伝子（鋳型DNA）を増幅する。あるいは、上記のようにして調製されたプローブを鋳型DNAとハイブリダイズさせて、目的の遺伝子多型を有するDNAを検出する。鋳型となるDNAの調製は、公知の手法、例えば塩化セシウム密度勾配超遠心法、SDS溶解法又はフェノール・クロロホルム抽出法等により行うことができる。

【００４７】

(1) PCRによる検出

増幅は、ポリメラーゼ連鎖反応(PCR)により行うことができる。DNAポリメラーゼとしてはLA Taq DNAポリメラーゼ(Takara)、Ex Taq ポリメラーゼ（Takara社）、Gold Taq ポリメラーゼ（Perkin Elmer），AmpliTaq（Perkin Elmer）、Pfu

DNAポリメラーゼ（Stratagene社）等が挙げられる。

【００４８】

増幅の条件は、85℃～105℃で10秒～40秒、好ましくは94℃で20秒～30秒の変性工程、50℃～72℃で30秒～1分、好ましくは60℃で20秒～1分のアニーリング工程、及び65℃～75℃で1分～4分、好ましくは72℃で2分～3分の伸長工程を１サイクルとしてこれを30～40サイクル行う。但し、鋳型DNA及びプライマーを十分変性させるために、上記増幅サイクルの前に95℃で1分～5分〔但し、Gold Taq ポリメラーゼ（Perkin Elmer）を使用の際は、最低8分～15分、好ましくは10分から12分の変性工程を加えてもよく、また、増幅されたDNAを完全に伸長するために、増幅サイクルの後に72℃で1分～10分の伸長工程を加えてもよい。さらに、増幅産物の検出を直ちに行わない場合は、非特異的な増幅が起こらないようにするために、増幅産物を4℃で保存する工程を加えることが好ましい。このようにして、薬物代謝酵素をコードする遺伝子を増幅することができる。

【００４９】

その後は、増幅産物についてアガロースゲル電気泳動を行い、臭化エチジウム、SYBR Green液等により染色し、そして増幅産物を1本又は２～３本のバンド（DNA フラグメント）として検出することにより、薬物代謝酵素をコードする遺伝子中の遺伝子多型を含む薬物代謝酵素の一部分をDNAフラグメントとして検出することができる。アガロースゲル電気泳動の代わりにポリアクリルアミドゲル電気泳動、あるいはキャピラリー電気泳動を実施してもよい。また、予め蛍光色素等により標識したプライマーを用いてPCRを行い、増幅産物を検出することもできる。また、マイクロプレート等の固相に増幅産物を結合させ、蛍光又は酵素反応等により検出する等、電気泳動を必要としない検出方法も採用することができる。

【００５０】

(2) TaqMan PCR法による検出

TaqMan PCR法は、蛍光標識したアレル特異的オリゴとTaq DNAポリメラーゼによるPCR反応とを利用した方法である。TaqMan PCR法で用いるアレル特異的オリゴ(TaqManプローブという)は、前記SNP情報に基づいて設計することができる。T

aqManプローブの5'末端はFAMやVICなどの蛍光レポーター色素Rによって標識されており、同時に3'末端がクエンチャーQ(消光物質)によって標識されている。（図１）。従って、この状態ではクエンチャーが蛍光エネルギーを吸収するため蛍光は検出できない。TaqMan プローブの3'末端はリン酸化されているため、PCR反応中にTaqManプローブからの伸長反応は起こらない（図１）。しかし、このTaqManプローブを、SNPを含む領域を増幅するように設計したプライマーとTaq DNAポリメラーゼとともにPCR反応を行うと、次の反応が起こる。

【００５１】

まず、TaqManプローブが鋳型DNAの特異的な配列にハイブリダイゼーションし（図2a）、同時にPCRプライマーから伸長反応が起こる（図2b）。この際、Taq DNAポリメラーゼは5'ヌクレアーゼ活性を有しているため、PCRプライマーの伸長反応が進む際にハイブリダイゼーションしたTaqManプローブを切断する。TaqManプローブが切断されると、蛍光色素がクエンチャーの影響を受けなくなり、蛍光を検出することができる（図2c）。

【００５２】

例えば、図3に示すように、SNP部位がAのアレル（アレル１とする）と、Gのアレル（アレル２とする）が存在すると仮定する。アレル１に特異的なTaqManプローブはFAMで、アレル２に特異的なTaqManプローブはVICで標識する（図3）。2種類のアレル特異的オリゴをPCR試薬に添加し、検出の対象となる鋳型とTaqMan PCRを行う。その後、蛍光検出器にてFAM及びVICの蛍光強度を測定する。その結果、アレルのSNP部位と、TaqManプローブのSNPに対応する部位とが相補的である場合は、プローブがアレルとハイブリダイズし、Taqポリメラーゼによりプローブの蛍光色素が切断されて、クエンチャーの影響を受けなくなり、蛍光強度が検出される。

【００５３】

なお、鋳型がアレル１のホモ接合体である場合はFAMの強い蛍光強度を認め、VICの蛍光はほとんど認められない。鋳型がアレル１とアレル２のヘテロ接合体である場合は、FAMとVICの両者の蛍光を検出することができる。

【００５４】

(3) インベーダー法によるSNPの検出

インベーダー法は、アレル特異的オリゴと鋳型とをハイブリダイゼーションすることによりSNPを検出する方法である。インベーダー法では、2種類の非標識オリゴと1種類の蛍光標識オリゴを用いる。2種類の非標識オリゴのうちのひとつは、アレルプローブと呼ばれるものである。アレルプローブは、ゲノムDNA（鋳型DNA）とハイブリダイズして相補二本鎖を形成する領域と、鋳型DNAの配列とは無関係な配列であってゲノムDNAとハイブリダイズしない配列の領域（フラップという）とから構成されており、ハイブリダイズする領域のうち最も5'側又は3'側の位置が、SNPに対応する塩基となっている（図4a）。上記フラップ配列は、後述するフレットプローブと相補的な配列を有するオリゴヌクレオチドである。もうひとつのオリゴは、インベーダープローブと呼ばれている。このオリゴは、SNP部位からゲノムDNAの3'側方向に向かって相補的にハイブリダイズするように設計されている（図4b）。但し、SNP部位に対応する配列（図4b中、「N」）は任意の塩基でよい。従って、鋳型であるゲノムDNAと上記２つのプローブをハイブリダイゼーションさせると、SNP部位にインベーダープローブの1塩基（N）が割り込むように侵入し（図4c）、SNP部位が３重鎖を形成する。

【００５５】

一方、蛍光標識オリゴはアレルと全く無関係な配列であり、SNPの種類によらず配列は共通である。このプローブをフレット（FRET）プローブ(fluorescence resonance energy transfer probe)という（図5）。FRETプローブの5'末端の塩基（レポーター）には蛍光色素Rが標識されており、その上流にはクエンチャーQが結合している。従って、この状態ではクエンチャーが蛍光色素を吸収してしまうため蛍光を検出できない。また、FRETプローブの5'末端（レポーター塩基）から一定領域（領域１とする）は、その領域１よりも3'側の領域と向き合って相補的な配列となるように設計されている（これを領域２という）。従って、領域１は領域２と自分自身で相補鎖を形成する（図5）。また、この相補鎖形成領域よりもさらに3'方向の領域は、アレルプローブのフラップとハイブリダイズして相補鎖を形成できるように設計されている（図5）。

【００５６】

インベーダー法では、DNAの特殊な構造を認識して切断する特殊なエンドヌクレアーゼ活性を有する酵素（5'ヌクレオチダーゼ）の１つであるクリーバーゼ（cleavase)を用いる。クリーバーゼは、ゲノムDNA、アレルプローブ及びインベーダープローブがSNP位置で３重になった時に、アレルプローブのSNP位置の3'側を切断する酵素である。従って、図4cのように３つの塩基が並び、5'末端がフラップ状になっている部分を認識して、そのフラップ部分を切断する。これによって、このSNP部位の構造がクリーバーゼにより認識され（図6a）、フラップの部位でアレルプローブが切断されフラップ部分が遊離する（図6b）。次に、アレルプローブから遊離したフラップ部分は、FRETプローブと相補的な配列をもつため相補結合する（図6c）。このとき、フラップのSNP部位がFRET自身の相補結合部位に割り込んで侵入する。クリーバーゼは再びこの構造を認識して蛍光色素部分を切断する。切断された蛍光色素は、クエンチャーの影響を受けなくなり、蛍光を発する（図6d）。SNP部位がアレルプローブのSNPに対応する配列とマッチしない場合は、図7のように、クリーバーゼが認識する特異的なDNA構造をとらないため、プローブは切断されず、蛍光は検出されない。

【００５７】

例えば、あるSNPがT/Cのときに、T用のインベーダープローブ、アレルプローブ、及びSNPに対応するレポーターにFAMを結合させたフレットプローブ、並びにこれとは別にC用のインベーダープローブ、アレルプローブ、及びSNPに対応するレポーターにVICを結合させたフレットプローブとを準備し、全て混合してSNP検出を行う。その結果、SNPがT／Tのホモの場合にはFAMの蛍光を発し、C／Cのホモの場合にはVICの蛍光を発し、T／Cヘテロの場合にはFAMとVIC両者の蛍光を発する。FAMとVICは蛍光波長が異なるため、両者を分別できることになる。

【００５８】

(4) SniPer法による検出

SniPer法でSNPを検出するためには、アレルの識別をRCAによる増幅の有無で行うことができる。すなわち、鋳型になるべきゲノムDNAを直鎖状にしておいて、このゲノムDNAにプローブをハイブリダイズさせる。プローブの配列と鋳型であるゲノムDNAの配列とが相補的にマッチして相補鎖を形成すると、ゲノムDNAはラ

イゲーション反応が起こって環状になることができる。その結果、環状DNAのRCAが進行する。これに対し、プローブの端がゲノムDNAとマッチしなければ、ライゲーションされず環状にならないため、RCAの反応は進まない。従ってSniPer法では、ゲノムDNAとアニールし、しかも環状になり得る一本鎖プローブを設計する。この一本鎖プローブをパドロックプローブという。このパドロックプローブの断端を検出目的となるSNPに対応する配列にしておいて、このパドロックプローブとゲノムDNAとを混ぜ、ライゲーション反応を行う。パドロックプローブの断端とゲノムDNAのSNP部分が相補的であれば、ライゲーション反応によってパドロックプローブは断端がつながり環状となるが、相補的でなければ環状にならない。従って、対象となるSNPに相当するパドロックプローブのみが環状となり、DNAポリメラーゼによって増幅する。SNPは、この増幅の有無を検出すればよい。検出は、両端に蛍光色素とクエンチャーをもち、ヘアピン構造を有する合成オリゴヌクレオチドを使用する。

【００５９】

(5) MALDI-TOF/MS法による検出

MALDI-TOF/MS (Matrix Assisted Laser Desorption-Time of Flight / Mass Spectrometry) 法は、質量分析計をSNPタイピングに応用した方法である。この方法は、以下のステップから構成される。

【００６０】

(i)SNPを含むDNA断片のPCR増幅及び精製

SNP部位の塩基とPCRプライマーは重複しないように設計した後DNA断片を増幅し、増幅反応産物からエキソヌクレアーゼやアルカリホスファターゼ処理によりプライマー、dNTP等を除去して増幅断片を精製する。

【００６１】

(ii) プライマー伸長反応（サーマルサイクル）及び精製

PCR産物である標的領域の鋳型に対して10倍以上のプライマーを加え、サーマルサイクル反応させてプライマー伸長反応を行う。ここで使用するプライマーは、その3'末端がSNP部位の塩基に隣接するように設計する。プライマーの長さは、15～30塩基、好ましくは20～25塩基である。マルチプレックス反応を行う場合

には、鋳型と相補的でない配列を5'末端に付加する。また、サーマルサイクルは、85～105℃（好ましくは94℃）と35～40℃（好ましくは37℃）の２温度間で20～30サイクル（好ましくは25サイクル）行う。

得られた反応産物を、質量分析機に適した状態にするため精製キット等を用いて精製する。

【００６２】

（iii）質量分析計によるDNAの質量分析

精製された伸長反応産物を質量分析機にアプライして、目的産物の質量を測定する。すなわち、精製産物をマトリックスと混合し、MALDIプレートに0.5～1.0μLスポットする。プレートを乾燥後、試料にレーザー光を照射し、スペクトログラムを作成する。

【００６３】

(6) 塩基配列決定法による検出

本発明においては、１塩基の伸長反応を利用した多型の検出を行うことができる。つまり、異なる蛍光化合物で標識された４種類のジデオキシヌクレオチドを、検出の対象となる遺伝子が含まれる反応系に添加し、１塩基の伸長反応を行う。この場合、伸長する塩基を多型部位としておき、また、DNA合成の停止とDNA分子の3'末端の蛍光標識という2つの反応を操作する。4種類の反応液をシークエンシング用ゲルの同一レーンやキャピラリー上で電気泳動を行ない、DNAバンドを標識した蛍光色素の違いを蛍光検出器により検出して配列決定を行う、あるいは１塩基伸長したオリゴヌクレオチドを蛍光検出装置や質量分析装置などを用いてどの塩基が伸長したかを蛍光色素の種類の違いを利用して調べる方法である。蛍光標識ジデオキシヌクレオチドの代わりにプライマーを蛍光標識し、非標識ジデオキシヌクレオチドと共に用いることもできる。

【００６４】

６．薬物の評価

本発明においては、前記のようにして得られる一塩基多型等の検出結果から、当該薬物代謝酵素によって代謝される薬物の有効性及び安全性を評価することができる。

薬物の評価は、タイピングシステムにより行うことができる。すなわち、上記いずれかの検出手法に従って、毒性（副作用）発現群と非発現群のアレル頻度を比較する。両者を比較した際、アレル頻度に差が生じるものを毒性発現認識のためのマーカーとして選出する。統計学的検定は、通常χ^2検定によるが、例えばFisher検定などの他の統計処理を行うこともできる。なお、この結果を、薬物の活性本体（薬物未変化体又は代謝物でもよい）の血中濃度、組織濃度に反映させることも可能である。当該全ての遺伝子多型に関して、毒性との因果関係を調べ、相関のあった遺伝子多型部位のみを選出する。その全ての遺伝子多型解析用プローブ又はプライマーと各手法に応じた試薬を、反応プレート、カード又はガラス基盤等に予め用意し、そこに予測したいヒトのゲノムDNAを添加し、反応させることで、アレルパターンを調べることができる。毒性と相関する遺伝子多型を有する場合には、そのヒトの副作用発現予測が可能となる。薬物の有効性についても同様である。また、薬物の違いにより、副作用又は有効性と相関する遺伝子多型も異なるので、それぞれに関して、当該遺伝子多型を用いてタイピング操作を行えば、有効性や副作用の予測をすることが可能となる。

【００６５】

このことを利用して、その遺伝子多型頻度と有効／無効又は副作用の有／無を比較し、アレル頻度に差がある時に判定することが可能となる。

例えば、薬物Aの投与によってある毒性（副作用）を示した者のSNPを解析した結果、統計的に全体の90％がT/Tを持つ者（例えばFAMの蛍光強度を検出）であることが判明し、毒性（副作用）を示さなかった者のSNPを解析した結果、T/Tを持つ者は全体の10％にすぎず、C/Cを持つものが90％を占めたことが判明したとすると、SNP解析の結果、T/Tを持つ者は薬物Aの投与はできないと評価することができる。

【００６６】

７．薬物のスクリーニング

本発明において前記の通り得られた遺伝子多型情報は、被験者から採取した当該薬物代謝酵素をコードする遺伝子の遺伝子多型情報と比較することにより、当該薬物代謝酵素によって代謝される薬物の有効性及び安全性を解析するための指

標として利用される。従って、本発明において得られた遺伝子多型情報は、どの薬物が治療に最も有効であるか、その使用すべき薬物を選択するための情報源となる。

【００６７】

手法としては「５．薬物の評価」に記載の評価方法を利用すればよい。つまり、前項で副作用又は有効性と相関が認められた遺伝子多型は、その酵素の活性、転写、翻訳に影響を与えるものであるといえる。また、副作用又は有効性の発現機構と間接的であっても何らかの因果関係があるといえる。ある薬物の代謝は、製薬会社などにおいて前臨床又は臨床試験にて調査・確認される。よって、それらの酵素遺伝子中に存在する遺伝子多型の中に重篤な副作用と相関する多型がある場合にはこれを削除すること、あるいは条件付きで使用することが可能となる。また、有効性についても同様である。この副作用と有効性の情報から薬物のスクリーニングが可能となる。

【００６８】

さらに、臨床試験（第I～III相試験）において副作用発現症例のボランティアと副作用非発現症例の遺伝子多型頻度解析を行うことで、前記した以外に副作用や有効性と相関する新たな遺伝子多型を検出することが可能となる。これを、上記と同様に調べることで薬物のスクリーニングが可能となる。

【００６９】

【実施例】

以下、実施例により本発明をさらに具体的に説明する。但し、本発明はこれら実施例にその技術的範囲が限定されるものではない。

【００７０】

〔実施例1〕 SNP情報の取得

(1) DNA抽出

血縁関係のない48人からEDTA存在下に採血を行った。DNAの抽出は、ゲノム解析ラボマニュアル（中村祐輔編 シュプリンガー・フェアラーク東京）の方法に従って以下の通り行った。

【００７１】

血液10mlを50mlのファルコンチューブに移し、室温で3000rpm、５分間遠心を行った。ピペットにて上清（血清）を採取した後、RBC溶解バッファー(10mM NH_4HCO_3, 144mM NH_3Cl)を30ml加えた。沈殿がほぐれるまで混和した後、室温で20分放置した。室温で3000rpm、５分間遠心を行った後、ピペットにて上清（血清）を捨て、白血球のペレットを得た。RBC溶解バッファーを30ml加え、同様の操作をさらに2回行った。白血球のペレットにProteinase Kバッファー(50mM Tris-HCl(pH7.4), 100mM NaCl, 1mM EDTA(pH8.0))を4ml、10% SDSを200μl、10mg/ml Proteinase Kを200μl加え、転倒混和した後、37℃で一晩静置した。フェノールを4ml加え、ローテーター（Rotator T-50, Taitec）にて4時間ゆっくりと転倒混和した。室温で3000rpm、10分間遠心を行い、上層を新しいチューブに回収した。4mlのフェノール-クロロホルム-イソアミルアルコール(容積比25:24:1)を加え、同様に2時間転倒混和した後、遠心した。上層を新しいチューブに回収し、4mlのクロロホルム-イソアミルアルコール(容積比24:1)を加え、同様に30分転倒混和した後、遠心した。上層を新しいチューブに回収し、8M 酢酸アンモニウム400μl、イソプロパノール4mlを加え、転倒混和した。糸状の白色析出物(DNA)を2ml容のチューブに回収し、70%エタノールを1ml加え、転倒混和した。新しい2ml容のチューブにDNAを回収し風乾した後、TE溶液(10mM Tris-HCl(pH7.4), 1mM EDTA(pH7.4))を500μl加え、溶解後、ゲノムDNAサンプルとした。

【００７２】

(2) PCR

ゲノムシークエンスは、GenBank DNAデータベースから得た。RepMask コンピュータプログラムを用い、リピート配列を除いた後、PCR産物が1kb前後になるようにPCRプライマーを設定した。ゲノムDNAは、同濃度に調製した血縁関係のない48人のDNAを使用した。それぞれ3人分のDNAを1本のチューブに同量混ぜ、このうち60ngをPCRに使用した。PCRは、Ex-Taq(2.5U; TaKaRa)を使用し、GeneAmp PCR System 9700(PE Applied Biosystems)を用いて行った。94℃で2分間反応後、94℃で30秒の変性、60℃又は55℃で30秒のアニーリング、72℃で1分の伸長を行い、これを１サイクルとして35サイクル行った。

【００７３】

(3) シークエンス

PCR産物は、Arraylt(Telechem)を使用し精製を行った後、BigDye Terminator RR Mix(PE Applied Biosystems)を用い、シークエンス反応を行った。GeneAmp PCR System 9700(PE Applied Biosystems)を用い、96℃で2分間反応後、96℃で20秒の変性、50℃で30秒のアニーリング、60℃で4分の伸長を行い、これを１サイクルとして25サイクル行った。シークエンス反応後、ABI PRISM 3700 DNA Analyzerにてシークエンス解析を行った。

【００７４】

(4) SNPの検出

SNPの検出には、PolyPhredコンピュータープログラム(Nickerson et al., 1997, Nucleic Acids Res., 25, 2745-2751)を使用し、解析を行った。

(5) 結果

表１に示すSNPの結果が得られた。また、解析を行った薬物代謝酵素名とその略号、データベース(GenBank)のACCESSION 番号、薬物代謝酵素の遺伝子の構造とSNPsの存在位置を図9～141に示した。図9～141において、エキソンは水平線で表示した遺伝子上に白抜きのボックス又は黒の線で示した。SNPsの存在位置は、遺伝子の上側に実線で示し、番号を付した。

【００７５】

〔実施例2〕

異なる２グループの被験者についてインベーダー法によりタイピングを行った。結果を図142に示す。図142において、横軸(Allele 1)はTに対応するFAMの蛍光の強さを、横軸（Allele 2）はCに対応するVICの蛍光の強さを表す。斜線入りの丸はSNPのパターンがT/Tであり、黒丸（●）はC/C、白丸（○）はT/Cであることを示す。黒四角（■）はバックグラウンド値を意味し、×印は判定不能を示す。パネルA（上）のグラフに示された被検者グループはSNPのパターンがC/Cのものが多く、パネルB（下）のグラフに示された被検者グループはSNPのパターンがT/Tのものが多いことが分かる。

【００７６】

〔実施例3〕SNPの検出

血縁関係のない5人から実施例1に記載した方法により採取したゲノムDNAを試料とし、3種類の薬物代謝酵素遺伝子(EPHX1, ABCB2, AANAT)中のSNPの検出を、インベーダー法により行った。EPHX1についてはNo.３（配列番号49）及びNo.17（配列番号63）、ABCB2についてはNo.４（配列番号4）及びNo.11（配列番号11）、AANATについてはNo.３（配列番号561）の各配列に基づいて設計されたインベーダープローブ及びアレルプローブを用いた。各SNPの存在位置は、表１に示されている。

結果を表２に示す。

【００７７】

【表２】

薬物代謝酵素遺伝子	EPHX1		ABCB2		AANAT
	No.3	No.17	No.4	No.11	No.3
	配列番号49	配列番号63	配列番号4	配列番号11	配列番号561
SNP	(T/G)	(A/G)	(G/T)	(G/A)	(T/A)
被験者Ⅰ	T/T	A/G	T/T	G/A	T/T
被験者Ⅱ	T/T	A/A	G/G	G/G	T/A
被験者Ⅲ	T/G	A/A	G/G	A/A	T/T
被験者Ⅳ	G/G	A/G	G/T	G/G	T/T
被験者Ⅴ	T/G	A/G	G/T	G/A	T/A

【００７８】

表２の結果より、本発明の方法により各被験者の薬物代謝酵素遺伝子中のSNPの検出及びそのパターンの同定が可能であることが分かった。

【００７９】

【発明の効果】

本発明により、SNPの解析方法が提供される。本発明の方法により、目的の疾患に応じた薬物の選択をすることが可能となるため、本発明の方法は極めて有用である。

【００８０】

【配列表】

SEQUENCE LISTING

<110> RIKEN

Nakamura Yusuke
Sekine Akihiro
Iida Aritoshi
Saito Susumu

<120> A method of detecting gene polymorphism

<130> RJH13-090S

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<150> JP2000-399443
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<150> JP2001-135256
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<400> 1485

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<210> 1486

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<212> DNA

<213> Homo sapiens

<400> 1486

actcgtttgc agattttaca yttgttttct tgttgacaca c 41

<210> 1487

<211> 41

<212> DNA

<213> Homo sapiens

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<222> 21

<223> n represents t or deletion

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<211> 41

<212> DNA

<213> Homo sapiens

<400> 1488

agggccgggg cccaggcttc ygtaggcatc agtatgatgg t 41

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tccttttcct gttttttgtt kttttttttt tcttggagtg g 41

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cattggtttt tagtgtattc wgtgttgtgc atccatcatc a 41

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<222> 21

<223> n represents tt

<400> 1494

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<210> 1495

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<212> DNA

<213> Homo sapiens

<400> 1495

tgtggtttag agctttctct gagacatttt tgctaaggtt 40

<210> 1496

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<400> 1496

agctgaagtg aattaagcac ratcaactca gtactcacac t 41

<210> 1497

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<220>

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<222> 21

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<400> 1497

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<400> 1498

agagggtttc ccaagcacac yctgtgtttg gggttattgc t 41

<210> 1499

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<220>

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<222> 21

<223> n represents a or deletion

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<210> 1500

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<400> 1500

aatttcagtt tttaggtcac ycaagccagt gggagtcaca t 41

<210> 1501

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<222> 21

<223> n represents 10 to 13 repeats of a

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<213> Homo sapiens

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<400> 1503

aaagagaata ggttagtgga ytagtattcc tgtgcttaat g 41

<210> 1504

<211> 41

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<400> 1505

gtttggctac tttgattaaa raagaaagaa gagataataa t 41

<210> 1506

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cctgcatcta ttctgaccta yactggggaa aacagtatgt g 41

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<222> 21

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<400> 1512

tttctcatca ggttacaaga ygagaagaaa ggtgatggcg t 41

<210> 1513

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gggaggtgac ccatgaattt yacttgagta tcatctccaa g 41

<210> 1517
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aaaggattca gcaggcatga rgaaagaaaa gctttgcaag a 41

<210> 1520

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ccattggcta atagcaatga mctatgacat ggtctaactt a 41

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<213> Homo sapiens

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tcaatgatgt tacagtgaga mtctaatatt gtattaaacc c 41

<210> 1522

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gtgtccaagt ttacggacta ygagctgaag gcctatgcca a 41

<210> 1524

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taatcattcc aaaccacgga mtttatttca ttaagaacat g　41

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tcattccaaa ccacggactt watttcatta agaacatgat a　41

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tttacagatt ggaaaagcca ytgaagtatt gcaggtccag a　41

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gaattcatta ataaaaataa wcacataatg gagcgtgaca t 41

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<210> 1532

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<400> 1532

gctatttggt aggaacatct rggcatgatc aggtagcctt c 41

<210> 1533

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<222> 21

<223> n represents a or deletion

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<210> 1534

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1534

tgtttccagt aatagggaat rgaggtgtct ttctctgaaa g 41

<210> 1535

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1535

gataaatgac aaggcaatta saacaatcag gaagcacagg t 41

<210> 1536

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1536

caaggcaatt acaacaatca rgaagcacag gttcttccca a 41

<210> 1537

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1537

cctcatcctt gccaatgttt yctttttactg gtttttgatg g 41

<210> 1538

<211> 41

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<213> Homo sapiens

<400> 1538

tctaaatgac ctcaacatgg ycattaaacc aggggaaatg a 41

<210> 1539

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1539

atggcagtat attgatcaaa yagaaaggtg tagcatacat t 41

<210> 1540

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<212> DNA

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<220>

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<222> 21

<223> n represents c

<400> 1540

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<210> 1541

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<400> 1541

ttattggcct ctatttttc tgcccattgg tcaagtatga 40

<210> 1542

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<400> 1542

catacattcc tgggagaaac yaagaggtca tagaaggaaa a 41

<210> 1543

<211> 41

<212> DNA

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<400> 1543

cacaattata cacatttctt ytcgtatgat tcccaagtca t 41

<210> 1544

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<212> DNA

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<400> 1544

tattgtgtca aaaacaattc rttgtatatc tccattctaa g 41

<210> 1545

<211> 41

<212> DNA

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<220>

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<222> 21

<223> n represents t

<400> 1545

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<210> 1546

<211> 40

<212> DNA

<213> Homo sapiens

<400> 1546

cagcctttgc attatatttt gctgtgttgt ctaacaggag 40

<210> 1547

<211> 41

<212> DNA

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<400> 1547

gctgtgttgt ctaacaggag maaagagaca cggatttgct c 41

<210> 1548

<211> 41

<212> DNA

<213> Homo sapiens

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tgagatagat atttaggacc rtgaccaatt tttattttgg t　　41

<210> 1549

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1549

gtgaccaatt tttattttgg ytgaaaaatc ttatttgaag t　　41

<210> 1550

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<210> 1551

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<400> 1551

ccttttctaa tgtctgcaca rcctatttaa gaatattccc a　　41

<210> 1552

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<220>

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<222> 21

<223> n represents 9 to 12 repeats of t

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<211> 41

<212> DNA

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<400> 1554

tccccaattc atgggttttt kgttagcttc tcatcttctt g 41

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<220>
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<222> 21
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<400> 1555
caattcatgg gtttttggtt nagcttctca tcttcttggg g　　41

<210> 1556
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<400> 1556
caattcatgg gtttttggtt agcttctcat cttcttgggg　　40

<210> 1557
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<220>
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<222> 21

<223> n represents aaaaaaagaaaa

<400> 1557

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<210> 1558

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<213> Homo sapiens

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<222> 21

<223> n represents aaaaaaaaaaaa

<400> 1558

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<210> 1559

<211> 41

<212> DNA

<213> Homo sapiens

<220>

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<222> 21

<223> n represents aaaaaaaaaa

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<210> 1560

<211> 41

<212> DNA

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<210> 1561

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tgttaaaata tctcattgta yatgctgacg gatttttctt g 41

<210> 1562

<211> 41

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ccttaagtct cctcctatca wgcaccttgt tctcaccagc t 41

<210> 1563

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<221> modified base

<222> 21

<223> n represents t or deletion

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ctctctcttc ctttctcagc nctactattt cactgttggc t 41

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<400> 1564

aatccccata tcctaccttа kccatctcat ccatgaatct t 41

<210> 1565

<211> 41

<212> DNA

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<400> 1565

atccccatat cctaccttag ycatctcatc catgaatctt g 41

<210> 1566

<211> 41

<212> DNA

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<400> 1566

aatatgagtt ttctaggtat rtatctagca gtgtttcaag t 41

<210> 1567

<211> 41

<212> DNA

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<400> 1567

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<210> 1568

<211> 41

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<210> 1569

<211> 41

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atgtatgaga tcaagtcagg rtcaaatatt agacacccat a 41

<210> 1570
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<400> 1570
ggaccatcct gtggggcaat sgttccagaa aatgctggta t 41

<210> 1571
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<400> 1571
ctcaccggta taaatacaac ygtagcaaag gttttctttt t 41

<210> 1572
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<210> 1573

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<400> 1573

tgcgtattcc ctcagttcag tttttattca agccacagca　　40

<210> 1574

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<222> 21

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<400> 1574

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<210> 1575

<211> 41

<212> DNA

<213> Homo sapiens

<220>

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<222> 21

<223> n represents c or deletion

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<400> 1578

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<210> 1579
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<400> 1579
aaacaccaca gaatgacata raactaaagg cggcaggaat c　　41

<210> 1580
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<210> 1581
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gagcagctga aggcaggtca katgaaggct aggtggctgg a　　41

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<400> 1582

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<400> 1584

gaggactttg cacatagtag rtgctcagct atattgttgg c 41

<210> 1585

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tttggaatct aaagactggg kcacgatgct agttgtgtga c 41

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<212> DNA

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<400> 1587

acctaagggt gtccatcctg raggagagca gtcctagggg g　　41

<210> 1588

<211> 41

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<210> 1595
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<210> 1597
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gcctgggttc ctcctcctgg yccctctatg ccccctccca t 41

<210> 1598
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<213> Homo sapiens

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<210> 1600
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<400> 1600
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<210> 1601
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<400> 1601
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<210> 1602
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<210> 1603

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1603

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<210> 1604

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<210> 1606

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<400> 1606

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<210> 1607

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<212> DNA

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<210> 1790

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agttcaagat gattttgtag sttcagggcc tagttgactt a 41

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<210> 1813

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<210> 1848
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<210> 1856
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<210> 1859
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<400> 1859

atattaaaca gagttacata yacttacaac ttcatacata t 41

<210> 1860
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<400> 1860
gtgtggatag taaatgccag rgtaaatcac atagcatcta a 41

<210> 1861
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<400> 1861
atggaagaga agttttagta raggggagga aggaggaggt g 41

<210> 1862
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<220>
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<222> 21
<223> n represents t or deletion

<400> 1862

gagagagact ttttttttt naaggcgaga gtttactacc t 41

<210> 1863
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<400> 1863
gtattaactc aaatctgatc wgccctactg ggccaggatt c 41

<210> 1864
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<213> Homo sapiens

<400> 1864
tttgcagtat cattgccttg ygatatatat tactttaatt a 41

<210> 1865
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<220>
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<222> 21
<223> n represents at or deletion

<400> 1865

atacatatat atgcacacac naaatatgta tatatacaca t 41

<210> 1866
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<212> DNA
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<400> 1866
taaatatgta tatatacaca wgtatacatg tataagtatg c 41

<210> 1867
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<213> Homo sapiens

<400> 1867
ggaagtataa atttgtaaat mactgagacc caaacttaca a 41

<210> 1868
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<213> Homo sapiens

<400> 1868
tgctattgac taatagtaat wattttaggg cagctttatg a 41

<210> 1869
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<213> Homo sapiens

<400> 1869
tggtagttct atgtggaaac mgtgaggaaa taattttata t 41

<210> 1870
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<400> 1870
caaaaaggta tggaagtcag mggagaagga gacccctatg t 41

<210> 1871
<211> 41
<212> DNA
<213> Homo sapiens

<220>
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<222> 21
<223> n represents a or deletion

<400> 1871
aagtatgcaa aaaaaaaaaa ngaaataaat cactgacaca c 41

<210> 1872
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<213> Homo sapiens

<400> 1872
cattaataaa ataacaaatc rtatctattc aaagaatggc a 41

<210> 1873
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<212> DNA
<213> Homo sapiens

<400> 1873
tgacatttgt gatatgatta ytctaattta gtctttttca g 41

<210> 1874
<211> 41
<212> DNA
<213> Homo sapiens

<220>
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<222> 21
<223> n represents t or deletion

<400> 1874
ttacctttaa ctttttttnt nagtttgatc agctctcttt a 41

<210> 1875
<211> 41
<212> DNA

<213> Homo sapiens

<400> 1875
atgcttttgg agttgggtct yataaatgta tagaaatgtt t 41

<210> 1876
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1876
atgtggaaca atcatgacta yatgcctttt actttctcta t 41

<210> 1877
<211> 41
<212> DNA
<213> Homo sapiens

<220>
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<222> 21
<223> n represents at or deletion

<400> 1877
agaatcaata ttaaacacac ngttttatta tatggagtca t 41

<210> 1878
<211> 41
<212> DNA

<213> Homo sapiens

<220>
<221> modified base
<222> 21
<223> n represents a or deletion

<400> 1878
ctgtcctaaa gtttaaaaag naaaaaaaaa ggaagaagga a 41

<210> 1879
<211> 41
<212> DNA
<213> Homo sapiens

<220>
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<222> 21
<223> n represents 12 to 14 repeats of t

<400> 1879
cctttacaaa ctcttagaca nagtttaaca tgttacaaaa c 41

<210> 1880
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1880

actcttcccc cttgtcaaca yatgatgaag cttttaaata c 41

<210> 1881
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<212> DNA
<213> Homo sapiens

<400> 1881
gggtgaagct ctttccccac yggaactcaa gcaagtgcaa g 41

<210> 1882
<211> 41
<212> DNA
<213> Homo sapiens

<220>
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<222> 21
<223> n represents t or deletion

<400> 1882
ggatgaatta agtttttttt naaaaaagaa acatttggta a 41

<210> 1883
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1883

aaaggggctg aaggggtctt yctttgtgt tcccctgact g 41

<210> 1884
<211> 41
<212> DNA
<213> Homo sapiens

<220>
<221> modified base
<222> 21
<223> n represents cac or deletion

<400> 1884
caccccacca ccaccaccac naaggtaacg ttctgcccca c 41

<210> 1885
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1885
agcctgggca acatagtgag rccccccccg ccctttctac a 41

<210> 1886
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<212> DNA
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<400> 1886

aggaggactg tgaatcccag mctgcatgtt tgggtcggat t　41

<210> 1887
<211> 41
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<213> Homo sapiens

<400> 1887
catctcacta aggaagaatc yagtaaccag caaggatgag a　41

<210> 1888
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1888
cccagactgc actcctgcag ygctgcctgg ctcctgtagt t　41

<210> 1889
<211> 41
<212> DNA
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<400> 1889
tttcagagct gtctggaaat wtaggggggca ggtgggaggg g　41

<210> 1890
<211> 41
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<213> Homo sapiens

<400> 1890
ccctacccct agcccagggg ycccacatg agtatgaatg g 41

<210> 1891
<211> 41
<212> DNA
<213> Homo sapiens

<220>
<221> modified base
<222> 21
<223> n represents cca

<400> 1891
agagaaccct tcattaacca ngggcgtggc tgaccagtgt c 41

<210> 1892
<211> 40
<212> DNA
<213> Homo sapiens

<400> 1892
agagaaccct tcattaacca gggcgtggct gaccagtgtc 40

<210> 1893
<211> 41
<212> DNA

<213> Homo sapiens

<400> 1893

taaagcacaa gttatcaccc rtggatggat ttgtcctttt c 41

<210> 1894

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1894

ttatctcccc ttgaaaggac rctccacaga gccagaaatt c 41

<210> 1895

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1895

cagagccaga aattctagaa sagggaaaag tggaggggag g 41

<210> 1896

<211> 41

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<213> Homo sapiens

<400> 1896

ctgtgaactg cagggacaga rggaaatggg tattgggaga a 41

<210> 1897

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<213> Homo sapiens

<400> 1897

tgaactgcag ggacagaagg maatgggtat tgggagaatg g 41

<210> 1898

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gacagaagga aatgggtatt rggagaatgg ccagccctcc a 41

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<400> 1899

tgggtattgg gagaatggcc rgccctccaa ggggctgatg t 41

<210> 1900

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<400> 1900

ggggacagcc ttcagctgtg raattcctcc agtcctagag a 41

<210> 1901

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<400> 1901

cattattcca gtcctgaggc rtgagagcag aaggccgatg c 41

<210> 1902

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<400> 1902

ccgatgcttc tgccctccat sctaatgtcc tcctgcaggg a 41

<210> 1903

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<400> 1903

ccatcctaat gtcctcctgc mgggacccaa ggtggatggc a 41

<210> 1904

<211> 41

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<400> 1904

ggtgagggta agcaggccac ytgggccagg gtggggtggg a 41

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<210> 1907

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<400> 1907

gttcgctgag gttggcggat ractttccgt agaaagggaa g 41

<210> 1908
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<400> 1908
tgtattcata tcgtcacgct sgtaaatgaa tgagtaagtg t　　41

<210> 1909
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<400> 1909
ggcattaggt caaaatcctg rtgggacaaa aggggaaact g　　41

<210> 1910
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tctgtagaaa gtacatgggg rcatgaagat cattggcttg a　　41

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<400> 1911

gattcccagg gaatgttaaa maggaccggg tcttcctaaa c　41

<210> 1912

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tctgacccag taccagccag sggggcaagt ttccatcccc c　41

<210> 1913

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1913

gttgccatct gagatcttgc yggaagtaca caagagaccc t　41

<210> 1914

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1914

ttccactggc cttttctgct yagtaattgc tacattacag g　41

<210> 1915

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1915

gaggaagctg cctcccggtg rggacaggaa gcgggcatgg c 41

<210> 1916

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1916

cccaggagtc caacctccct ktgtccagct agaccatggt g 41

<210> 1917

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<212> DNA

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<400> 1917

cctgggacat gttttcttat rtaaacagca tcaaaagatg t 41

<210> 1918

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<212> DNA

<213> Homo sapiens

<400> 1918

gcccgcccag gactcctcac stgtccaagt cacctaggga g 41

<210> 1919
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<220>
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<400> 1919
tccgaggatg tgtttttttt nccctccgtt agtcagcagt g 41

<210> 1920
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<400> 1920
tcctgctcat atgcggcacc rtcagacttc tgggcaggca a 41

<210> 1921
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<400> 1921

ggtattgatt aaaagcctca ygggcagaga aattcgccat c 41

<210> 1922
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<400> 1922
tgtgtattgt agaagtgatg rgaaatccag aacagaaagc t 41

<210> 1923
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<400> 1923
gccctctcat ttcccttcca rtgctgagcg tttccagtgt g 41

<210> 1924
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<400> 1924
gcctctgtcc acagactttc rtgggccacg tcagcttctt c 41

<210> 1925
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<400> 1925

accaagaatg aggccatccc ktccccacgt ggctgcccca t 41

<210> 1926

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<212> DNA

<213> Homo sapiens

<400> 1926

tgggttcaaa gatggaatgg kgcataactc agcaaaatta t 41

<210> 1927

<211> 41

<212> DNA

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<400> 1927

gggagggagg ctggacaggg satgaaggca gagcctggtg g 41

<210> 1928

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<212> DNA

<213> Homo sapiens

<400> 1928

ggaggtggga cccaggatgg ygtttcttgg gaccacaagg a 41

<210> 1929

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actcccccgg ccccactcac rtctgccacc ttccctccct g 41

<210> 1930

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<212> DNA

<213> Homo sapiens

<400> 1930

actcattcca agtattgatc ragaagagag gtaggtactg g 41

<210> 1931

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1931

ttgaagatct taagttgttt ytggttcact catttcgcaa a 41

<210> 1932

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<212> DNA

<213> Homo sapiens

<400> 1932

agctaaaagc aaaacagcct ytgacctggc aagcattccc a 41

<210> 1933

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1933

tgtcctactt ttcttttgac scttataact tcctgacttc g 41

<210> 1934

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1934

ccagctccta gtgggctgga rggaaggaca tgcggttggg g 41

<210> 1935

<211> 41

<212> DNA

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<400> 1935

ttgcaaactg agttagggcc yggagagctt actgtgtgct g 41

<210> 1936

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<400> 1936

tgcacttgcc gcctacttat kccagaccca atgattgggt c　　41

<210> 1937

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1937

tatagattaa tgaggctctg rgtccctcaa aaccttccct c　　41

<210> 1938

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<400> 1938

cccttacctc tccaaaaaac rcttgagata ccctagaggt g　　41

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<400> 1939

ctcaggatct tcctggagga yatggttcac tcccatgaga g　　41

<210> 1940
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<213> Homo sapiens

<400> 1940
actaagcaga tttctaccaa ytgcacctcc ccatcccctt g 41

<210> 1941
<211> 41
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<213> Homo sapiens

<400> 1941
gaacaagccc ctgagaatgc yttccgcacc ccctactccc g 41

<210> 1942
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1942
acaagcccct gagaatgcct yccgcacccc ctactcccgc c 41

<210> 1943
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1943

gcccttccat cgatcaccca yacccagcca tctcactccc c 41

<210> 1944

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1944

tctcactccc caggtgctta yctgcactcc agcctctcca t 41

<210> 1945

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1945

cataggggag agggcaggaa yggagggaag ggagagagcc c 41

<210> 1946

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1946

tagtatttaa cctgcccaaa ygctgtgtga agtgctgacc t 41

<210> 1947

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1947

tcccctccac aagcttagac raacaggatt ctcctgtgac t 41

<210> 1948

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1948

tttggtgaca gggcatcaac ytgtctggtg gtcaacgcca g 41

<210> 1949

<211> 41

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents c or deletion

<400> 1949

caaggatagc acaaatgacc nattgcagac ttcagatgga g 41

<210> 1950

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1950

gaaggtgggt atatccaggg rtggccaagc agccacccct g 41

<210> 1951

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1951

gttctgctag aacctgaact yataaaggtc ttcctgtcct t 41

<210> 1952

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1952

gtgagcgtct gcacatccaa staaagattg ttttctcctc c 41

<210> 1953

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1953

cgataagtgg gtgtaatttg yccatcccca cccatgagtt c 41

<210> 1954
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1954
cagctccctg ccctcccctc rctctctctc cctcagccag c 41

<210> 1955
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1955
gacagctgct gagtcaggcc ragccggcag ctgagaaagg c 41

<210> 1956
<211> 41
<212> DNA
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<400> 1956
cagctgagaa aggcggcagt sgtcagatgg gcttgagaaa c 41

<210> 1957
<211> 41
<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents aaaa or deletion

<400> 1957

cctccaaaaa ataaaaacaa ncagaaatga aggaaataga a 41

<210> 1958

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1958

tggggtaagc ggaagacggg rttgaacgct ttgagtttgg t 41

<210> 1959

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1959

ctcttaggga tcttgtctaa ktaaagaaga gcagagcaaa g 41

<210> 1960

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1960
cagatcccag cttcctgtaa rcagcctcag atcaggccaa a　　41

<210> 1961
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1961
gcgcctcaca ctcctataac rcgcacatgc cctgatgcac a　　41

<210> 1962
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1962
atgccctgat gcacacacat yttcaacacg cacttactct a　　41

<210> 1963
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1963
agacacgtca ccctcccaca ygtctccacc ctgggggtgt g　　41

<210> 1964

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1964

tcagtcccct cagacacatg mcctctctcc acgcagagac a 41

<210> 1965

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1965

gcggccaagg agagtgatga yggcagccca ggttgatcag a 41

<210> 1966

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1966

gctcctgggg ctccagcctt ygcagccctt gtgtgtgtct g 41

<210> 1967

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1967

ggcttcgcag tcacctcgtg kccctccagg gccgaggcct c 41

<210> 1968

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1968

agggacctgg gggcagacag ygaggccacc cttgtattga g 41

<210> 1969

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1969

cccagggaca ggactggcct sttgtggccg tcatcagtgc a 41

<210> 1970

<211> 41

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents c or deletion

<400> 1970

aggacattct ggccacatgc ntcatcctcc tcctccaagc c　　41

<210> 1971

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1971

tggcccccac cgcgggtggt rttcccacca tcctgacccg c　　41

<210> 1972

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1972

tgttgtttct ccttaaagag mtatttgttt ttccccccaa a　　41

<210> 1973

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1973

gctggccttc tggcttgcag wagttgtatt ttaagaatca g　　41

<210> 1974

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<212> DNA

<213> Homo sapiens

<400> 1974

tgcagaagtt gtattttaag ratcagagct cttgtgagga g　　41

<210> 1975

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<400> 1975

ttctgtggaa atcagaggct stctaaaata ttcctaattt t　　41

<210> 1976

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<212> DNA

<213> Homo sapiens

<400> 1976

tggacgcact caacattttc ragttattac tccttcaact c　　41

<210> 1977

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<212> DNA

<213> Homo sapiens

<400> 1977

aggatatcat gaaacactga mtcttagtaa aaactatctt t　　41

<210> 1978

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1978

tactgtggaa tttttcttgc macagagata tgtatttttc a 41

<210> 1979

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1979

cagtggtaga tgtgttttct rttgccatca tctacaaata t 41

<210> 1980

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<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents 7 to 9 repeats of t

<400> 1980

tgttcaaata ggctttttnt ncagagaatt gaatgctttc t 41

<210> 1981

<211> 41

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents a or deletion

<400> 1981

tcagtcgtat tcctactaaa ncaaaatttt gtaagttatg t 41

<210> 1982

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1982

ctttttattt gctgcttacc rttttactaa ggttggatat a 41

<210> 1983

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1983

cttttaataa atgcaaactg yacacctggt ctataaaaag a 41

<210> 1984
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1984
cctatagaat ttttcttttc kttttttctca aaaaaattaa a 41

<210> 1985
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1985
tttctttttt ctcaaaaaaa ytaaatgttt gttatttatt t 41

<210> 1986
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1986
ttctgtagat gaagcttaag wgctagatct tatttgaaaa a 41

<210> 1987
<211> 41
<212> DNA
<213> Homo sapiens

<400> 1987

tttttaactt attgtttgcc ktttcatttt ttaatagaaa a 41

<210> 1988

<211> 41

<212> DNA

<213> Homo sapiens

<400> 1988

cgaatttgct gcttttagag waatctttgc aaataataaa a 41

<210> 1989

<211> 41

<212> DNA

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<210> 1990

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<210> 1991

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<210> 1992

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<210> 1993

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<222> 21

<223> n represents taac or deletion

<400> 1993

caaaacagaa taatgaaaag ntattatcta aaataataaa a　　41

<210> 1994

<211> 41

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<213> Homo sapiens

<220>

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<222> 21

<223> n represents ctcttt

<400> 1994

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<210> 1995

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<212> DNA

<213> Homo sapiens

<220>

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<222> 21

<223> n represents ct

<400> 1995

aacatactct cctcctctct naagtcaaaa tatattagta t 41

<210> 1996

<211> 40

<212> DNA

<213> Homo sapiens

<400> 1996

aacatactct cctcctctct aagtcaaaat atattagtat 40

<210> 1997

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<213> Homo sapiens

<400> 1997

ttctgtgaaa gtgtcccaaa wtgtgccttt aaattgtttt t 41

<210> 1998

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<400> 1998

agtgtcacat gtatttttc yggtattcct atgtttatca a 41

<210> 1999

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<213> Homo sapiens

<400> 1999

ctcatttcaa acttggctat ytggactctc cccaggcatt g 41

<210> 2000

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<212> DNA

<213> Homo sapiens

<400> 2000

atcccctagt gatgtacact ragcttgcct ccatctttcc t 41

<210> 2001

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<400> 2001

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<210> 2002

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<220>

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<222> 21

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<400> 2002

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<210> 2004

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<400> 2004

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<210> 2005

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<212> DNA

<213> Homo sapiens

<220>

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<222> 21

<223> n represents t or deletion

<400> 2005

aatcctggtg ttttttttnt nctttttcat ttttcagtag g 41

<210> 2006

<211> 41

<212> DNA

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<400> 2006

aagtaactca aggaaagatg rtttaacttg tgaaatcgta a 41

<210> 2007

<211> 41

<212> DNA

<213> Homo sapiens

<400> 2007

ctcatagttc agaagagttc mgagcccaat tcagaagagt t 41

<210> 2008

<211> 41

<212> DNA

<213> Homo sapiens

<220>

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<222> 21

<223> n represents g or deletion

<400> 2008

tgaacctata aaattctaat nccatctttg gatgaggtgc a 41

<210> 2009

<211> 41

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<213> Homo sapiens

<400> 2009

ccagggacaa aagaagatga ygtaaactta aggattggga c 41

<210> 2010

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<400> 2010

agcaagccag gaagaaagtc sattaagttg tatttagaaa t 41

<210> 2011

<211> 41

<212> DNA

<213> Homo sapiens

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<222> 21

<223> n represents aattagaa or deletion

<400> 2011

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<210> 2012

<211> 41

<212> DNA

<213> Homo sapiens

<220>

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<222> 21

<223> n represents tttaaaa or ttttaa

<400> 2012

aactctttct cttcatctgc ngcaagcctt gaaggagagt g 41

<210> 2013

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<213> Homo sapiens

<400> 2013

gcatgcaaaa taatgaagaa racaatcttg tctgacattg a 41

<210> 2014

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<400> 2014

aaatatttca gaatttgggg rtgtagagca tttgccgtca t 41

<210> 2015

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<220>

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<222> 21

<223> n represents t or deletion

<400> 2015

cttgtaagtc ttttttttt naaagtaatg aaaatttcta a 41

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<211> 41

<212> DNA

<213> Homo sapiens

<400> 2016

agacaacact gctttttgt rtgttcacaa ttcaacgaca g 41

<210> 2017

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<400> 2017

aactggctga aaggaaaaaa wtcatattgc tgtaaatatt t 41

<210> 2018

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<400> 2018

tgcttttgct ttccacttca rtatccagaa aactctctca t 41

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<400> 2019

aacatggaac tatagtaaat rtagtttttt tggggttcag a 41

<210> 2020

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<222> 21

<223> n represents t or deletion

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aatttacact ttttttttt ngcaggagaa tattttgcaa a 41

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tatttcctta gccagcggta ycacagtgtg tttagtgaat t 41

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<400> 2023

tcacattgcc ttgacatcac mcctactgct cctccaccct a 41

<210> 2024

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<222> 21

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<210> 2025

<211> 41

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<220>

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<222> 21

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<400> 2026

tctgaagtca aatatgcggg kcacttttttg aaatccttgt t 41

<210> 2027

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<400> 2027

aagggaatcc ctgagctgag matgaccagc ccagtggttt c 41

<210> 2028

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<210> 2029

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tgcttccaag gaagttcatc kcagtattat ttgtaattag c 41

<210> 2030

<211> 41

<212> DNA

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<222> 21

<223> n represents aaa or deletion

<400> 2030

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<210> 2031

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<212> DNA

<213> Homo sapiens

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<222> 21

<223> n represents a or deletion

<400> 2031

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<213> Homo sapiens

<400> 2032

gagaatatgg gacacccctt kttcatcctc tcatccagca t 41

<210> 2033

<211> 41

<212> DNA

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<400> 2033

tccttcttgc atttatttttrgctggatgt ttttatgcct c 41

<210> 2034

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<400> 2034

aaccagctca atgggttagg raggacattg atcgtcatcc c 41

<210> 2035

<211> 41

<212> DNA

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gagtcaaggc agtcccctga ygggctgatc ctttgctctg g 41

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<210> 2038
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<400> 2039
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<210> 2040
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<210> 2041
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<400> 2041
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<210> 2042
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<400> 2043

tgtggtcctg aaggtcctgc tgacatctct gctccccacc 40

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gaggtgggca gagggtcagc ycactactgg attcctcagt c 41

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<210> 2046

<211> 41

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<400> 2046

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<210> 2047

<211> 41

<212> DNA

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<210> 2049

<211> 41

<212> DNA

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<400> 2049

cctccaaaat caacaatcca rttatcgcct gtctgctagt t 41

<210> 2050

<211> 41

<212> DNA

<213> Homo sapiens

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aggaactatc caaagagaaa yacattcata tacttcgcag g 41

<210> 2051

<211> 41

<212> DNA

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<210> 2059

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<210> 2062

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<400> 2062

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<210> 2063

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catttgggat gctaagatta maaattagca taacacttcc a 41

<210> 2064

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cattcacaaa agctctttct yctatggttg gctctgagtt t 41

<210> 2065

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caaatatttg gctctaattc ygcttccacc tcagacagct a 41

<210> 2066

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gcgcctctgg gcatctcact rtgcatgctt aggcgccttg c 41

<210> 2067

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gtgcatgctt aggcgccttg sggctctgtt gtttttcaga a 41

<210> 2068

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<400> 2068

aacggtgatg aaagaggcga ygtgagaagg aaggtggctt t　　41

<210> 2069
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<400> 2069
ttgcatggca cttactgacc rttgcacagg cctgcaacac c　　41

<210> 2070
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<400> 2070
atttctggat tctgttagta ygtagaaagc tctaaagcat g　　41

<210> 2071
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<400> 2071
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<210> 2072
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<210> 2073
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<400> 2073
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<210> 2074
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<220>
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<222> 21
<223> n represents a or deletion

<400> 2074

aatgctaaaa aaaaaaaaaa ntcactgtgg tactttgggg a 41

<210> 2075
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<400> 2075
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<210> 2076
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<400> 2076
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<210> 2081
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<210> 2082

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<210> 2084

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<210> 2086

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<210> 2087

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<400> 2087

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<210> 2088

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<222> 21

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<400> 2247

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<220>

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<222> 21

<223> n represents 16 to 18 repeats of a

<400> 2249

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<223> n represents g

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<400> 2251

ttcatgacag atcagatgtt cttttatgga tttacaaaga 40

<210> 2252

<211> 41

<212> DNA

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<220>

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<222> 21

<223> n represents c or deletion

<400> 2252

tttccttctt caaacccccc nagactagga gaaggtctgt c 41

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<222> 21

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<400> 2256
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<222> 21

<223> n represents 11 to 13 repeats of gt

<400> 2258

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<210> 2259

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<222> 21

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<400> 2259

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<210> 2261

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<220>

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<222> 21

<223> n represents 9 to 11 repeats of t

<400> 2262

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<222> 21

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<400> 2265

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<211> 41

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<222> 21

<223> n represents 7 to 9 repeats of a

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<220>

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<222> 21

<223> n represents 9 to 11 repeats of t

<400> 2267

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taaaaccgtc ttgtttgttt nttacatggt ttttagggcc c 41

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<220>

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<210> 2301

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<220>

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<222> 21

<223> n represents 22 to 26 repeats of t

<400> 2348

cgtgaactac cacgtcctgc naagagatgg agtctcactc t 41

<210> 2349

<211> 41

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents 8 to 10 repeats of g

<400> 2349

ggggactctg agggtctggt nactctgagg gtctgggggc c 41

<210> 2350

<211> 41

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents 6 to 7 repeats of c

<400> 2350

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<210> 2351

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<212> DNA

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<222> 21

<223> n represents 12 to 14 repeats of a

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<400> 2428

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<211> 41

<212> DNA

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<400> 2464

tatgcagtta catggacaga yacaacattg gagaccgagg g 41

<210> 2465

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<212> DNA

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<220>

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<222> 21

<223> n represents tcac or deletion

<400> 2474

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<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents t or deletion

<400> 2475

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<210> 2476

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<212> DNA

<213> Homo sapiens

<220>
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<222> 21
<223> n represents 9 to 11 repeats of t

<400> 2476
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<220>
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<222> 21
<223> n represents 7 to 8 repeats of a

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<400> 2491

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<210> 2495

<211> 41

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<220>

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<222> 21

<223> n represents 13 to 16 repeats of t

<400> 2495

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<210> 2496

<211> 41

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents 9 to 10 repeats of t

<400> 2496

tacatttgtc aaaatttata ngcagataat catttcatct c 41

<210> 2497

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<220>

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<222> 21

<223> n represents 14 to 16 repeats of t

<400> 2497

taaattcaca tgattctgta naggatcctc ctgactggca g 41

<210> 2498

<211> 41

<212> DNA

<213> Homo sapiens

<220>

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<222> 21

<223> n represents 13 to 17 repeats of t

<400> 2498

tctttcaaac ttatatttgc ncatagtttc atgtttgatg a 41

<210> 2499

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<212> DNA

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<220>

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<222> 21

<223> n represents t

<400> 2499

ttgctctgtt tcaaatctct nattcatggg ccagcagctc g 41

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<212> DNA

<213> Homo sapiens

<400> 2500

ttgctctgtt tcaaatctct attcatgggc cagcagctcg 40

<210> 2501

<211> 41

<212> DNA

<213> Homo sapiens

<220>

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<222> 21

<223> n represents 8 to 9 repeats of a

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<211> 41

<212> DNA

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<220>

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<222> 21

<223> n represents 8 to 9 repeats of t

<400> 2502

ttccaatttt ccattgttac ncttgccaga ttactcctga a 41

<210> 2503

<211> 41

<212> DNA

<213> Homo sapiens

<220>
<221> modified base
<222> 21
<223> n represents gcagtattactgtagt or deletion

<400> 2503
tcctctgcat tttggcttct natttgtcat tttcaaatta a 41

<210> 2504
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<220>
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<222> 21
<223> n represents 13 to 14 repeats of t

<400> 2504
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<220>

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<222> 21

<223> n represents 9 to 10 repeats of t

<400> 2505

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<211> 41

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<220>

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<222> 21

<223> n represents 10 to 11 repeats of t

<400> 2506

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<400> 2507

taaatggaga aaataacacc racctgatag cattgttgtg a 41

<210> 2508

<211> 40

<212> DNA

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<400> 2508

aaactcccca agcatgctca ctagatcctt accctaggtc　　40

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<210> 2514
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<400> 2514
gcgctgccac agatcaggcc raggtggggg acagaaatgc c 41

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cccagaattc tgaatacagc rgcgatgacg ggactacgag g 41

<210> 2516

<211> 40

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aacagatcca caggaccaga agcaaagggg aggaacatgc 40

<210> 2517

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<400> 2518

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<210> 2523

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<400> 2523

ataactggta caggtttact sgtgtctaca ctggcagaga a 41

<210> 2524

<211> 41

<212> DNA

<213> Homo sapiens

<220>

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<222> 21

<223> n represents t or deletion

<400> 2524

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<212> DNA

<213> Homo sapiens

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<222> 21

<223> n represents 12 to 15 repeats of t

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<212> DNA

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<210> 2528

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<400> 2528

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<210> 2529

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<400> 2529

ggatgagcac tgcccagctg rtccctgccc accttccaca g　41

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<210> 2531

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<212> DNA

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<210> 2534

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gtctgaagag gccccgagaa yagaaatcta gaacctgcca g　41

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<210> 2561

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<210> 2568

<211> 41

<212> DNA

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<210> 2569

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<212> DNA

<213> Homo sapiens

<400> 2569

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ggccctgcta atgtggacag yagactttat ccctccttct t 41

<210> 2574

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<210> 2575

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<400> 2575

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ttccaaggct acagacatgg ygccatcctc acaggcctag c 41

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tacgagacac cccttcacrg catacactgc catggtatg 39

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agacaggagt gttgggccag yggtcagggg gcctggggat g 41

<210> 2585

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<212> DNA

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<210> 2586

<211> 41

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<222> 21

<223> n represents a or deletion

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<210> 2587

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<213> Homo sapiens

<220>

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<222> 21

<223> n represents at or deletion

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<213> Homo sapiens

<400> 2588

ctgggtggag tggggtggca yggagttgaa gacccagtcc t 41

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tgtgccggcc ccagccctga scatgcatcc ctttggggac c 41

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accacccttc tgcgtagcac rgagggtggg tggcatcaag g 41

<210> 2591

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<212> DNA

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<400> 2591

tgtaggctga ggtcagcccc atccagtcca aagcccaccc 40

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<210> 2593

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<400> 2593

gatctggggc ggagggtaca yggggctggc gctgggtgaa g 41

<210> 2594

<211> 41

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents t or deletion

<400> 2594

tggtgtaaat ttttttttt ngcttcaaaa atatagtatt t 41

<210> 2595

<211> 41

<212> DNA

<213> Homo sapiens

<220>

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<222> 21

<223> n represents ttc or deletion

<400> 2595

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ggaaatgctg gctaaataaa nggtatcaaa ctaactctga a 41

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tcgttggatg gtagtattgt ktgaacaaca gaagaaattc a 41

<210> 2598

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<400> 2598

ccaaatgcat gccagcagag ygtggcagga aggtacacaa g　41

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<210> 2603

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caacttctgc catcttattg ratctgtact tacctagtaa t 41

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<210> 2611
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ctactgaaac gggataaatg yagcttgatg attttcagct g 41

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<210> 2650
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<400> 2650
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<210> 2651
<211> 41
<212> DNA
<213> Homo sapiens

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<223> n represents 9 to 11 repeats of c

<400> 2651

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<213> Homo sapiens

<220>
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<222> 21
<223> n represents 15 to 21 repeats of a

<400> 2652
ctgtatccat tggaaggcac ntgcaaagga aacaaggcaa a 41

<210> 2653
<211> 41
<212> DNA
<213> Homo sapiens

<220>
<221> modified base
<222> 21
<223> n represents ggggtggcggggtggg or deletion

<400> 2653
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<210> 2654

<211> 41

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents t or deletion

<400> 2654

ctcactggaa ctttttttt naatttaatt tttaaaattt t 41

<210> 2655

<211> 41

<212> DNA

<213> Homo sapiens

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<222> 21

<223> n represents a

<400> 2655

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<210> 2656

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<212> DNA

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<400> 2656
cacttccatt ctgactgtta cggtgtgatt cttcctgcca 40

<210> 2657
<211> 41
<212> DNA
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<220>
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<222> 21
<223> n represents a or deletion

<400> 2657
gcgcgtgctg tttctccctt ntctgtcctt gtacacgtgt g 41

<210> 2658
<211> 41
<212> DNA
<213> Homo sapiens

<220>
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<222> 21
<223> n represents 10 to 12 repeats of t

<400> 2658
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<210> 2659

<211> 41

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents tt

<400> 2659

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<210> 2660

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<212> DNA

<213> Homo sapiens

<400> 2660

aattccccca ttgcttctct ctgtagacat tttaaaccta　　40

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<220>

<221> modified base

<222> 21

<223> n represents tccctccttgaagctgatcgt or deletion

<400> 2661

ccctccttga agctgatcgt ngtccaagat agttgctagg a 41

<210> 2662

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<212> DNA

<213> Homo sapiens

<220>

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<222> 21

<223> n represents 12 to 18 repeats of ca

<400> 2662

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<210> 2663

<211> 41

<212> DNA

<213> Homo sapiens

<400> 2663

ttaataaatg tttattcaat kaaaccaact gctaatattc t 41

<210> 2664

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<400> 2664

cctggagatt ttaactttct rcgaagtttt taaaaacaac t　　41

<210> 2665

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ggagaagggg accgcatgca ragggtggca ggcagggagg g　　41

<210> 2666

<211> 41

<212> DNA

<213> Homo sapiens

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ccccttggga cggttctcac ytgtgcccca cttccccagt c　　41

<210> 2667

<211> 41

<212> DNA

<213> Homo sapiens

<400> 2667

gcccgcaagc attgctgtat rgcacccagg cctccagtga g　　41

<210> 2668
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<400> 2668
cgagtaaaat ttttctaccg stttgtttta gagtggtgtc t 41

<210> 2669
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<400> 2669
aaaaaatttg tagatatggg kactccctat gttgcccagg c 41

<210> 2670
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<400> 2671

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<210> 2672

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<212> DNA

<213> Homo sapiens

<400> 2672

tccagcatct tccctttcca yttttaagtt agacttttt t 41

<210> 2673

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<210> 2674

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<400> 2674

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<212> DNA

<213> Homo sapiens

<400> 2675

ggtttatagt gttccccccc wccccgcccc caaaagaccc a 41

<210> 2676

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<400> 2676

gaagctgccg ctccaggaag sagtctgtcg ttggagaaga g 41

<210> 2677

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<400> 2677

ggaaagctgg ggaactgttt kcctggaaca gagtctcaaa a 41

<210> 2678

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<212> DNA

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<400> 2678

tgtcaactgc gtaacacagg ygtagaagtg gacattgttt t　41

<210> 2679
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<400> 2679
tttaatagaa aatggtattc ytgtcttttc tttcccatct c　41

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<400> 2680
gggtaaaccc attttgaata ytagcattgc caatatcctg t　41

<210> 2681
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<400> 2681
tatttgcttt ccttctctct ytgttttctt tttctctgaa a　41

<210> 2682
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<213> Homo sapiens

<400> 2682
cagcacgttt ttcctatgaa yaagacattc tccaaataac t 41

<210> 2683
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tggctctgtg tgcatgaaca ygcacgcgtg cacgcgcaca c 41

<210> 2684
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<212> DNA
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<400> 2684
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<210> 2685
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<222> 21
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<400> 2686
ccccttcaat actagaacaa ngcagacaca ttaaatgtta c 41

<210> 2687
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<400> 2687
ccccttcaat actagaacaa gcagacacat taaatgttac 40

<210> 2688
<211> 41
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<213> Homo sapiens

<220>
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<222> 21
<223> n represents t or deletion

<400> 2688
actatttcaa ttttttttt nggaggggga gacagagtct c 41

<210> 2689
<211> 41
<212> DNA
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<220>
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<222> 21
<223> n represents 9 to 13 repeats of t

<400> 2689
cccagcatta taagaatgac naagtgcaga tgtggggagg g 41

<210> 2690
<211> 41
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<220>

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<222> 21

<223> n represents aa or deletion

<400> 2690

tagcatttgg caaaggagaa ntgccaagaa gtatcttcga a 41

<210> 2691

<211> 41

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents ttgaca or gtccaatat

<400> 2691

agaaaactgg atgtctgaaa ncactgcact tgtatgtgtt g 41

<210> 2692

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<213> Homo sapiens

<220>

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<222> 21

<223> n represents cta or deletion

<400> 2692

ggattttaga ttcctcccta nttctttccg accttccacc c 41

<210> 2693

<211> 41

<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> 21

<223> n represents 9 to 10 repeats of t

<400> 2693

tttccatttt taagttagac ncacctctct cgttacttca g 41

<210> 2694

<211> 41

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<213> Homo sapiens

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<222> 21

<223> n represents gagatgttgtggctcacat

<400> 2694

tcctcttcat gtctctatgt nagtcatcct ctttgtgaga c 41

<210> 2695
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<400> 2695
tcctcttcat gtctctatgt agtcatcctc tttgtgagac　　40

<210> 2696
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<220>
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<222> 21
<223> n represents cc or deletion

<400> 2696
acacacacac acacacacac ntgctctgga gttgggcaac t　　41

<210> 2697
<211> 41
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<220>
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<222> 21

<223> n represents act or deletion

<400> 2697

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<210> 2698

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ataacatctt ctgcagagaa cttcaatgga aatacactca 40

<210> 2700

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<210> 2702

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aaattattca atctctttgg rcagtggttt ctttttcttt g 41

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<211> 41

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<210> 2710

<211> 41

<212> DNA

<213> Homo sapiens

<400> 2710

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<210> 2711

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<400> 2714
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<210> 2715
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<210> 2716
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<400> 2718
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<210> 2719

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<210> 2722

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<210> 2723

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acaaatcagc catgttttac ratagcagac attatgccat t　　41

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<210> 2734

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attttattag atataactgg atgctaacaa ttttaaaagc 40

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<210> 2739

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<400> 2739

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<210> 2741
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<222> 21

<223> n represents atattcacttggtatctg or deletion

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<222> 21
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<400> 3004
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<220>

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<222> 21

<223> n represents 4 to 5 repeats of at

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<212> DNA

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<222> 21

<223> n represents 7 to 8 repeats of t

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<210> 3010

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<212> DNA

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<222> 21

<223> n represents 19 to 23 repeats of t

<400> 3010

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<210> 3011

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<212> DNA

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<222> 21

<223> n represents t or deletion

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<222> 21

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<400> 3012

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<212> DNA

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<220>

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<222> 21

<223> n represents 8 to 10 repeats of t

<400> 3013

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<222> 21

<223> n represents a or deletion

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<210> 3018

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gaaccagatg cccccagcct ygactcagtc ccagtctcca c 41

<210> 3021

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<222> 21

<223> n represents 13 to 15 repeats of a

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<210> 3022

<211> 41

<212> DNA

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<220>

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<222> 21

<223> n represents 12 to 15 repeats of t

<400> 3022

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<400> 3023

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<210> 3024

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cacatccatc attcgagaca mactcgtctc agctgccatg a 41

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actagactgc tagtgtcctc yggtgagccc agtcccatag g 41

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<210> 3038

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<400> 3043
tacatttggt ccccaggggg agcggctgat caggagagaa 40

<210> 3044
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<400> 3044

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<400> 3045
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<222> 21
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<400> 3046
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<210> 3047
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<220>

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<222> 21

<223> n represents 11 to 13 repeats of t

<400> 3047

ttttgaactg aagaacttac nataacgaac gttgacatct t 41

<210> 3048

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<400> 3048

gcatgcagct tagaagtttt rttttatgag ggtctctaac c 41

<210> 3049

<211> 41

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<220>

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<222> 21

<223> n represents a or deletion

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<210> 3050

<211> 41

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<400> 3050

tcagctcttt agtgagactt staaattttc taagacaagc a 41

<210> 3051

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<222> 21

<223> n represents 9 to 11 repeats of t

<400> 3051

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<213> Homo sapiens

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<210> 3053

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<212> DNA

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ttgggaccca catagagtca ytacttaaaa taaatgacca g 41

<210> 3054

<211> 41

<212> DNA

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<222> 21

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<211> 41

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<400> 3055

gacttttata attttgtata rctgatatta taggaataca c 41

<210> 3056

<211> 41

<212> DNA

<213> Homo sapiens

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<222> 21

<223> n represents t or deletion

<400> 3056

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<210> 3057

<211> 41

<212> DNA

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<400> 3057

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<210> 3058

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<400> 3058

ccttccaaac ctttacttaa sattgtctgt tttggtcata a 41

<210> 3059

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<212> DNA

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<400> 3059

cataaattgt cagtcaaact rcatgttaat agaggacttc a 41

<210> 3060

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<212> DNA

<213> Homo sapiens

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<222> 21

<223> n represents t or deletion

<400> 3060

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<212> DNA

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<210> 3062

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aactccaggt tgcaaataga ygtttctggt attttaagta g　　41

<210> 3063

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<400> 3064

agataaattg atgaattatt yactctgtgc tgctgataga t　　41

<210> 3065

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<213> Homo sapiens

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<222> 21

<223> n represents aaga

<400> 3065

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<210> 3066

<211> 40

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<400> 3066

taaaaagaat ttctaaaaga ccttttttt gaataactct 40

<210> 3067

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<400> 3067

ctgaaataga aacctttcag wgtaccttgc agagcagtga a 41

<210> 3068

<211> 41

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<213> Homo sapiens

<400> 3068

cagtgtcata aagatccagc rgaaatcaaa atgtttcata t 41

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<222> 21
<223> n represents aaaa or deletion

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<210> 3070
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<210> 3071
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<400> 3071

ttggttcaaa gccttcttca rccttaggat atgcattgag g 41

<210> 3072
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gtttgagaca ttaacttcta rttcaactga agatgctagt t 41

<210> 3073
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<222> 21
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<400> 3073
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<210> 3074
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<210> 3075
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<400> 3075
taatacaaat catttgaagc rtttactatt aaaaaaacaa a　41

<210> 3076
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<400> 3076
ctttgagcac ctactgcatt wtaagtgctg ttaagatgtg g　41

<210> 3077
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<400> 3077
ttaatcacct caatctttaa ygaatttctt gatttttctt t　41

<210> 3078
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<210> 3079

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<210> 3080

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<222> 21

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tcactccatt ttttaactgt scttcctaaa tgtgtggtta a 41

<210> 3084
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gaataaaagg atagggacat kggtaagacc acttttccc t 41

<210> 3086

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gcctctcaat tttctcatgt ktaatagaga gaaaaccctg c 41

<210> 3087

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<400> 3087

gactgactgg ttcataagtt sagaaatttc actgtggtgc t 41

<210> 3088

<211> 41

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<210> 3090

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<210> 3103

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<213> Homo sapiens

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<400> 3103

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<210> 3104

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<210> 3106

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<400> 3106

tctgatttta tcactgttta yagattgctt agtcatactc a 41

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<400> 3112
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<210> 3113
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<223> n represents gga

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<211> 40

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<211> 41

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<220>

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<223> n represents c

<400> 3310

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<210> 3311

<211> 40

<212> DNA

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<222> 21

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<222> 21

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<213> Homo sapiens

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【００８１】

【配列表フリーテキスト】

配列番号39：nはtを表す（存在位置21）。

配列番号64：nはcを表す（存在位置21）。

配列番号580：nはa又は欠失を表す（存在位置21）。

配列番号634：nはa又は欠失を表す（存在位置21）。

配列番号656：nはa又は欠失を表す（存在位置21）。

配列番号658：nはc又は欠失を表す（存在位置21）。

配列番号671：nはa又は欠失を表す（存在位置21）。

配列番号672：nはg又は欠失を表す（存在位置21）。

配列番号673：nはc又は欠失を表す（存在位置21）。

配列番号674：nは(cctgy)χを表す（存在位置21）。

配列番号676：nはgaa又は欠失を表す（存在位置21）。

配列番号677：nはag又は欠失を表す（存在位置21）。

配列番号785：nはtaを表す（存在位置21）。

配列番号797：nはacacを表す（存在位置21）。

配列番号806：nはgatttgtggtatccagを表す（存在位置21）。

配列番号808：nはag又は欠失を表す（存在位置21）。

配列番号809：nはta又は欠失を表す（存在位置21）。

配列番号815：nはtを表す（存在位置21）。

配列番号828：nはcagaggctを表す（存在位置21）。

配列番号830：nはca又は欠失を表す（存在位置21）。

配列番号831：nはag又は欠失を表す（存在位置21）。

配列番号843：nはgtaaaを表す（存在位置21）。

配列番号845：nはaを表す（存在位置21）。

配列番号888：nはtcを表す（存在位置21）。

配列番号890：nはt又は欠失を表す（存在位置21）。

配列番号913：nはt又は欠失を表す（存在位置21）。

配列番号932：nはt又は欠失を表す（存在位置21）。

配列番号933：nはt又は欠失を表す（存在位置21）。

配列番号955：nはat又は欠失を表す（存在位置21）。

配列番号956：nはa又は欠失を表す（存在位置21）。

配列番号957：nはc又は欠失を表す（存在位置21）。

配列番号987：nはcを表す（存在位置21）。

配列番号999：nはgtt又は欠失を表す（存在位置21）。

配列番号1164：nはatを表す（存在位置21）。

配列番号1166：nはc又は欠失を表す（存在位置21）。

配列番号1167：nはt又は欠失を表す（存在位置21）。

配列番号1168：nはt又は欠失を表す（存在位置21）。

配列番号1169：nはgを表す（存在位置21）。

配列番号1171：nはcを表す（存在位置21）。

配列番号1173：nはtを表す（存在位置21）。

配列番号1175：nはc又は欠失を表す（存在位置21）。

配列番号1200：nはa又は欠失を表す（存在位置21）。

配列番号1204：nはaを表す（存在位置21）。

配列番号1207：nはttを表す（存在位置21）。

配列番号1210：nはatを表す（存在位置21）。

配列番号1245：nはtを表す（存在位置21）。

配列番号1248：nはt又は欠失を表す（存在位置21）。

配列番号1249：nはtを表す（存在位置21）。

配列番号1251：nはa又は欠失を表す（存在位置21）。

配列番号1252：nはtgt又は欠失を表す（存在位置21）。

配列番号1260：nはt又は欠失を表す（存在位置21）。

配列番号1309：nはa又は欠失を表す（存在位置21）。

配列番号1389：nはg又は欠失を表す（存在位置21）。

配列番号1411：nはa又は欠失を表す（存在位置21）。

配列番号1417：nはaaagを表す（存在位置21）。

配列番号1424：nはgtg又は欠失を表す（存在位置21）。

配列番号1426：nはgg又はtggtggggtggaを表す（存在位置21）。

配列番号1429：nはat又は欠失を表す（存在位置21）。

配列番号1436：nはaを表す（存在位置21）。

配列番号1453：nはc又は欠失を表す（存在位置21）。

配列番号1456：nはggを表す（存在位置21）。

配列番号1465：nはgtc又は欠失を表す（存在位置21）。

配列番号1487：nはt又は欠失を表す（存在位置21）。

配列番号1494：nはttを表す（存在位置21）。

配列番号1497：nはtの９～12回の繰り返しを表す（存在位置21）。

配列番号1499：nはa又は欠失を表す（存在位置21）。

配列番号1501：nはaの10～13回の繰り返しを表す（存在位置21）。

配列番号1504：nはct又は欠失を表す（存在位置21）。

配列番号1507：nはcagatcttcttcagctaatttagaaatgtを表す（存在位置21）。

配列番号1533：nはa又は欠失を表す（存在位置21）。

配列番号1540：nはcを表す（存在位置21）。

配列番号1545：nはtを表す（存在位置21）。

配列番号1552：nはtの9～12回の繰り返しを表す（存在位置21）。

配列番号1555：nはtを表す（存在位置21）。

配列番号1557：nはaaaaaaagaaaaを表す（存在位置21）。

配列番号1558：nはaaaaaaaaaaaaを表す（存在位置21）。

配列番号1559：nはaaaaaaaaaaを表す（存在位置21）。

配列番号1563：nはt又は欠失を表す（存在位置21）。

配列番号1572：nはcを表す（存在位置21）。

配列番号1574：nはa又は欠失を表す（存在位置21）。

配列番号1575：nはc又は欠失を表す（存在位置21）。

配列番号1596：nはcct又は欠失を表す（存在位置21）。

配列番号1598：nはtcを表す（存在位置21）。

配列番号1616：nはca又は欠失を表す（存在位置21）。

配列番号1638：nはgを表す（存在位置21）。

配列番号1661：nはt又は欠失を表す（存在位置21）。

配列番号1690：nはgccagを表す（存在位置21）。

配列番号1718：nはtを表す（存在位置21）。

配列番号1723：nはc又は欠失を表す（存在位置21）。

配列番号1729：nはtc又は欠失を表す（存在位置21）。

配列番号1740：nはct又は欠失を表す（存在位置21）。

配列番号1771：nはaを表す（存在位置21）。

配列番号1781：nはa又は欠失を表す（存在位置21）。

配列番号1787：nはt又は欠失を表す（存在位置21）。

配列番号1791：nはt又は欠失を表す（存在位置21）。

配列番号1792：nはg又は欠失を表す（存在位置21）。

配列番号1800：nはt又は欠失を表す（存在位置21）。

配列番号1801：nはt又は欠失を表す（存在位置21）。

配列番号1802：nはa又は欠失を表す（存在位置21）。

配列番号1815：nはa又は欠失を表す（存在位置21）。

配列番号1819：nはca又は欠失を表す（存在位置21）。

配列番号1820：nはt又は欠失を表す（存在位置21）。

配列番号1824：nはt又は欠失を表す（存在位置21）。

配列番号1829：nはt又は欠失を表す（存在位置21）。

配列番号1830：nはc又は欠失を表す（存在位置21）。

配列番号1838：nはa又は欠失を表す（存在位置21）。

配列番号1840：nはt又は欠失を表す（存在位置21）。

配列番号1847：nはgatt又は欠失を表す（存在位置21）。

配列番号1848：nはtを表す（存在位置21）。

配列番号1853：nはt又は欠失を表す（存在位置21）。

配列番号1854：nはgtを表す（存在位置21）。

配列番号1857：nはa又は欠失を表す（存在位置21）。

配列番号1858：nはa又は欠失を表す（存在位置21）。

配列番号1862：nはt又は欠失を表す（存在位置21）。

配列番号1865：nはat又は欠失を表す（存在位置21）。

配列番号1871：nはa又は欠失を表す（存在位置21）。

配列番号1874：nはt又は欠失を表す（存在位置21）。

配列番号1877：nはat又は欠失を表す（存在位置21）。

配列番号1878：nはa又は欠失を表す（存在位置21）。

配列番号1879：nはtの12～14の繰り返しを表す（存在位置21）。

配列番号1882：nはt又は欠失を表す（存在位置21）。

配列番号1884：nはcac又は欠失を表す（存在位置21）。

配列番号1891：nはccaを表す（存在位置21）。

配列番号1919：nはt又は欠失を表す（存在位置21）。

配列番号1949：nはc又は欠失を表す（存在位置21）。

配列番号1957：nはaaaa又は欠失を表す（存在位置21）。

配列番号1970：nはc又は欠失を表す（存在位置21）。

配列番号1980：nはtの7～9の繰り返しを表す（存在位置21）。

配列番号1981：nはa又は欠失を表す（存在位置21）。

配列番号1993：nはtaac又は欠失を表す（存在位置21）。

配列番号1994：nはctctttを表す（存在位置21）。

配列番号1995：nはctを表す（存在位置21）。

配列番号2002：nはa又は欠失を表す（存在位置21）。

配列番号2005：nはt又は欠失を表す（存在位置21）。

配列番号2008：nはg又は欠失を表す（存在位置21）。

配列番号2011：nはaattagaa又は欠失を表す（存在位置21）。

配列番号2012：nはtttaaaa又はttttaaを表す（存在位置21）。

配列番号2015：nはt又は欠失を表す（存在位置21）。

配列番号2020：nはt又は欠失を表す（存在位置21）。

配列番号2024：nはg又は欠失を表す（存在位置21）。

配列番号2025：nはt又は欠失を表す（存在位置21）。

配列番号2030：nはaaa又は欠失を表す（存在位置21）。

配列番号2031：nはa又は欠失を表す（存在位置21）。

配列番号2042：nはcを表す（存在位置21）。

配列番号2072：nはa又は欠失を表す（存在位置21）。

配列番号2074：nはa又は欠失を表す（存在位置21）。

配列番号2243：nはtcaの14～16の繰り返しを表す（存在位置21）。

配列番号2244：nはaの8～10の繰り返しを表す（存在位置21）。

配列番号2245：nはcacagtcat又は欠失を表す（存在位置21）。

配列番号2246：nはtt又は欠失を表す（存在位置21）。

配列番号2247：nはaの10～12の繰り返しを表す（存在位置21）。

配列番号2248：nはc又は欠失を表す（存在位置21）。

配列番号2249：nはaの16～18の繰り返しを表す（存在位置21）。

配列番号2250：nはgを表す（存在位置21）。

配列番号2252：nはc又は欠失を表す（存在位置21）。

配列番号2253：nはt又は欠失を表す（存在位置21）。

配列番号2254：nはa又は欠失を表す（存在位置21）。

配列番号2255：nはtgを表す（存在位置21）。

配列番号2257：nはtの10～13の繰り返しを表す（存在位置21）。

配列番号2258：nはgtの11～13の繰り返しを表す（存在位置21）。

配列番号2259：nはa又は欠失を表す（存在位置21）。

配列番号2260：nはg又は欠失を表す（存在位置21）。

配列番号2261：nはg又は欠失を表す（存在位置21）。

配列番号2262：nはtの9～11の繰り返しを表す（存在位置21）。

配列番号2263：nはgを表す（存在位置21）。

配列番号2265：nはtt又は欠失を表す（存在位置21）。

配列番号2266：nはaの7～9の繰り返しを表す（存在位置21）。

配列番号2267：nはtの9～11の繰り返しを表す（存在位置21）。

配列番号2268：nはaの9～10の繰り返しを表す（存在位置21）。

配列番号2269：nはgt又は欠失を表す（存在位置21）。

配列番号2270：nはa又は欠失を表す（存在位置21）。

配列番号2271：nはtを表す（存在位置21）。

配列番号2273：nはa又は欠失を表す（存在位置21）。

配列番号2274：nはct又は欠失を表す（存在位置21）。

配列番号2275：nはg又は欠失を表す（存在位置21）。

配列番号2276：nはa又は欠失を表す（存在位置21）。

配列番号2277：nはa又は欠失を表す（存在位置21）。

配列番号2278：nはa又は欠失を表す（存在位置21）。

配列番号2279：nはc又は欠失を表す（存在位置21）。

配列番号2280：nはaaag又は欠失を表す（存在位置21）。

配列番号2348：nはtの22～26の繰り返しを表す（存在位置21）。

配列番号2349：nはgの8～10の繰り返しを表す（存在位置21）。

配列番号2350：nはcの6～7の繰り返しを表す（存在位置21）。

配列番号2351：nはaの12～14の繰り返しを表す（存在位置21）。

配列番号2427：nはcaccaggcagcagactctgatgaggaggggaggggを表す（存在位置21）。

配列番号2429：nはgを表す（存在位置21）。

配列番号2474：nはtcac又は欠失を表す（存在位置21）。

配列番号2475：nはt又は欠失を表す（存在位置21）。

配列番号2476：nはtの9～11の繰り返しを表す（存在位置21）。

配列番号2477：nはaの7～8の繰り返しを表す（存在位置21）。

配列番号2495：nはtの13～16の繰り返しを表す（存在位置21）。

配列番号2496：nはtの9～10の繰り返しを表す（存在位置21）。

配列番号2497：nはtの14～16の繰り返しを表す（存在位置21）。

配列番号2498：nはtの13～17の繰り返しを表す（存在位置21）。

配列番号2499：nはtを表す（存在位置21）。

配列番号2501：nはaの8～9の繰り返しを表す（存在位置21）。

配列番号2502：nはtの8～9の繰り返しを表す（存在位置21）。

配列番号2503：nはgcagtattactgtagt又は欠失を表す（存在位置21）。

配列番号2504：nはtの13～14の繰り返しを表す（存在位置21）。

配列番号2505：nはtの9～10の繰り返しを表す（存在位置21）。

配列番号2506：nはtの10～11の繰り返しを表す（存在位置21）。

配列番号2524：nはt又は欠失を表す（存在位置21）。

配列番号2525：nはtの12～15の繰り返しを表す（存在位置21）。

配列番号2586：nはa又は欠失を表す（存在位置21）。

配列番号2587：nはat又は欠失を表す（存在位置21）。

配列番号2594：nはt又は欠失を表す（存在位置21）。

配列番号2595：nはttc又は欠失を表す（存在位置21）。

配列番号2606：nはcttを表す（存在位置21）。

配列番号2651：nはcの9～11の繰り返しを表す（存在位置21）。

配列番号2652：nはaの15～21の繰り返しを表す（存在位置21）。

配列番号2653：nはggggtggcggggtggg又は欠失を表す（存在位置21）。

配列番号2654：nはt又は欠失を表す（存在位置21）。

配列番号2655：nはaを表す（存在位置21）。

配列番号2657：nはa又は欠失を表す（存在位置21）。

配列番号2658：nはtの10～12の繰り返しを表す（存在位置21）。

配列番号2659：nはttを表す（存在位置21）。

配列番号2661：nはtccctccttgaagctgatcgt又は欠失を表す（存在位置21）。

配列番号2662：nはcaの12～18の繰り返しを表す（存在位置21）。

配列番号2685：nはaの18～20の繰り返しを表す（存在位置21）。

配列番号2686：nはaaを表す（存在位置21）。

配列番号2688：nはt又は欠失を表す（存在位置21）。

配列番号2689：nはtの9～13の繰り返しを表す（存在位置21）。

配列番号2690：nはaa又は欠失を表す（存在位置21）。

配列番号2691：nはttgaca又はgtccaatatを表す（存在位置21）

配列番号2692：nはcta又は欠失を表す（存在位置21）。

配列番号2693：nはtの9～10の繰り返しを表す（存在位置21）。

配列番号2694：nはgagatgttgtggctcacatを表す（存在位置21）。

配列番号2696：nはcc又は欠失を表す（存在位置21）。

配列番号2697：nはact又は欠失を表す（存在位置21）。

配列番号2755：nはtat又は欠失を表す（存在位置21）。

配列番号2756：nはacの14～17の繰り返しを表す（存在位置21）。

配列番号2757：nはaの16～27の繰り返しを表す（存在位置21）。

配列番号2758：nはt又は欠失を表す（存在位置21）。

配列番号2759：nはaの8～10の繰り返しを表す（存在位置21）。

配列番号2760：nはgtの9～11の繰り返しを表す（存在位置21）。

配列番号2761：nはaa又は欠失を表す（存在位置21）。

配列番号2762：nはt又は欠失を表す（存在位置21）。

配列番号2763：nはacの8～12の繰り返しを表す（存在位置21）。

配列番号2764：nはa又は欠失を表す（存在位置21）。

配列番号2810：nはaを表す（存在位置21）。

配列番号2812：nはaa又は欠失を表す（存在位置21）。

配列番号2813：nはca又は欠失を表す（存在位置21）。

配列番号2814：nはt又は欠失を表す（存在位置21）。

配列番号2815：nはtgtgtg又は欠失を表す（存在位置21）。

配列番号2912：nはaを表す（存在位置21）。

配列番号2914：nはgを表す（存在位置21）。

配列番号2916：nはactt又は欠失を表す（存在位置21）。

配列番号2917：nはttta又は欠失を表す（存在位置21）。

配列番号2918：nはaの11～13の繰り返しを表す（存在位置21）。

配列番号2919：nはtの8～10の繰り返しを表す（存在位置21）。

配列番号2920：nはaの12～14の繰り返しを表す（存在位置21）。

配列番号2921：nはcttgta又は欠失を表す（存在位置21）。

配列番号2922：nはaの9～10の繰り返しを表す（存在位置21）。

配列番号2923：nはctt又は欠失を表す（存在位置21）。

配列番号2924：nはcttを表す（存在位置21）。

配列番号2926：nはa又は欠失を表す（存在位置21）。

配列番号2927：nはaの9～11の繰り返しを表す（存在位置21）。

配列番号2928：nはtgt又は欠失を表す（存在位置21）。

配列番号2929：nはaの24～27の繰り返しを表す（存在位置21）。

配列番号2930：nはtaの10～21の繰り返しを表す（存在位置21）。

配列番号2931：nはaの8～10の繰り返しを表す（存在位置21）。

配列番号2932：nはaの11～13の繰り返しを表す（存在位置21）。

配列番号2933：nはaの8～10の繰り返しを表す（存在位置21）。

配列番号2999：nはtatc又は欠失を表す（存在位置21）。

配列番号3000：nはatattcacttggtatctg又は欠失を表す（存在位置21）。

配列番号3001：nはttta又は欠失を表す（存在位置21）。

配列番号3002：nはtを表す（存在位置21）。

配列番号3004：nはg又は欠失を表す（存在位置21）。

配列番号3005：nはa又は欠失を表す（存在位置21）。

配列番号3006：nはaの9～11の繰り返しを表す（存在位置21）。

配列番号3007：nはg又は欠失を表す（存在位置21）。

配列番号3008：nはatの4～5の繰り返しを表す（存在位置21）。

配列番号3009：nはtの7～8の繰り返しを表す（存在位置21）。

配列番号3010：nはtの19～23の繰り返しを表す（存在位置21）。

配列番号3011：nはt又は欠失を表す（存在位置21）。

配列番号3012：nはtgat又は欠失を表す（存在位置21）。

配列番号3013：nはtの8～10の繰り返しを表す（存在位置21）。

配列番号3014：nはa又は欠失を表す（存在位置21）。

配列番号3021：nはaの13～15の繰り返しを表す（存在位置21）。

配列番号3022：nはtの12～15の繰り返しを表す（存在位置21）。

配列番号3042：nはgを表す（存在位置21）。

配列番号3044：nはa又は欠失を表す（存在位置21）。

配列番号3046：nはg又は欠失を表す（存在位置21）。

配列番号3047：nはtの11～13の繰り返しを表す（存在位置21）。

配列番号3049：nはa又は欠失を表す（存在位置21）。

配列番号3051：nはtの9～11の繰り返しを表す（存在位置21）

配列番号3054：nはt又は欠失を表す（存在位置21）。

配列番号3056：nはt又は欠失を表す（存在位置21）。

配列番号3060：nはt又は欠失を表す（存在位置21）。

配列番号3065：nはaagaを表す（存在位置21）。

配列番号3069：nはaaaa又は欠失を表す（存在位置21）。

配列番号3073：nはtの9～11の繰り返しを表す（存在位置21）。

配列番号3081：nはa又は欠失を表す（存在位置21）。

配列番号3103：nはtの11～13の繰り返しを表す（存在位置21）。

配列番号3119：nはactaを表す（存在位置21）。

配列番号3125：nはgtg又は欠失を表す（存在位置21）。

配列番号3130：nはtの11～12の繰り返しを表す（存在位置21）。

配列番号3140：nはtta又は欠失を表す（存在位置21）。

配列番号3154：nはgを表す（存在位置21）。

配列番号3156：nはaを表す（存在位置21）。

配列番号3158：nはcct又は欠失を表す（存在位置21）。

配列番号3169：nはggaを表す（存在位置21）。

配列番号3179：nはtの12～14の繰り返しを表す（存在位置21）。

配列番号3184：nはtの16～17の繰り返しを表す（存在位置21）。

配列番号3196：nはgを表す（存在位置21）。

配列番号3273：nはagを表す（存在位置21）。

配列番号3306：nはgを表す（存在位置21）。

配列番号3310：nはcを表す（存在位置21）。

配列番号3315：nはct又は欠失を表す（存在位置21）。

配列番号3317：nはgc又は欠失を表す（存在位置21）。

配列番号3352：nはtの9～11の繰り返しを表す（存在位置21）。

配列番号3355：nはaを表す（存在位置21）。

配列番号3358：nはt又は欠失を表す（存在位置21）。

【図面の簡単な説明】

【図１】

TaqMan プローブを示す図である。

【図２】

TaqMan PCR法の概要を示す図である。

【図３】

蛍光色素を付したプローブを示す図である。

【図４】

インベーダー法の概要を示す図である。

【図５】

フレットプローブを示す図である。

【図６】

インベーダー法の概要を示す図である。

【図７】

アレルとマッチしないプローブを示す図である。

【図８】

ライゲーション反応によるアレルの識別の概要を示す図である。

【図９】

ATP結合カセットサブファミリーBメンバー２（ABCB2）遺伝子の構造とSNPの存在位置を示す図である。

【図１０】

ATP結合カセットサブファミリーBメンバー４（ABCB4）遺伝子の構造とSNPの存在位置を示す図である。

【図１１】

ミクロソームエポキシドハイドロラーゼ1(EPHX1)遺伝子の構造とSNPの存在位置を示す図である。

【図１２】

細胞質エポキシドハイドロラーゼ（EPHX2)遺伝子の構造とSNPの存在位置を示す図である。

【図１３】

グアニジノアセテートN-メチルトランスフェラーゼ(GAMT）遺伝子の構造とSNPの存在位置を示す図である。

【図１４】

ニコチンアミドN-メチルトランスフェラーゼ(NNMT）遺伝子の構造とSNPの存在位置を示す図である。

【図１５】

フェニルエタノールアミンN-メチルトランスフェラーゼ(PNMT）遺伝子の構造とSNPの存在位置を示す図である。

【図１６】

ホスファチジルエタノールアミンN-メチルトランスフェラーゼ(PEMT）遺伝子の構造とSNPの存在位置を示す図である。

【図１７】

グルタチオン-S-トランスフェラーゼ3(GSTM3）遺伝子の構造とSNPの存在位置

を示す図である。

【図１８】

アルデヒドデヒドロゲナーゼ5(ALDH5)遺伝子の構造とSNPの存在位置を示す図である。

【図１９】

トランスグルタミナーゼ1(TGM1）遺伝子の構造とSNPの存在位置を示す図である。

【図２０】

ガンマ-グルタミルトランスフェラーゼ1(GGT1）遺伝子の構造とSNPの存在位置を示す図である。

【図２１】

NAD(P)H: キノンオキシドレダクターゼ1(NQO1）遺伝子の構造とSNPの存在位置を示す図である。

【図２２】

キノンオキシドレダクターゼ相同体のp53誘導遺伝子3（PIG3）の構造とSNPの存在位置を示す図である。

【図２３】

NRH: キノンオキシドレダクターゼ2(NQO2）遺伝子の構造とSNPの存在位置を示す図である。

【図２４】

スルホトランスフェラーゼ1A1(SULT1A1/STP1）遺伝子の構造とSNPの存在位置を示す図である。

【図２５】

スルホトランスフェラーゼ1A2(SULT1A2/STP2）遺伝子の構造とSNPの存在位置を示す図である。

【図２６】

スルホトランスフェラーゼ-関連タンパク質3(SULTX3）遺伝子の構造とSNPの存在位置を示す図である。

【図２７】

チロシルタンパク質スルホトランスフェラーゼ1(TPST1) 遺伝子の構造とSNPの存在位置を示す図である。

【図２８】

チロシルタンパク質スルホトランスフェラーゼ2(TPST2) 遺伝子の構造とSNPの存在位置を示す図である。

【図２９】

スルホトランスフェラーゼ1A3(SULT1A3/STM/HAST) 遺伝子の構造とSNPの存在位置を示す図である。

【図３０】

セレブロシドスルホトランスフェラーゼ(CST) 遺伝子の構造とSNPの存在位置を示す図である。

【図３１】

スルホトランスフェラーゼ1C1(SULT1C1) 遺伝子の構造とSNPの存在位置を示す図である。

【図３２】

スルホトランスフェラーゼ1C2(SULT1C2) 遺伝子の構造とSNPの存在位置を示す図である。

【図３３】

甲状腺ホルモンスルホトランスフェラーゼ(ST1B2) 遺伝子の構造とSNPの存在位置を示す図である。

【図３４】

炭水化物スルホトランスフェラーゼ2(CHST2) 遺伝子の構造とSNPの存在位置を示す図である。

【図３５】

スルホトランスフェラーゼ2A1(SULT2A1) 遺伝子の構造とSNPの存在位置を示す図である。

【図３６】

スルホトランスフェラーゼ2B1(SULT2B1) 遺伝子の構造とSNPの存在位置を示す図である。

【図３７】

炭水化物スルホトランスフェラーゼ4(CHST4) 遺伝子の構造とSNPの存在位置を示す図である。

【図３８】

炭水化物スルホトランスフェラーゼ5(CHST5) 遺伝子の構造とSNPの存在位置を示す図である。

【図３９】

HNK-スルホトランスフェラーゼ(NHK-1ST) 遺伝子の構造とSNPの存在位置を示す図である。

【図４０】

エストロゲンスルホトランスフェラーゼ(STE) 遺伝子の構造とSNPの存在位置を示す図である。

【図４１】

アルコールデヒドロゲナーゼ1(ADH1) 遺伝子の構造とSNPの存在位置を示す図である。

【図４２】

アルコールデヒドロゲナーゼ2(ADH2) 遺伝子の構造とSNPの存在位置を示す図である。

【図４３】

アルコールデヒドロゲナーゼ3(ADH3) 遺伝子の構造とSNPの存在位置を示す図である。

【図４４】

アルコールデヒドロゲナーゼ6(ADH6) 遺伝子の構造とSNPの存在位置を示す図である。

【図４５】

アルコールデヒドロゲナーゼ7(ADH7) 遺伝子の構造とSNPの存在位置を示す図である。

【図４６】

短鎖アルコールデヒドロゲナーゼファミリー遺伝子(HEP27)の構造とSNPの存在

位置を示す図である。

【図４７】

L1 細胞接着分子(L1CAM) 遺伝子の構造とSNPの存在位置を示す図である。

【図４８】

アリールアルキルアミン N-アセチルトランスフェラーゼ(AANAT) 遺伝子の構造とSNPの存在位置を示す図である。

【図４９】

サッカロミセス・セレビシエ(Saccharomyces cerevisiae)のN-アセチルトランスフェラーゼ相同体(ARD1) 遺伝子の構造とSNPの存在位置を示す図である。

【図５０】

N-アセチルトランスフェラーゼ(NAT1) 遺伝子の構造とSNPの存在位置を示す図である。

【図５１】

N-アセチルトランスフェラーゼ2(NAT2) 遺伝子の構造とSNPの存在位置を示す図である。

【図５２】

グランザイムA(GZMA)遺伝子の構造とSNPの存在位置を示す図である。

【図５３】

グランザイムB(GZMB)遺伝子の構造とSNPの存在位置を示す図である。

【図５４】

エステラーゼD/ホルミルグルタチオンハイドロラーゼ(ESD) 遺伝子の構造とSNPの存在位置を示す図である。

【図５５】

ドリシル-ジホスホオリゴサッカライド-タンパク質グリコシルトランスフェラーゼ(DDOST) 遺伝子の構造とSNPの存在位置を示す図である。

【図５６】

ミクロソームグルタチオン-S-トランスフェラーゼ(MGST1) 遺伝子の構造とSNPの存在位置を示す図である。

【図５７】

アルコールデヒドロゲナーゼ５(ADH5) 遺伝子の構造とSNPの存在位置を示す図である。

【図５８】

グルタチオンＳトランスフェラーゼＭ１(GSTM1) 遺伝子の構造とSNPの存在位置を示す図である。

【図５９】

グルタチオンＳトランスフェラーゼＭ２(GSTM２) 遺伝子の構造とSNPの存在位置を示す図である。

【図６０】

グルタチオンＳトランスフェラーゼＭ４(GSTM4) 遺伝子の構造とSNPの存在位置を示す図である。

【図６１】

グルタチオンＳトランスフェラーゼＺ１(GSTZ1) 遺伝子の構造とSNPの存在位置を示す図である。

【図６２】

グルタチオンＳトランスフェラーゼＰｉ(GSTZPi) 遺伝子の構造とSNPの存在位置を示す図である。

【図６３】

グルタチオンＳトランスフェラーゼＴ１(GSTT1) 遺伝子の構造とSNPの存在位置を示す図である。

【図６４】

ミクロソームのグルタチオンＳトランスフェラーゼ１like１(MGST1L1) 遺伝子の構造とSNPの存在位置を示す図である。

【図６５】

ミクロソームのグルタチオンＳトランスフェラーゼＴ２(MGST2) 遺伝子の構造とSNPの存在位置を示す図である。

【図６６】

ミクロソームのグルタチオンＳトランスフェラーゼＴ３(MGST3) 遺伝子の構造とSNPの存在位置を示す図である。

【図６７】

グルタチオンＳトランスフェラーゼＡ１(GSTA1）遺伝子の構造とSNPの存在位置を示す図である。

【図６８】

グルタチオンＳトランスフェラーゼＡ４(GSTA4）遺伝子の構造とSNPの存在位置を示す図である。

【図６９】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼ１αサブコンプレックス１(NDUFA1）遺伝子の構造とSNPの存在位置を示す図である。

【図７０】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼ１αサブコンプレックス２(NDUFA2）遺伝子の構造とSNPの存在位置を示す図である。

【図７１】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼ１αサブコンプレックス３(NDUFA3）遺伝子の構造とSNPの存在位置を示す図である。

【図７２】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼ１αサブコンプレックス５(NDUFA5）遺伝子の構造とSNPの存在位置を示す図である。

【図７３】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼ１αサブコンプレックス６(NDUFA6）遺伝子の構造とSNPの存在位置を示す図である。

【図７４】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼ１αサブコンプレックス７(NDUFA7）遺伝子の構造とSNPの存在位置を示す図である。

【図７５】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼ１αサブコンプレックス８(NDUFA8）遺伝子の構造とSNPの存在位置を示す図である。

【図７６】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼ１α/βサブコンプレックス１(

NDUFAB1）遺伝子の構造とSNPの存在位置を示す図である。

【図７７】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼ１αサブコンプレックス９（NDUFA9）遺伝子の構造とSNPの存在位置を示す図である。

【図７８】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼＦｅ－Ｓタンパク質１（NDUFS1）遺伝子の構造とSNPの存在位置を示す図である。

【図７９】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼＦｅ－Ｓタンパク質３（NDUFS3）遺伝子の構造とSNPの存在位置を示す図である。

【図８０】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼＦｅ－Ｓタンパク質４（NDUFS4）遺伝子の構造とSNPの存在位置を示す図である。

【図８１】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼＦｅ－Ｓタンパク質５（NDUFS5）遺伝子の構造とSNPの存在位置を示す図である。

【図８２】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼＦｅ－Ｓタンパク質６（NDUFS6）遺伝子の構造とSNPの存在位置を示す図である。

【図８３】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼＦｅ－Ｓタンパク質８（NDUFS8）遺伝子の構造とSNPの存在位置を示す図である。

【図８４】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼ１βサブコンプレックス３（NDUFB3）遺伝子の構造とSNPの存在位置を示す図である。

【図８５】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼ１βサブコンプレックス５（NDUFB5）遺伝子の構造とSNPの存在位置を示す図である。

【図８６】

ＮＡＤＨ－ユビキノン　オキシドリダクターゼ１βサブコンプレックス７(NDUFB7) 遺伝子の構造とSNPの存在位置を示す図である。

【図８７】

ＡＴＰ結合カセット　サブファミリーＡメンバー１(ABCA1) 遺伝子の構造とSNPの存在位置を示す図である。

【図８８】

カテコール-O-メチルトランスフェラーゼ(COMT) 遺伝子の構造とSNPの存在位置を示す図である。

【図８９】

ヒスタミン N-メチルトランスフェラーゼ(HNMT) 遺伝子の構造とSNPの存在位置を示す図である。

【図９０】

チトクロームＰ４５０サブファミリー１（アロマティック化合物誘発性）ポリペプチド１(CYP1A1) 遺伝子の構造とSNPの存在位置を示す図である。

【図９１】

チトクロームＰ４５０サブファミリー１（アロマティック化合物誘発性）ポリペプチド２ (CYP1A2) 遺伝子の構造とSNPの存在位置を示す図である。

【図９２】

チトクロームＰ４５０サブファミリー１（ジオキシン誘発性）ポリペプチド１(CYP1B1) 遺伝子の構造とSNPの存在位置を示す図である。

【図９３】

アリルアセタミド デアセチラーゼ(AADAC) 遺伝子の構造とSNPの存在位置を示す図である。

【図９４】

ニューロパチーターゲットエステラーゼ(NTE) 遺伝子の構造とSNPの存在位置を示す図である。

【図９５】

ＡＴＰ結合カセット　サブファミリーＣ(CFTR/MRP)メンバー２(MRP2) 遺伝子の構造とSNPの存在位置を示す図である。

【図９６】

ＡＴＰ結合カセット　サブファミリーBメンバー１(ABCB1) 遺伝子の構造とSNPの存在位置を示す図である。

【図９７】

ＡＴＰ結合カセット　サブファミリーBメンバー３(ABCB3) 遺伝子の構造とSNPの存在位置を示す図である。

【図９８】

ＡＴＰ結合カセット　サブファミリーBメンバー7(ABCB7) 遺伝子の構造とSNPの存在位置を示す図である。

【図９９】

ＡＴＰ結合カセット　サブファミリーBメンバー８(ABCB8) 遺伝子の構造とSNPの存在位置を示す図である。

【図１００】

ＡＴＰ結合カセット　サブファミリーBメンバー９(ABCB9) 遺伝子の構造とSNPの存在位置を示す図である。

【図１０１】

ＡＴＰ結合カセット　サブファミリーBメンバー１０(ABCB10) 遺伝子の構造とSNPの存在位置を示す図である。

【図１０２】

ＡＴＰ結合カセット　サブファミリーBメンバー１１(ABCB11) 遺伝子の構造とSNPの存在位置を示す図である。

【図１０３】

チトクロームＰ４５０サブファミリーIVB　ポリペプチド１ (CYP4B1) 遺伝子の構造とSNPの存在位置を示す図である。

【図１０４】

チトクロームＰ４５０サブファミリーXXVIIA　ポリペプチド１ (CYP27A1) 遺伝子の構造とSNPの存在位置を示す図である。

【図１０５】

チトクロームＰ４５０サブファミリーIVF　ポリペプチド２(CYP4F2) 遺伝子の

構造とSNPの存在位置を示す図である。

【図１０６】

チトクロームＰ４５０サブファミリー4F　ポリペプチド３（CYP4F3）遺伝子の構造とSNPの存在位置を示す図である。

【図１０７】

チトクロームＰ４５０サブファミリー4F　ポリペプチド８（CYP4F8）遺伝子の構造とSNPの存在位置を示す図である。

【図１０８】

アルデヒドデヒドロゲナーゼ１(ALDH1)遺伝子の構造とSNPの存在位置を示す図である。

【図１０９】

アルデヒドデヒドロゲナーゼ２(ALDH2)遺伝子の構造とSNPの存在位置を示す図である。

【図１１０】

アルデヒドデヒドロゲナーゼ７(ALDH7)遺伝子の構造とSNPの存在位置を示す図である。

【図１１１】

アルデヒドデヒドロゲナーゼ８(ALDH8)遺伝子の構造とSNPの存在位置を示す図である。

【図１１２】

アルデヒドデヒドロゲナーゼ９(ALDH9)遺伝子の構造とSNPの存在位置を示す図である。

【図１１３】

アルデヒドデヒドロゲナーゼ１０(ALDH10)遺伝子の構造とSNPの存在位置を示す図である。

【図１１４】

ＡＴＰ結合カセット　サブファミリーCメンバー７(ABCC7)遺伝子の構造とSNPの存在位置を示す図である。

【図１１５】

ＡＴＰ結合カセット　サブファミリーCメンバー８(ABCC8) 遺伝子の構造とSNPの存在位置を示す図である。

【図１１６】

ＡＴＰ結合カセット　サブファミリーCメンバー９(ABCC9) 遺伝子の構造とSNPの存在位置を示す図である。

【図１１７】

カルボキシルエステラーゼ１(CES1) 遺伝子の構造とSNPの存在位置を示す図である

【図１１８】

ＡＴＰ結合カセット　サブファミリーAメンバー４(ABCA4) 遺伝子の構造とSNPの存在位置を示す図である。

【図１１９】

ＡＴＰ結合カセット　サブファミリーAメンバー７(ABCA7) 遺伝子の構造とSNPの存在位置を示す図である。

【図１２０】

ＡＴＰ結合カセット　サブファミリーGメンバー１(ABCG1) 遺伝子の構造とSNPの存在位置を示す図である。

【図１２１】

ＡＴＰ結合カセット　サブファミリーGメンバー２(ABCG2) 遺伝子の構造とSNPの存在位置を示す図である。

【図１２２】

ＡＴＰ結合カセット　サブファミリーGメンバー４(ABCG4) 遺伝子の構造とSNPの存在位置を示す図である。

【図１２３】

ＡＴＰ結合カセット　サブファミリーEメンバー１(ABCE1) 遺伝子の構造とSNPの存在位置を示す図である。

【図１２４】

カルボハイドレート　スルホトランスフェラーゼ１(CHST1) 遺伝子の構造とSNPの存在位置を示す図である。

【図１２５】

カルボハイドレート　スルホトランスフェラーゼ３(CHST3) 遺伝子の構造とSNPの存在位置を示す図である。

【図１２６】

ＮＡＤＨ：ユビキノン デハイドロゲナーゼフラボプロテイン１(NDUFV1) 遺伝子の構造とSNPの存在位置を示す図である。

【図１２７】

ＮＡＤＨ：ユビキノン オキシドレダクターゼ フラボプロテイン２(NDUFV2) 遺伝子の構造とSNPの存在位置を示す図である。

【図１２８】

ＮＡＤＨ：ユビキノン オキシドレダクターゼ フラボプロテイン３(NDUFV3) 遺伝子の構造とSNPの存在位置を示す図である。

【図１２９】

ＮＡＤＨ：ユビキノン オキシドレダクターゼ A10 (NDUFA10) 遺伝子の構造とSNPの存在位置を示す図である。

【図１３０】

high-mobility group protein 17-like 1 (HMG17L1) 遺伝子の構造とSNPの存在位置を示す図である。

【図１３１】

UDPグリコシルトランスフェラーゼ２ファミリー　ポリペプチドA1(UGT2A1) 遺伝子の構造とSNPの存在位置を示す図である。

【図１３２】

ヒト オーガニック　アニオン　トランスポーター　ポリペプチド１(hOATP1) 遺伝子の構造とSNPの存在位置を示す図である。

【図１３３】

ヒト オーガニック　アニオン　トランスポーター　ポリペプチド２(hOATP2) 遺伝子の構造とSNPの存在位置を示す図である。

【図１３４】

ヒト オーガニック　アニオン　トランスポーター　ポリペプチド８(hOATP8)

遺伝子の構造とSNPの存在位置を示す図である。

【図１３５】

ヒト オーガニック　アニオン　トランスポーター１(hOAT1) 遺伝子の構造とSNPの存在位置を示す図である。

【図１３６】

ヒト オーガニック　アニオン　トランスポーター２(hOAT2) 遺伝子の構造とSNPの存在位置を示す図である。

【図１３７】

ヒト オーガニック　アニオン　トランスポーター３(hOAT3) 遺伝子の構造とSNPの存在位置を示す図である。

【図１３８】

アルデヒド　デヒドロゲナーゼ１ファミリー　メンバーA2(ALDH1A2) 遺伝子の構造とSNPの存在位置を示す図である。

【図１３９】

アルデヒド　デヒドロゲナーゼ１ファミリー　メンバーA3(ALDH1A3) 遺伝子の構造とSNPの存在位置を示す図である。

【図１４０】

フォルミルテトラヒドロフォレート　デヒドロゲナーゼ(FTHFD/ALDH1L1) 遺伝子の構造とSNPの存在位置を示す図である。

【図１４１】

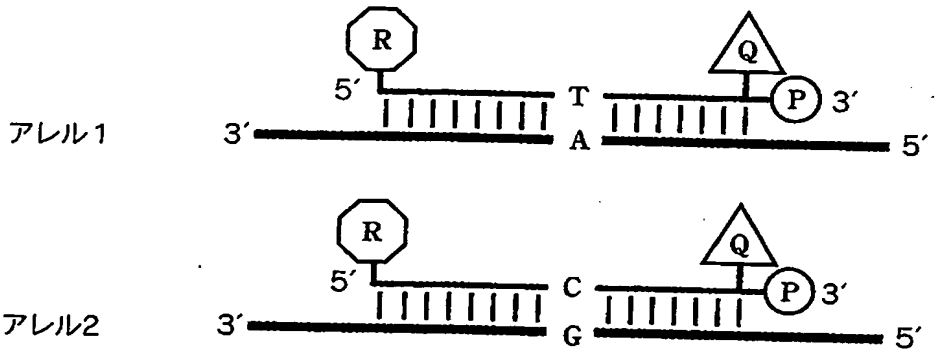
チトクロームＰ４５０サブファミリーIIIA（アロマティック化合物誘発性）ポリペプチド４(CYP3A4) 遺伝子の構造とSNPの存在位置を示す図である。

【図１４２】

異なる２グループの被験者についてインベーダー法によりタイピングを行った結果を示す図である。

【書類名】図面

【図１】



【図２】

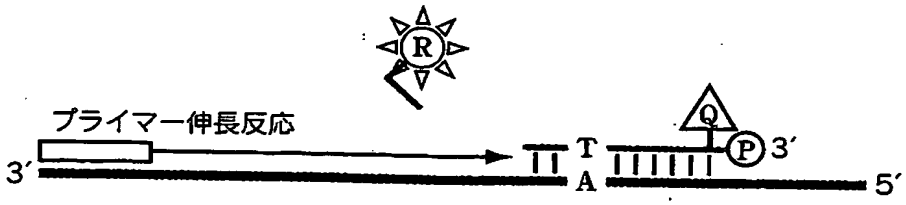
a. ハイブリダイゼーション



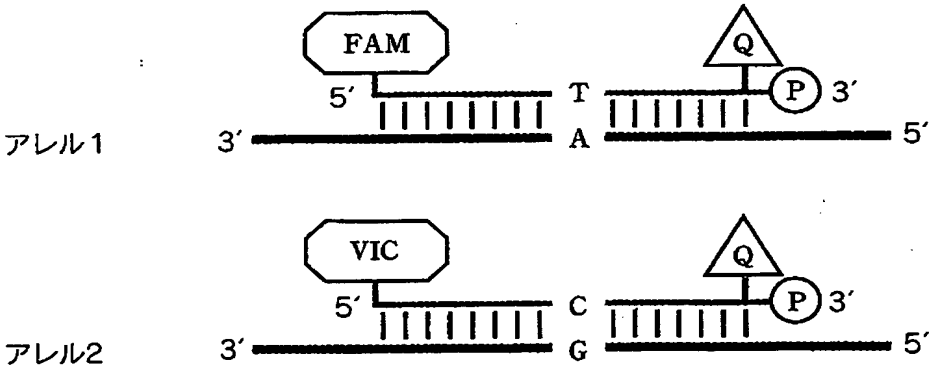
b. PCR反応



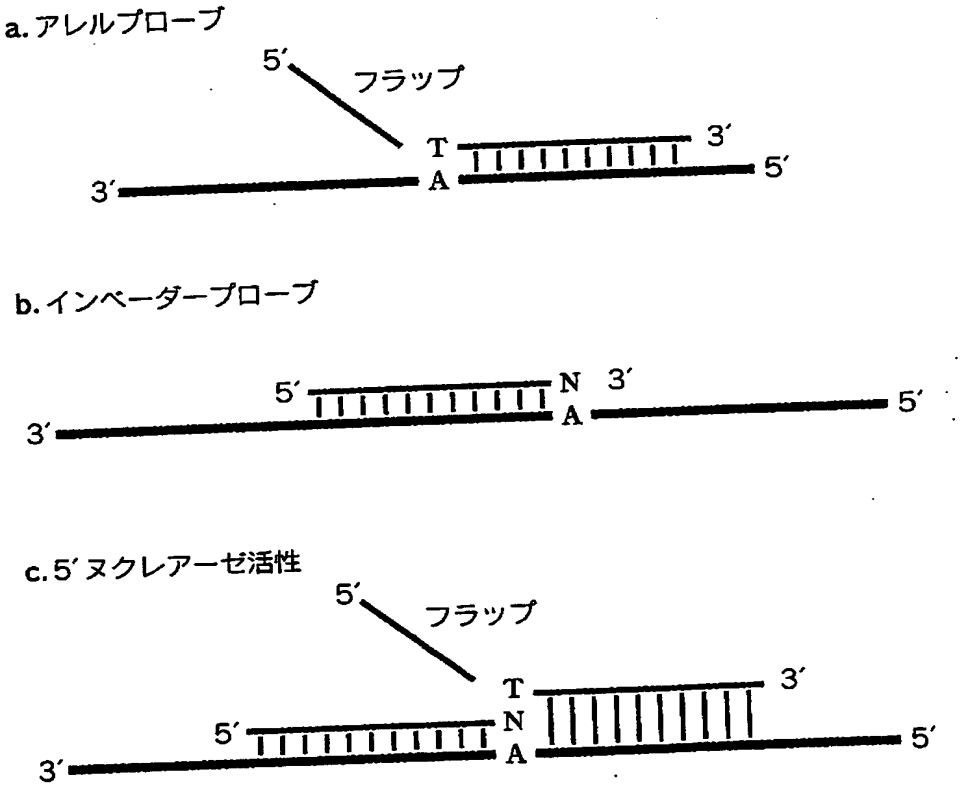
c. 5′ヌクレアーゼ活性



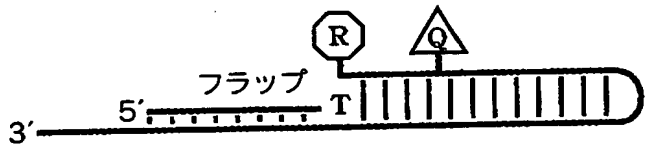
【図３】


アレル１
FAM
5′
T
A
3′
Q
P
3′
5′
アレル2
VIC
5′
C
G
3′
Q
P
3′
5′

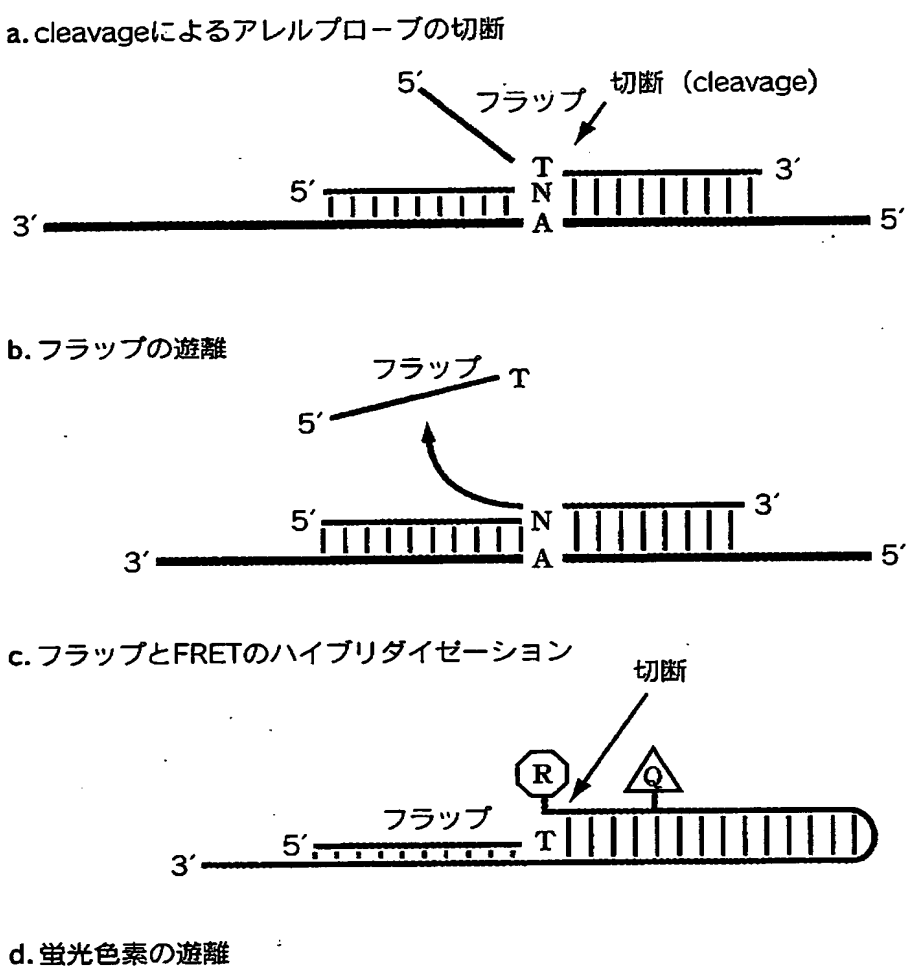
【図４】


a.アレルプローブ
5′
フラップ
T
A
3′
3′
5′
b.インベーダープローブ
5′
N
A
3′
3′
5′
c.5′ヌクレアーゼ活性
5′
フラップ
T
N
A
5′
3′
3′
5′

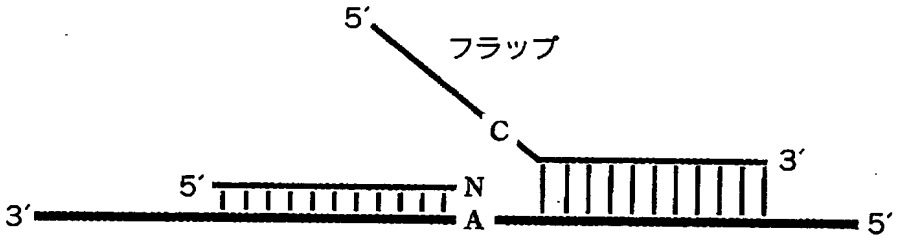
【図５】


R
Q
フラップ
5′
T
3′

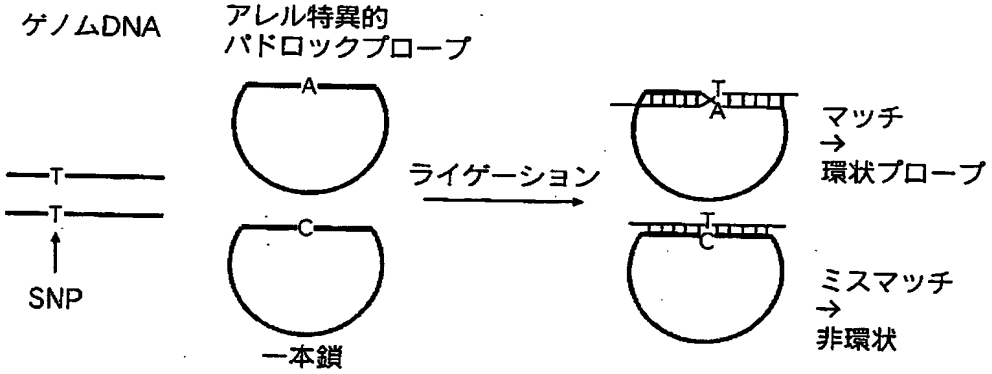
【図６】


a. cleavageによるアレルプローブの切断
5′
フラップ
切断（cleavage）
T
N
A
3′
5′
3′
5′
b. フラップの遊離
フラップ
T
5′
3′
5′
3′
5′
c. フラップとFRETのハイブリダイゼーション
切断
R
Q
フラップ
5′
T
3′
d. 蛍光色素の遊離
R
Q
フラップ
5′
T
3′

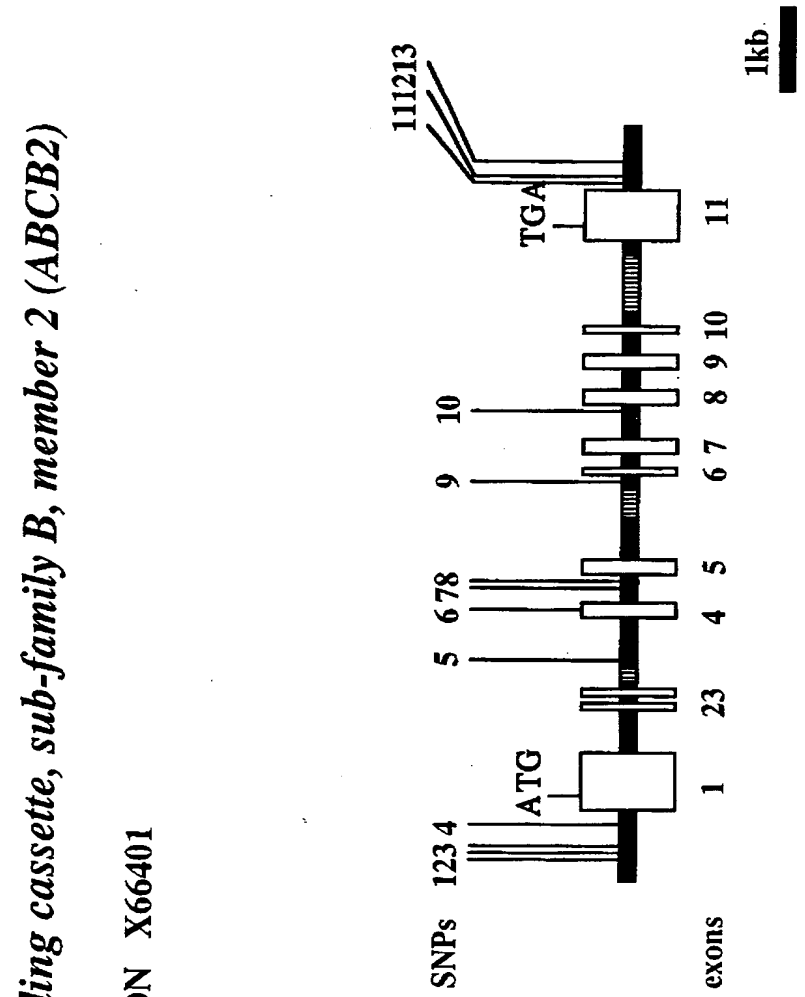
【図７】


5′
フラップ
C
3′
5′
N
A
3′
5′

【図８】


ゲノムDNA
アレル特異的
パドロックプローブ
A
T
T
SNP
C
一本鎖
ライゲーション
T
A
マッチ
→
環状プローブ
T
C
ミスマッチ
→
非環状

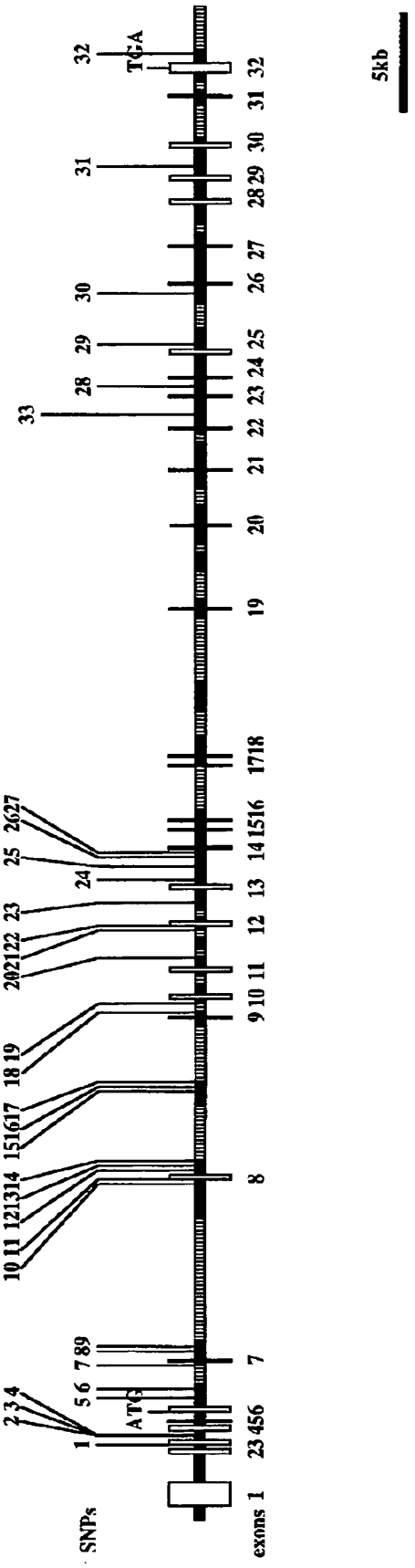
【図９】


ATP binding cassette, sub-family B, member 2 (ABCB2)
ACCESSION X66401
111213
1kb
TGA
ATG
SNPs 123 4
5 6 78
9
10
exons 1 23 4 5 6 7 8 9 10 11

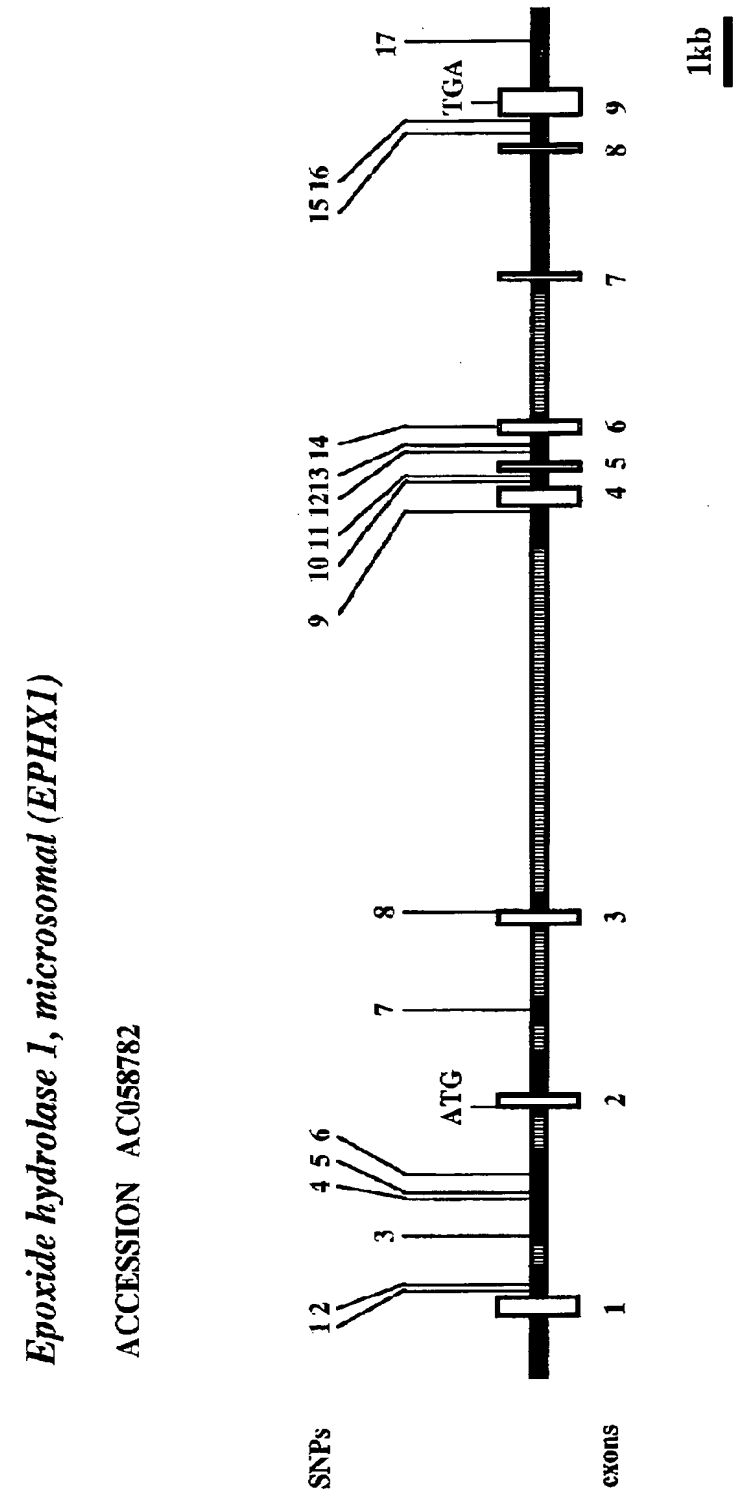
【図１０】

ATP-binding cassette, sub-family B, member 4 (ABCB4)

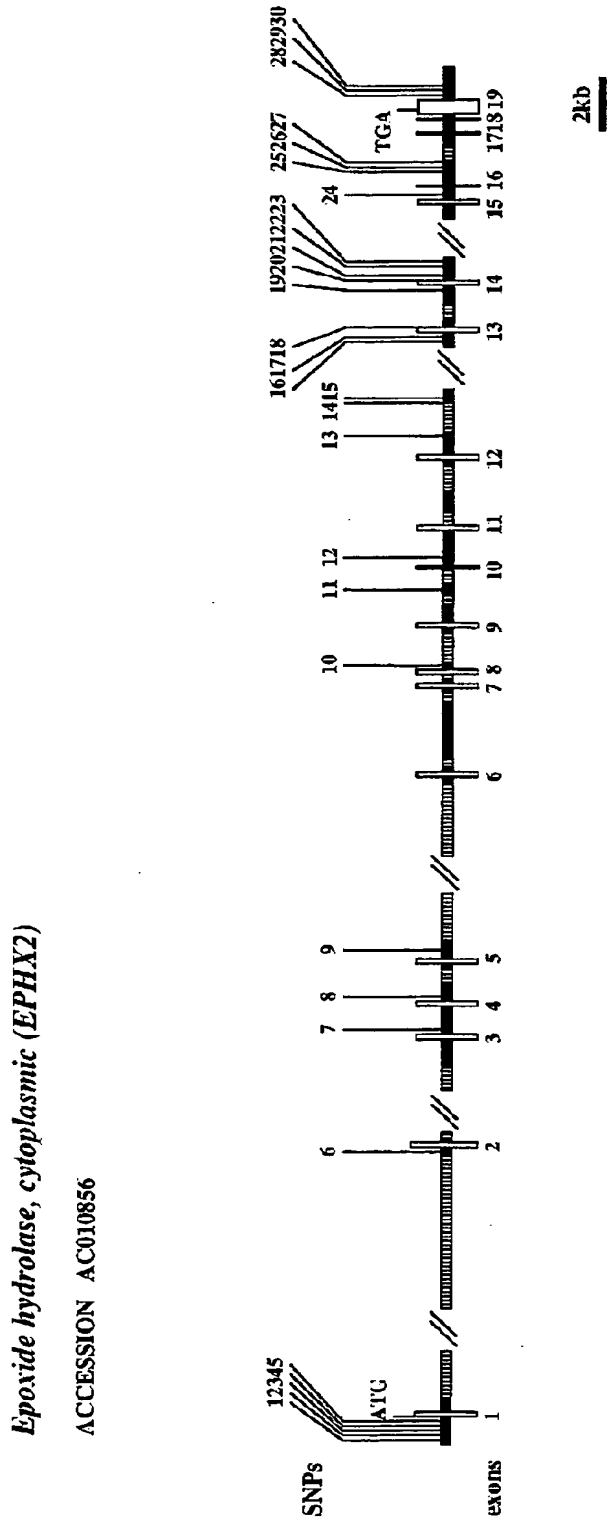
ACCESSION AC079591
AC079303
AC005045



【図１１】


Epoxide hydrolase 1, microsomal (EPHX1)
ACCESSION AC058782
SNPs
exons
ATG
TGA
1kb
1 2
3
4 5 6
7
8
9 10 11 12 13 14
15 16
17
1
2
3
4 5 6
7
8 9

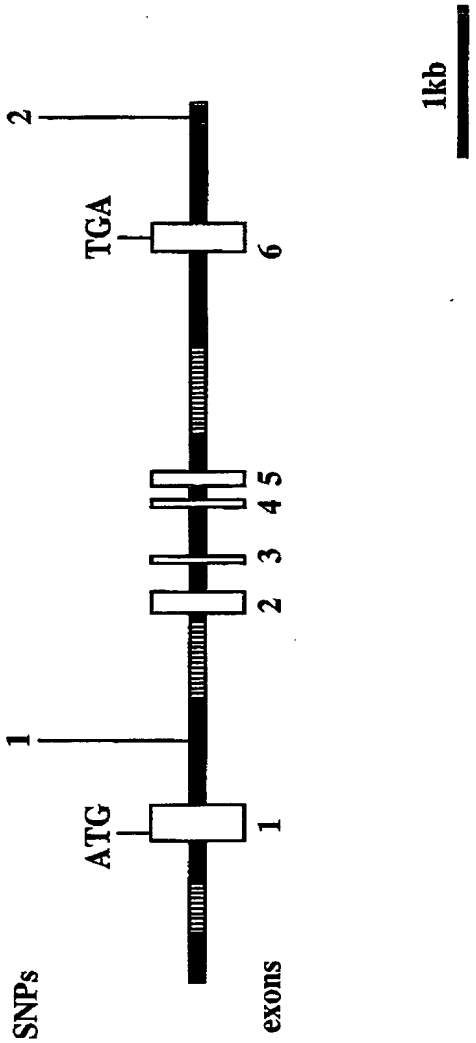
【図１２】


Epoxide hydrolase, cytoplasmic (EPHX2)
ACCESSION AC010856
SNPs
12345
ATG
TGA
exons
2kb

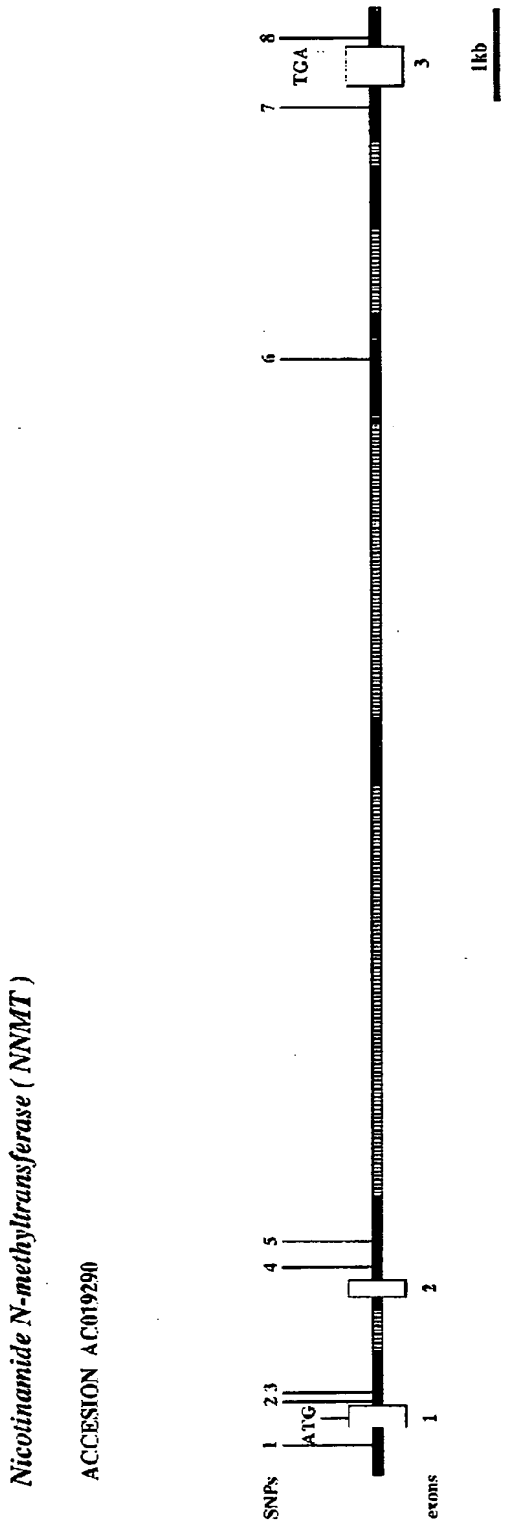
【図１３】

Guanidinoacetate N-methyltransferase (GAMT)

ACCESSION NT_000879



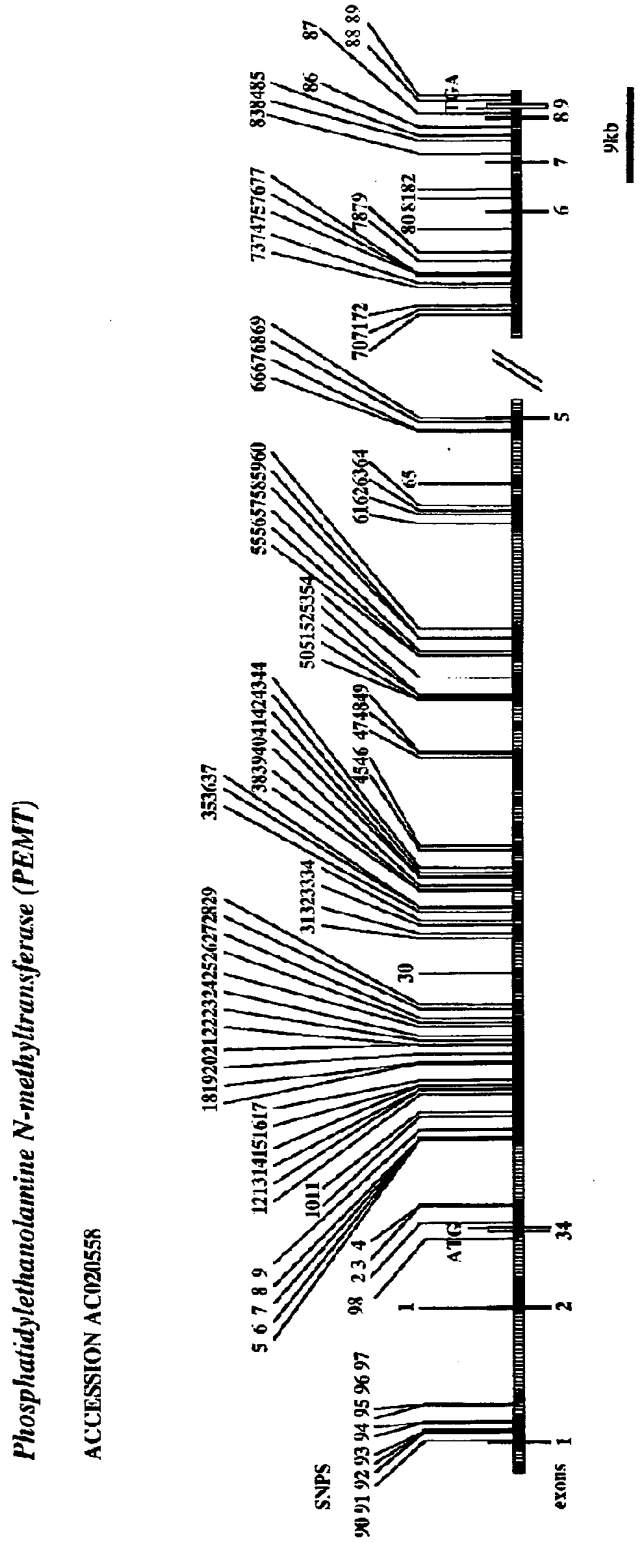
【図１４】


Nicotinamide N-methyltransferase (NNMT)
ACCESION AC019290
SNPs 1 2 3 4 5 6 7 8
exons ATG 1 2 3 TGA
1kb

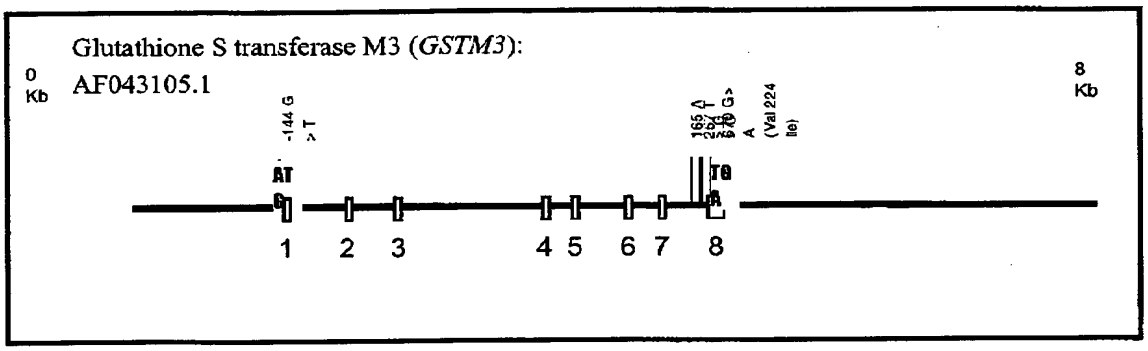
【図１５】


Phenylethanolamine N-methyltransferase (PNMT)
ACCESSION AC040933
SNPs
1
ATG
TGA
1
2
3
exons
1kb

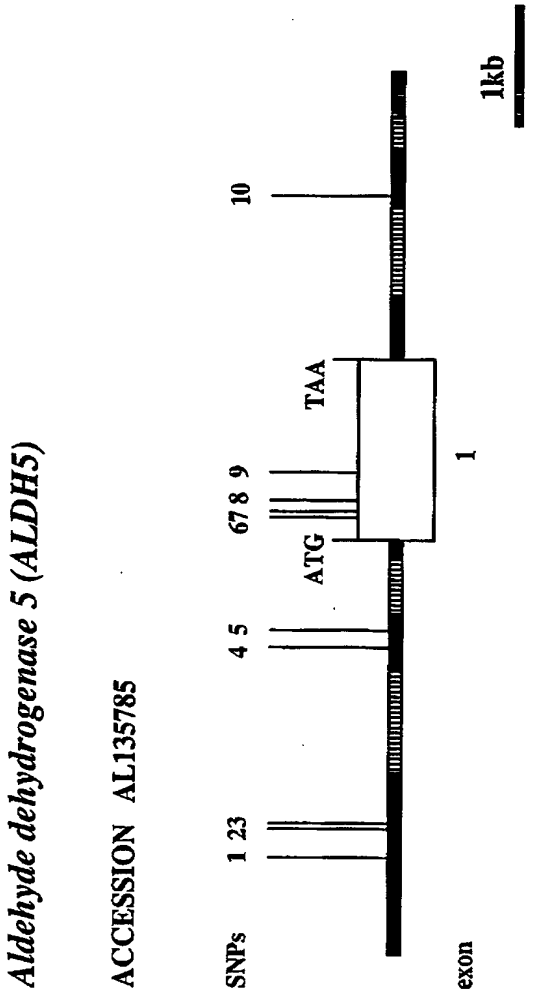
【図１６】


Phosphatidylethanolamine N-methyltransferase (PEMT)
ACCESSION AC020558
SNPS
exons
ATG
TGA
9kb

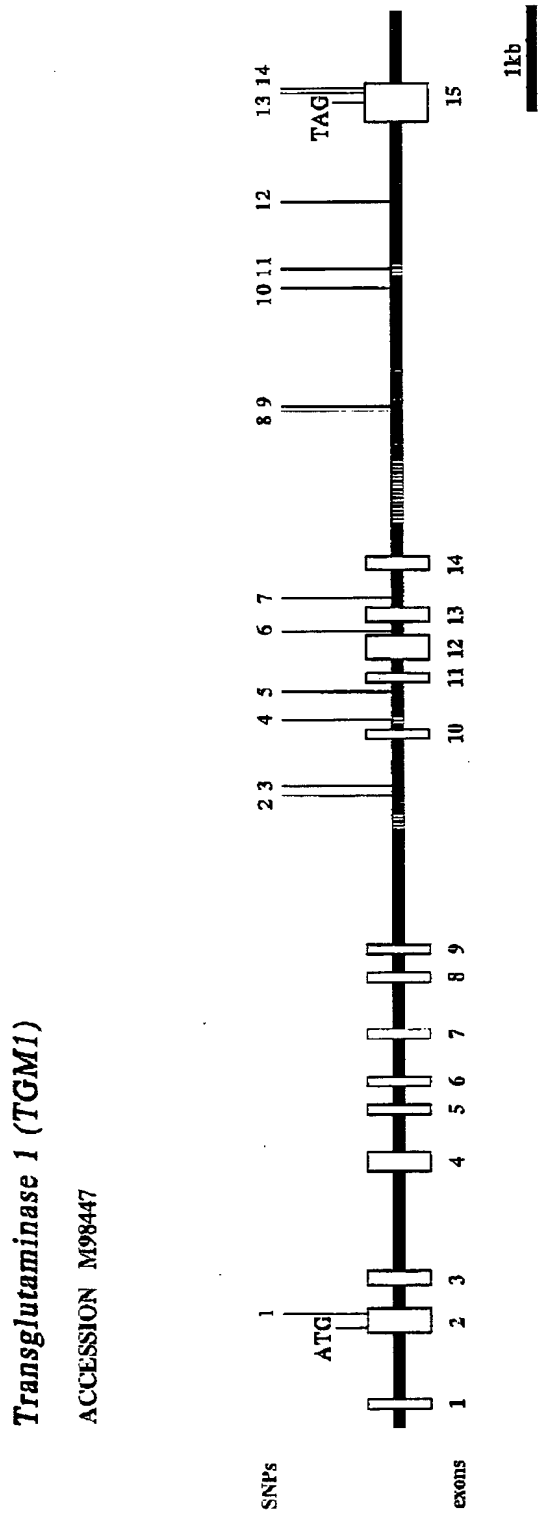
【図１７】


Glutathione S transferase M3 (GSTM3):
AF043105.1
0 Kb
8 Kb
-144 G >T
AT
TG
(Val224 Ile)
1 2 3 4 5 6 7 8

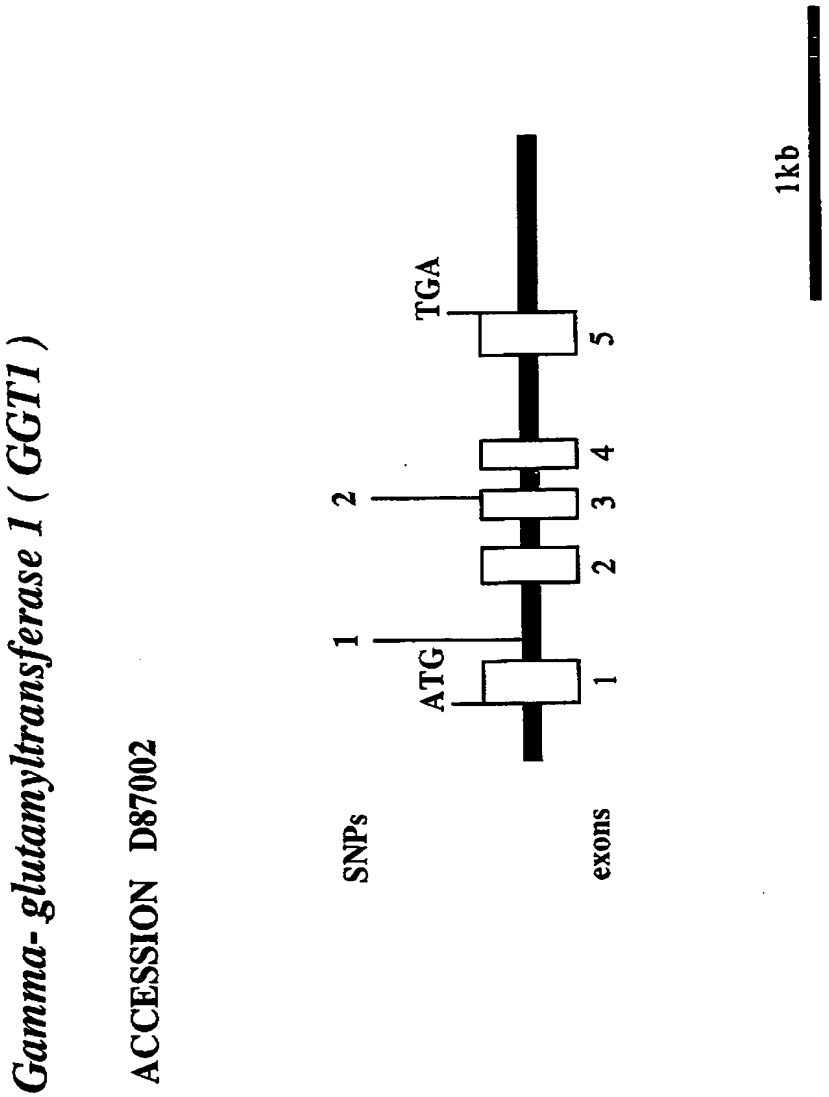
【図１８】


Aldehyde dehydrogenase 5 (ALDH5)
ACCESSION AL135785
SNPs
1 23
4 5
6 7 8 9
ATG
TAA
10
1
exon
1kb

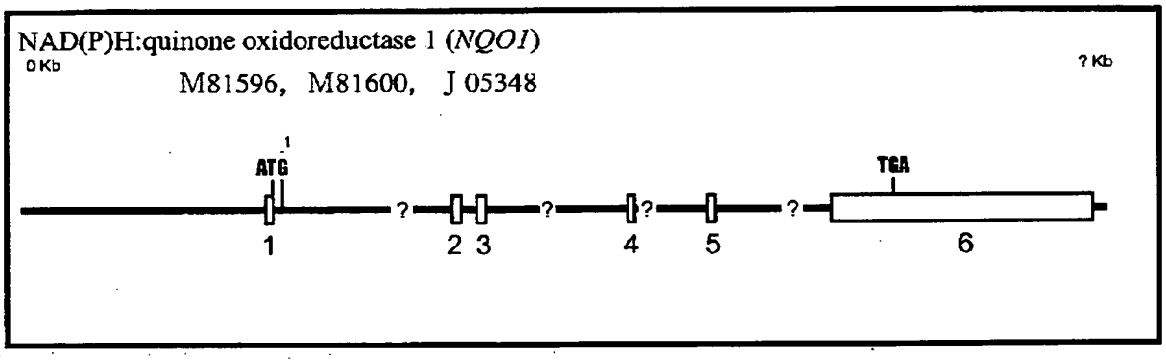
【図１９】


Transglutaminase 1 (TGM1)
ACCESSION M98447
SNPs
exons
ATG
TAG
1kb
1
2 3
4 5
6 7
8 9
10 11
12
13 14
15

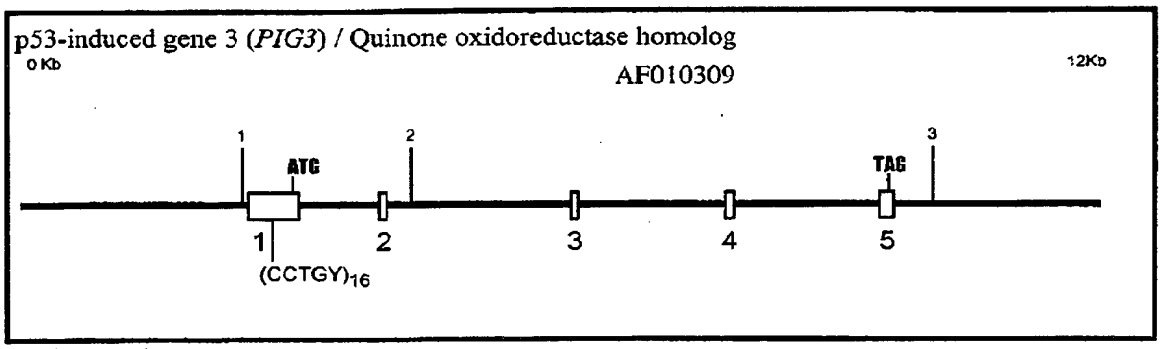
【図２０】


Gamma- glutamyltransferase 1 (GGT1)
ACCESSION D87002
SNPs
exons
ATG
TGA
1
2
1
2
3
4
5
1kb

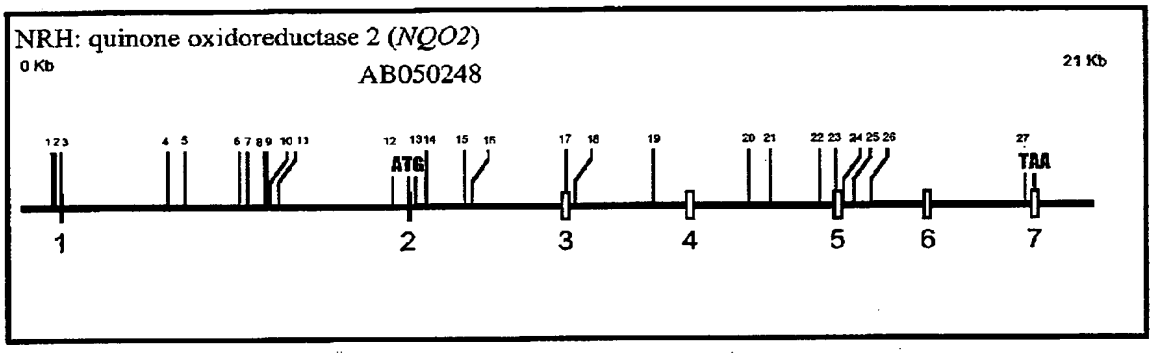
【図２１】


NAD(P)H:quinone oxidoreductase 1 (NQO1)
0 Kb
M81596, M81600, J 05348
? Kb
ATG
TGA
1
2 3
4
5
6

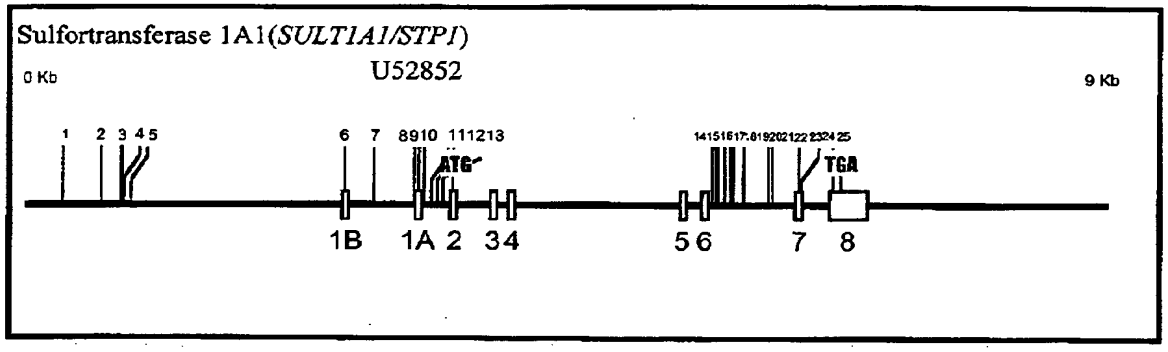
【図２２】



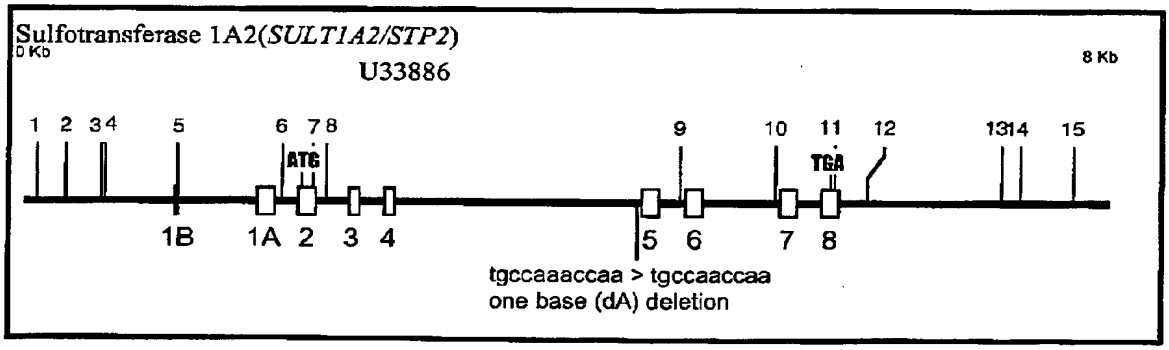
【図２３】



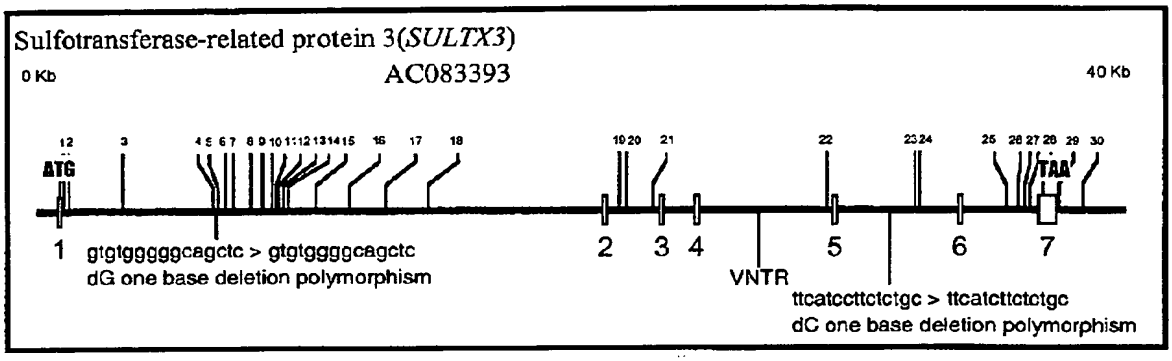
【図２４】



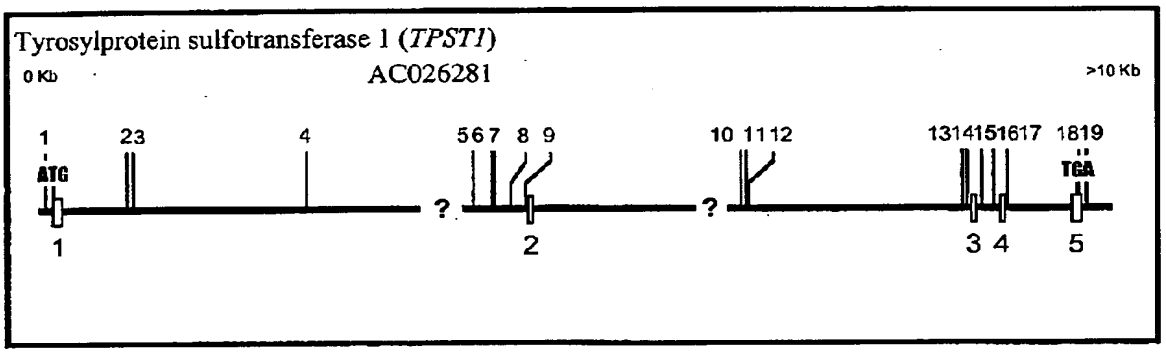
【図２５】



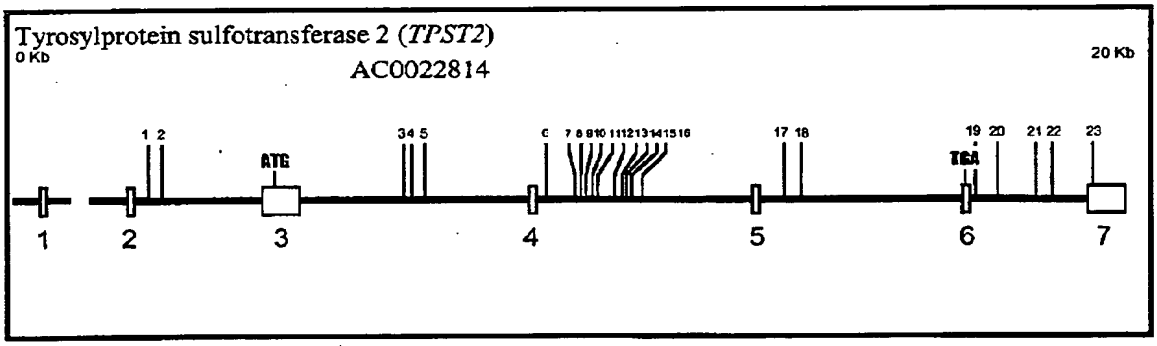
【図２６】



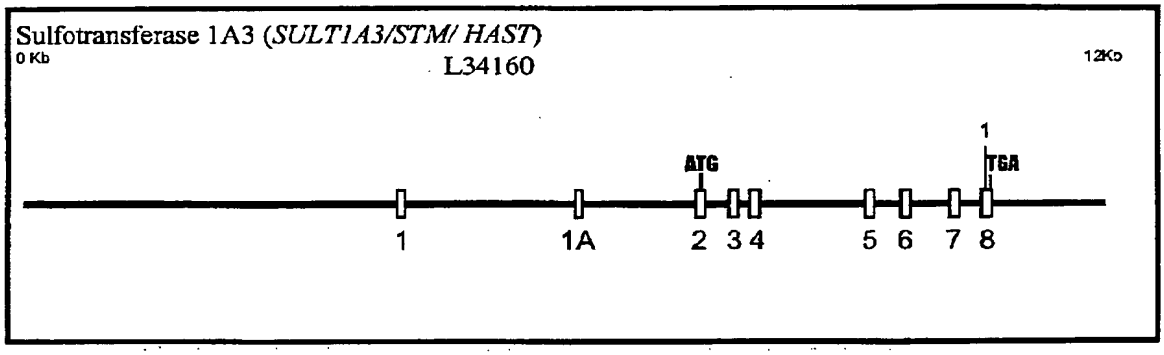
【図２７】



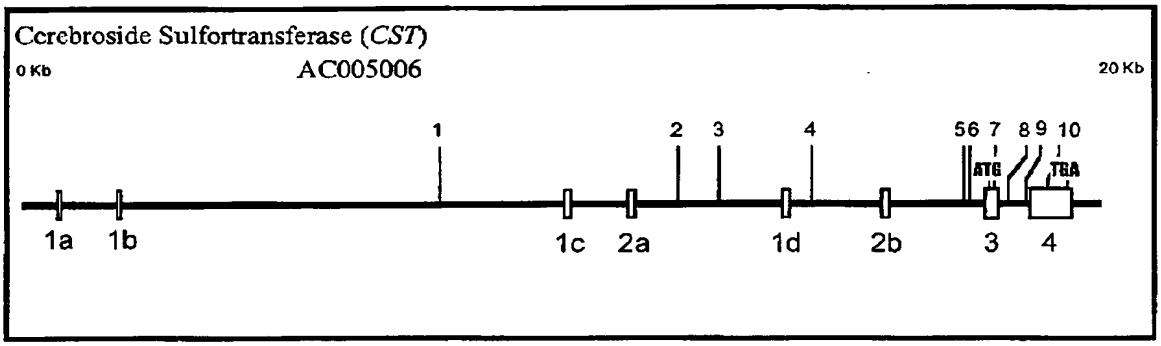
【図２８】



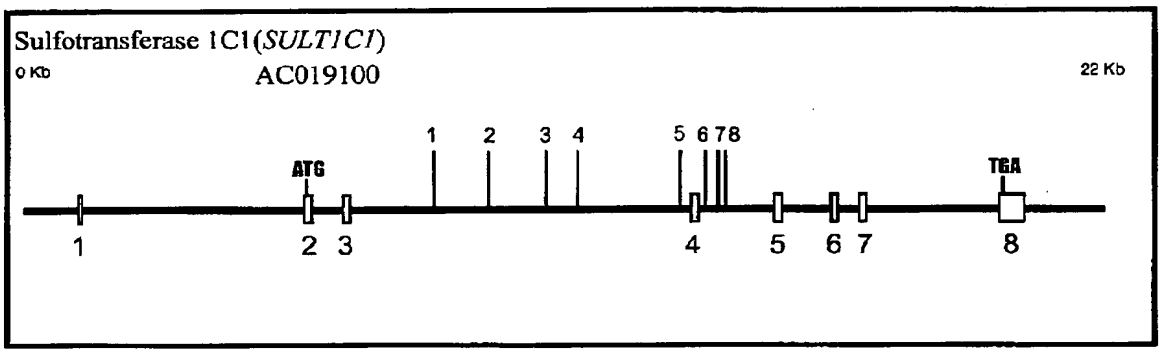
【図２９】



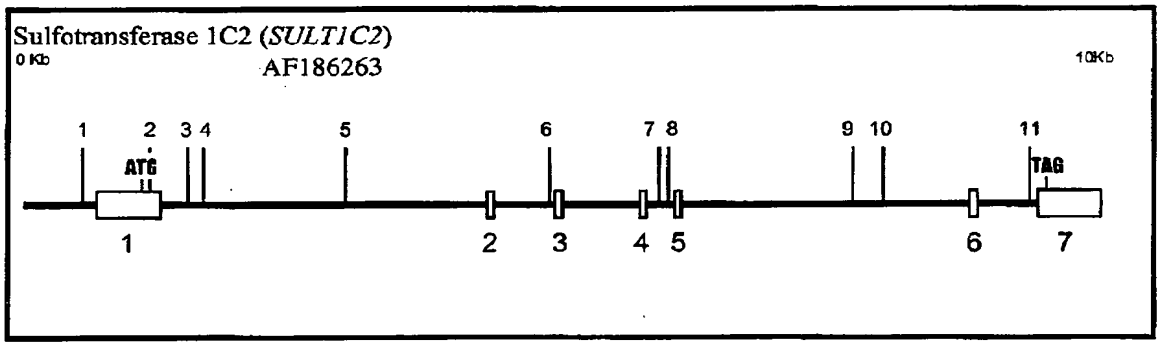
【図３０】



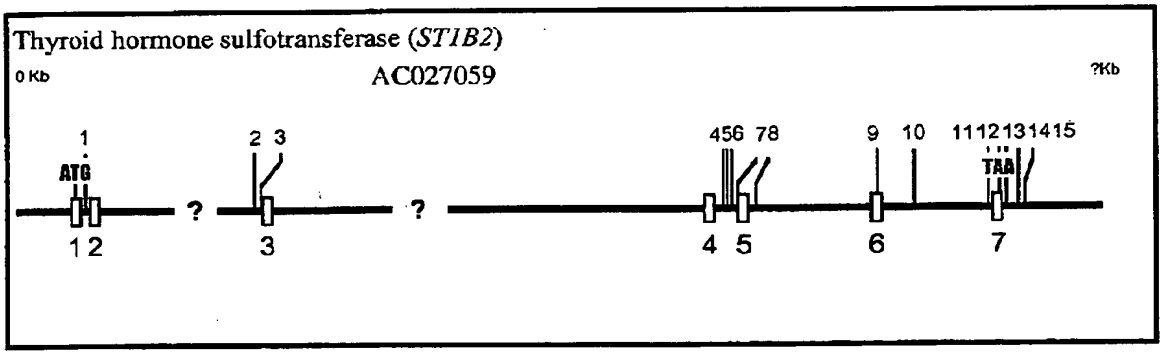
【図３１】



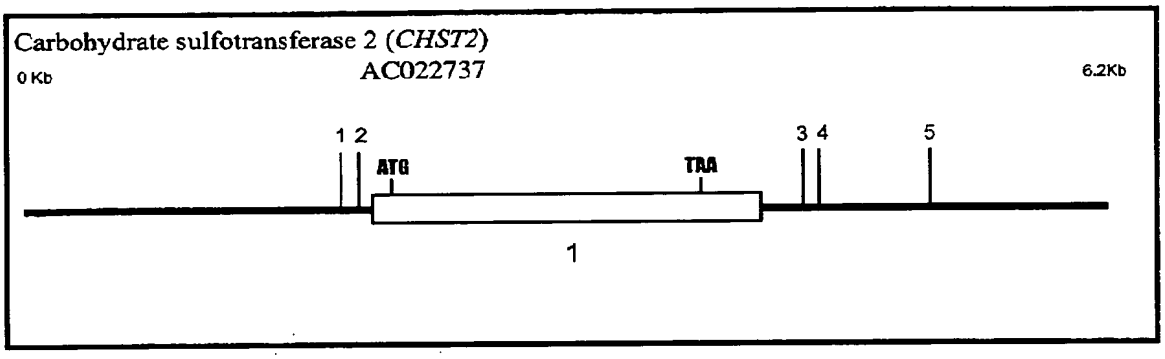
【図３２】



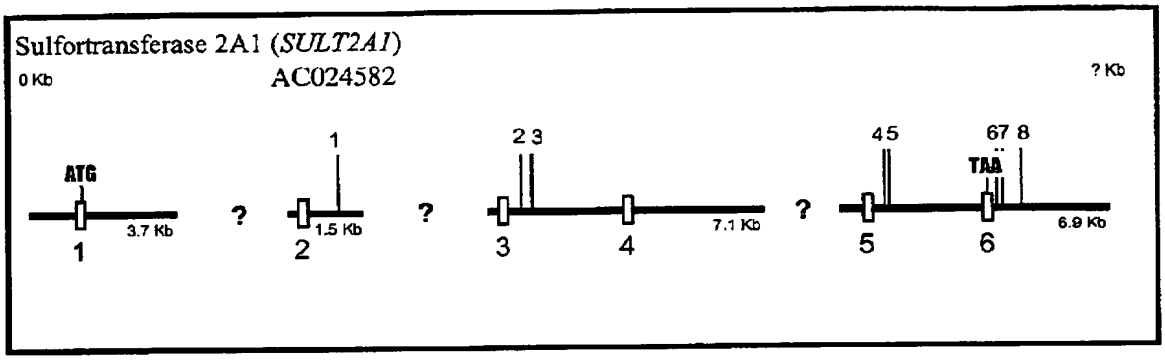
【図３３】



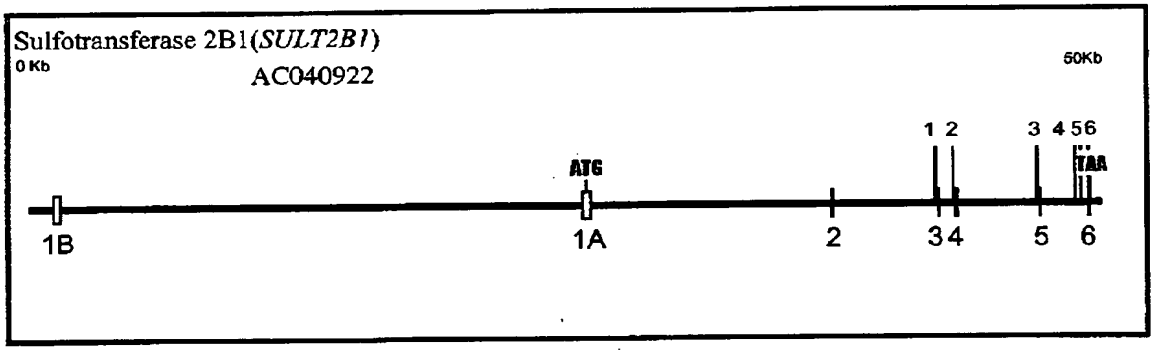
【図３４】


Carbohydrate sulfotransferase 2 (CHST2)
AC022737
0 Kb
6.2Kb
1 2
ATG
TAA
3 4
5
1

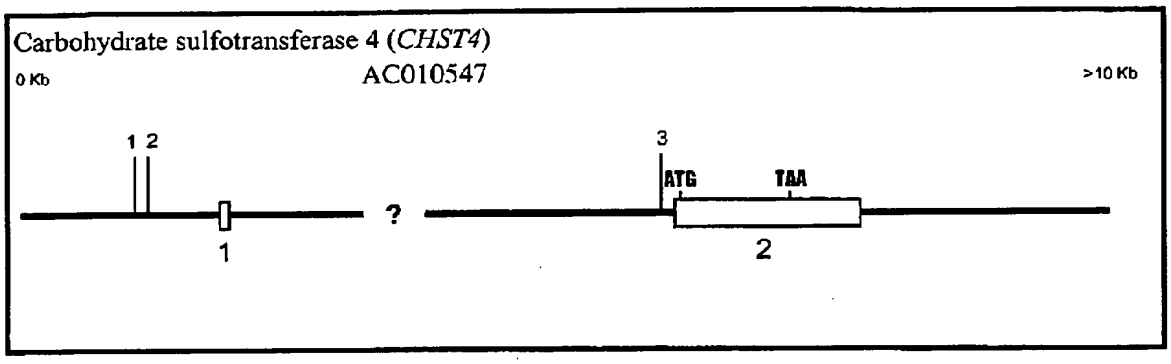
【図３５】


Sulfortransferase 2A1 (SULT2A1)
AC024582
0 Kb
? Kb
ATG
3.7 Kb
1
?
1
1.5 Kb
2
?
2 3
3
4
7.1 Kb
?
4 5
6 7 8
TAA
5
6
6.9 Kb

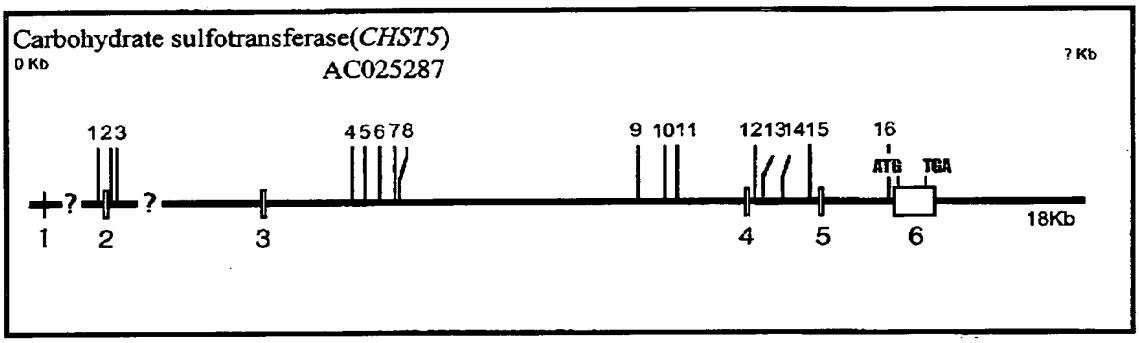
【図３６】


Sulfotransferase 2B1(SULT2B1)
AC040922
0 Kb
50Kb
1 2
3 4 5 6
ATG
TAA
1B
1A
2
3 4
5
6

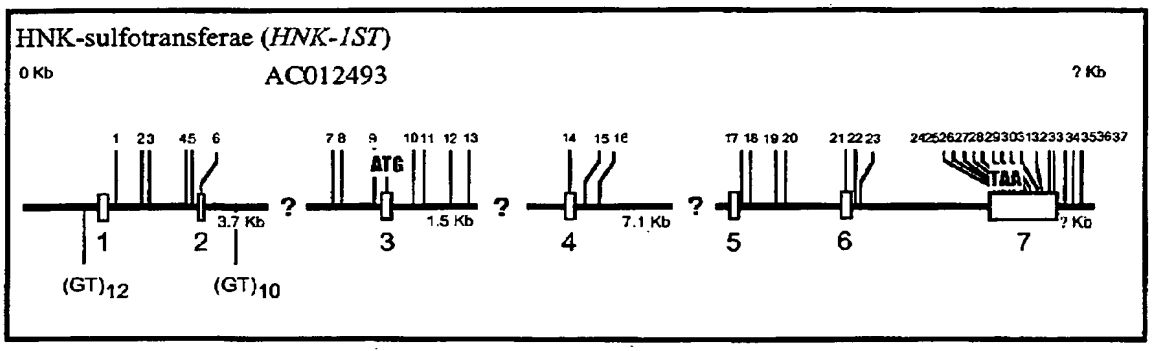
【図３７】


Carbohydrate sulfotransferase 4 (CHST4)
0 Kb
AC010547
>10 Kb
1 2
3
ATG
TAA
?
1
2

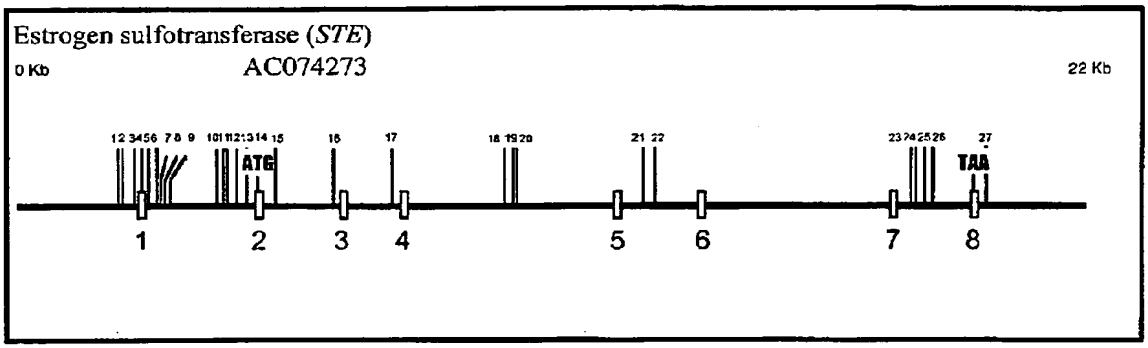
【図３８】


Carbohydrate sulfotransferase(CHST5)
0 Kb
AC025287
? Kb
123
45678
9 1011
12131415
16
ATG
TGA
18Kb
1 2 3 4 5 6

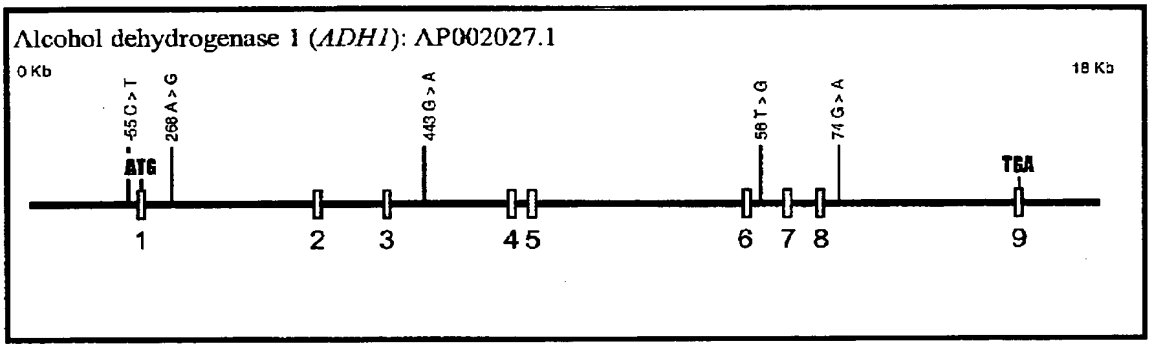
【図３９】


HNK-sulfotransferae (HNK-1ST)
0 Kb
AC012493
? Kb
ATG
TAA
3.7 Kb
1.5 Kb
7.1 Kb
? Kb
1 2 3 4 5 6 7
(GT)12
(GT)10

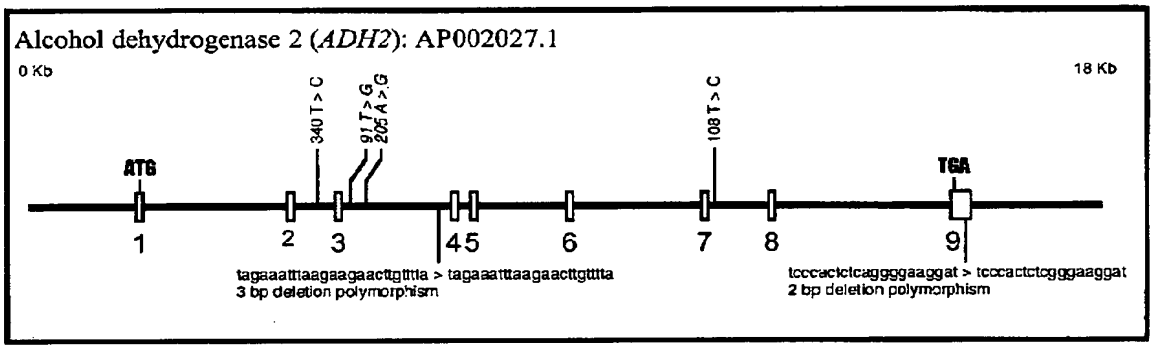
【図４０】



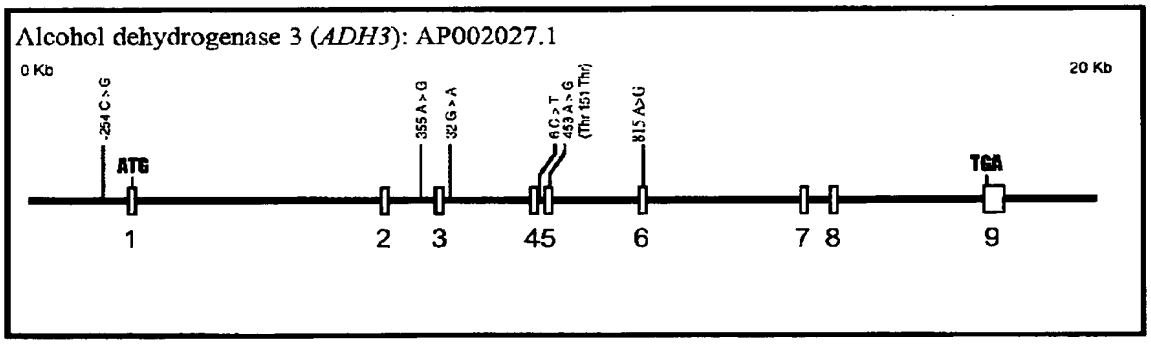
【図４１】



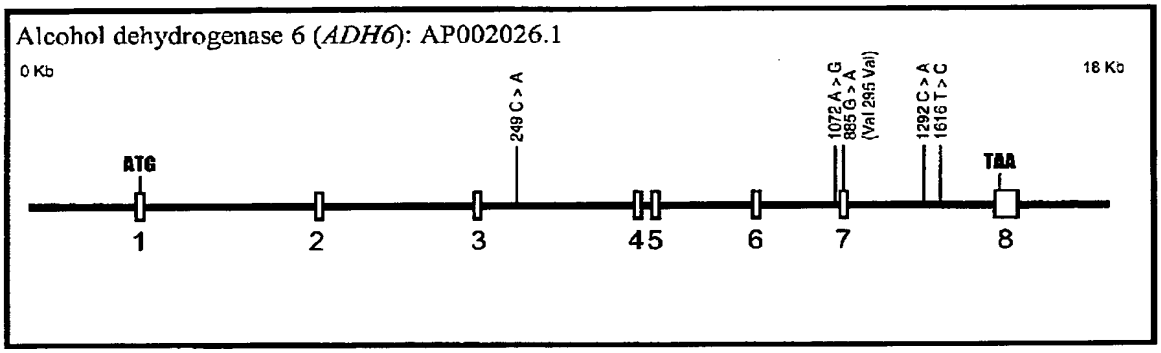
【図４２】



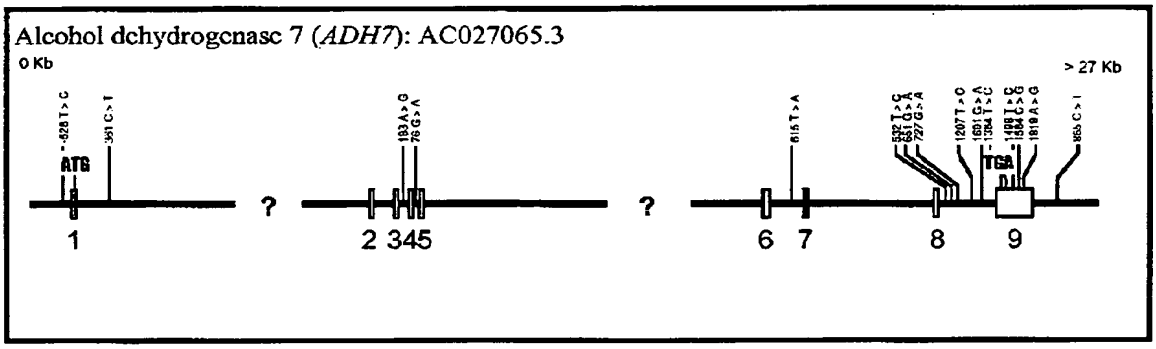
【図４３】



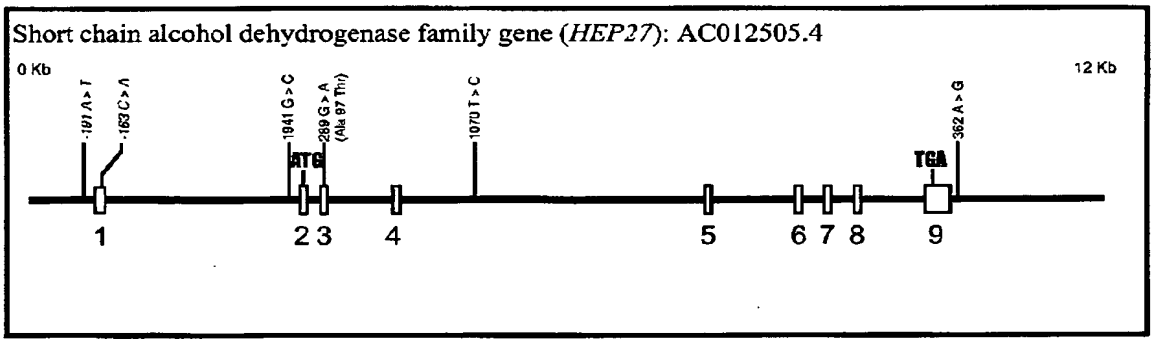
【図４４】


Alcohol dehydrogenase 6 (*ADH6*): AP002026.1
0 Kb
16 Kb
ATG
249 C > A
1072 A > G
885 G > A
(Val 295 Val)
1292 C > A
1616 T > C
TAA
1
2
3
45
6
7
8

【図４５】


Alcohol dehydrogenase 7 (*ADH7*): AC027065.3
0 Kb
> 27 Kb
ATG
TGA
?
?
1
2 345
6 7
8
9

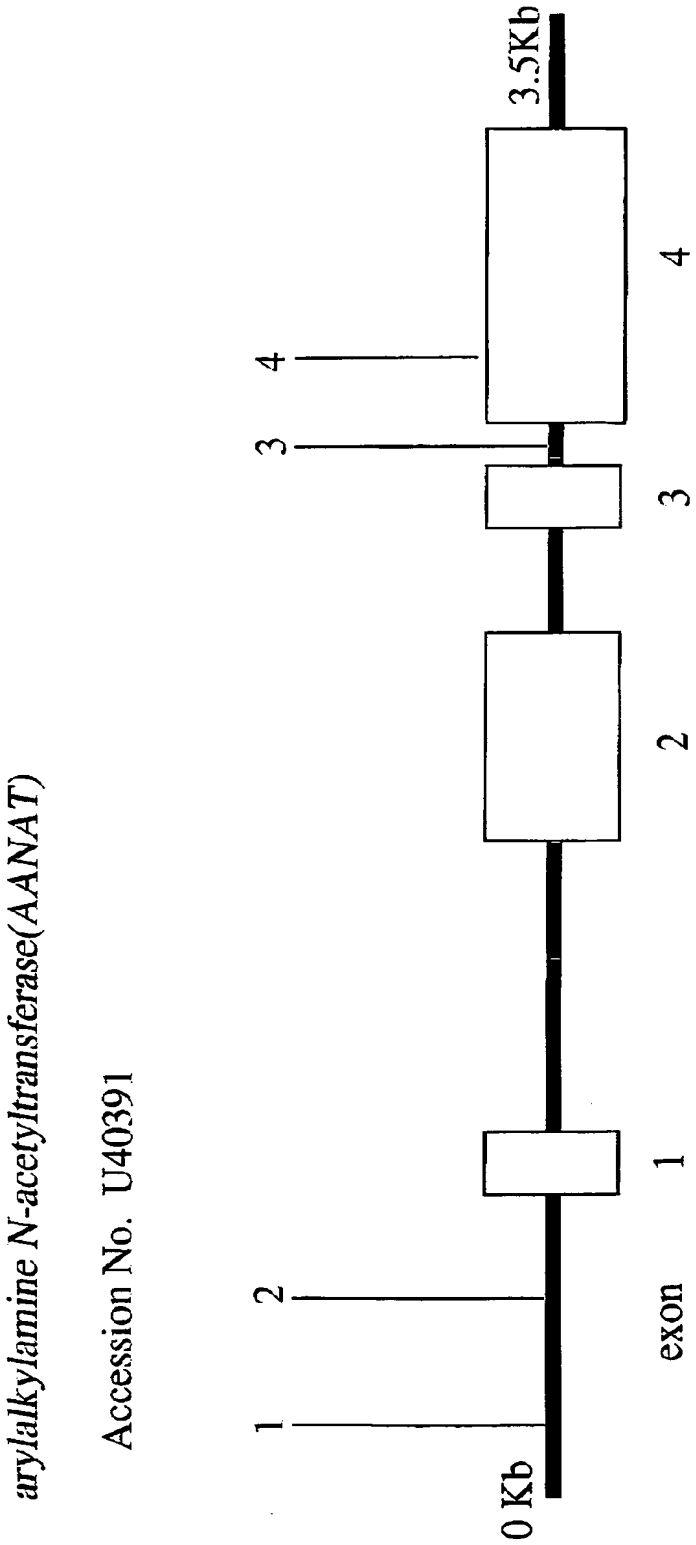
【図４６】


Short chain alcohol dehydrogenase family gene (*HEP27*): AC012505.4
0 Kb
12 Kb
ATG
TGA
1070 T > C
1
2 3
4
5
6 7 8
9

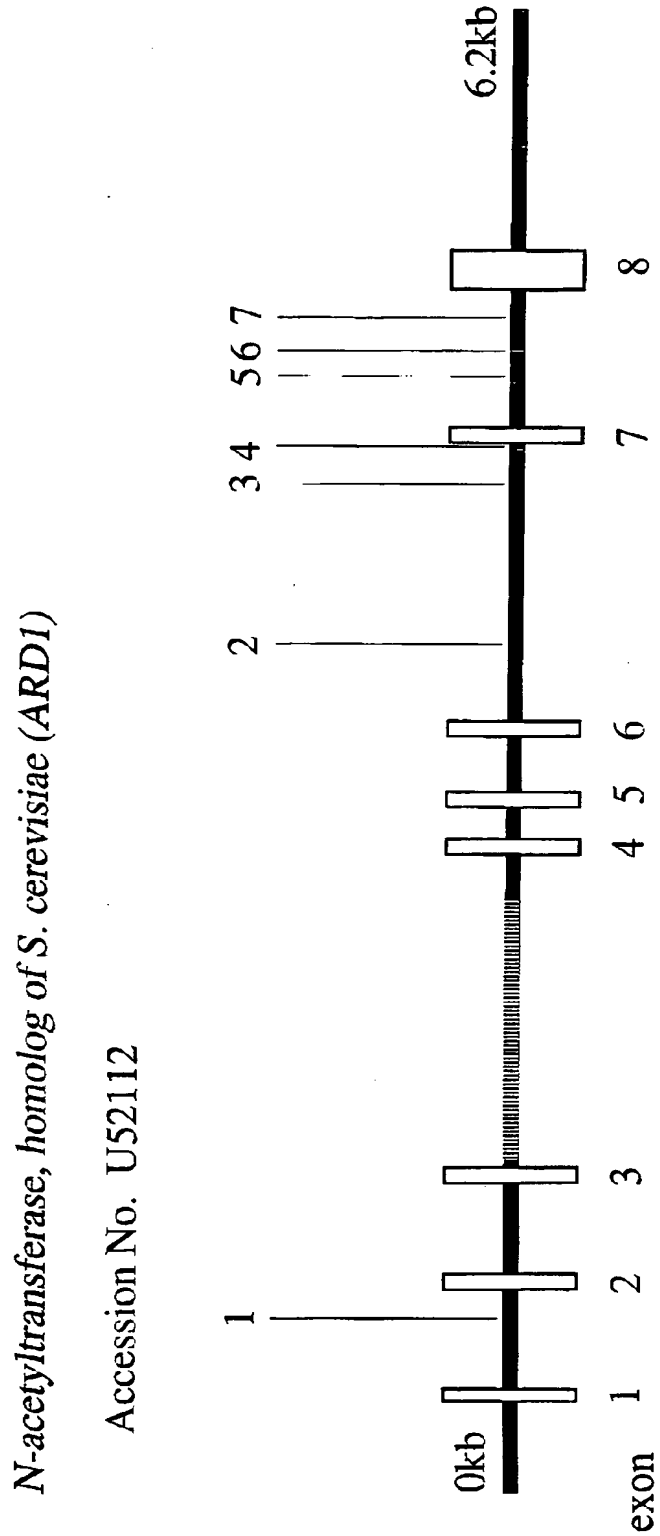
【図４７】


L1 cell adhesion molecule (L1CAM)
Accession No. U52112
0kb
16kb
exon 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28
1 2 3 4 5 6

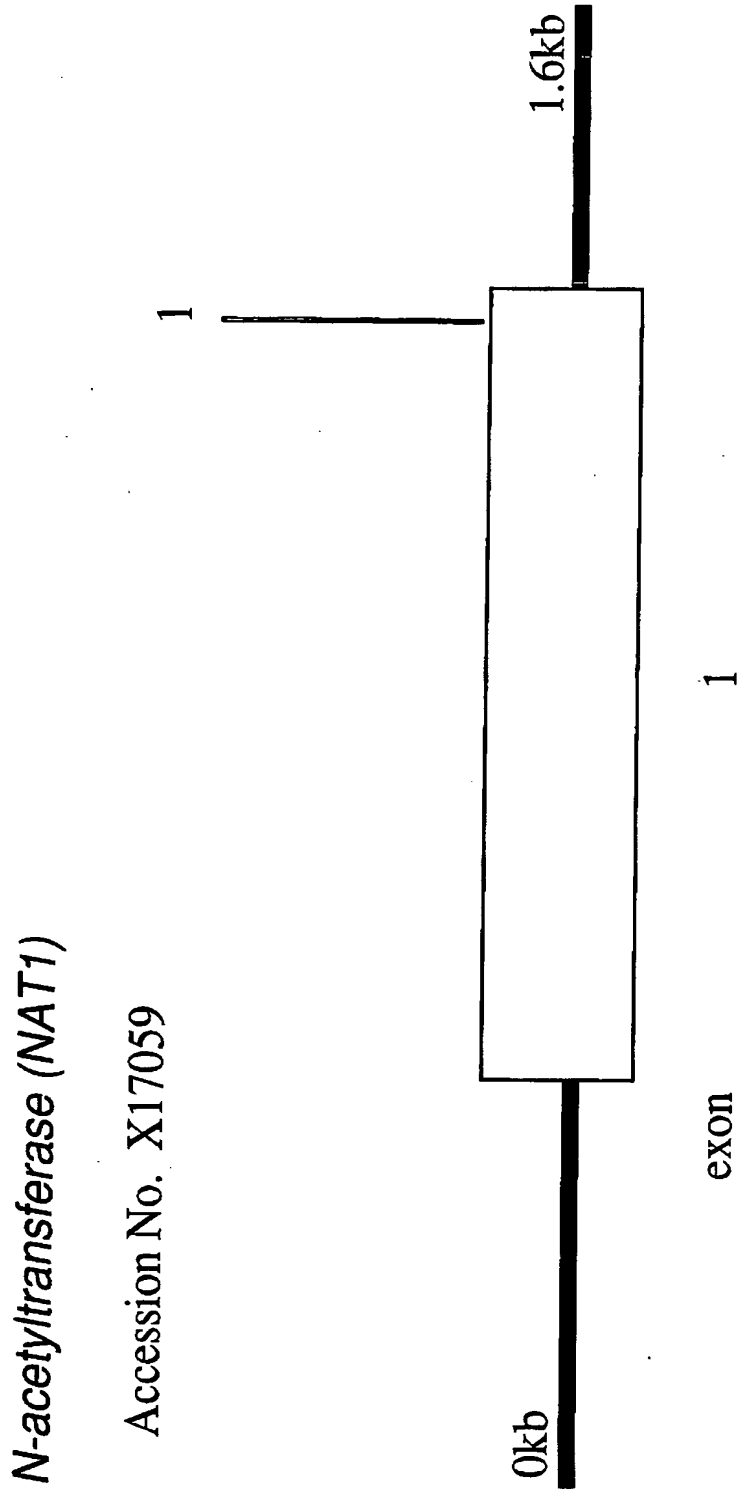
【図４８】


arylalkylamine N-acetyltransferase(AANAT)
Accession No. U40391
0 Kb
3.5Kb
1
2
3
4
exon
1
2
3
4

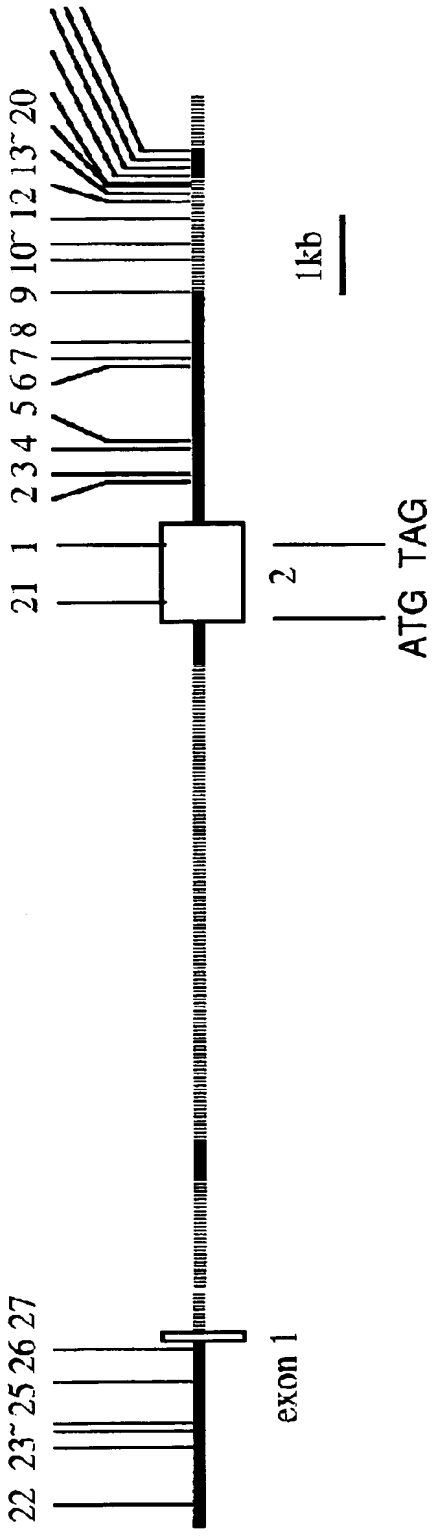
【図４９】


N-acetyltransferase, homolog of S. cerevisiae (ARD1)
Accession No. U52112
0kb
6.2kb
exon
1
2
3
4
5
6
7
8
1
2
3 4
5 6 7

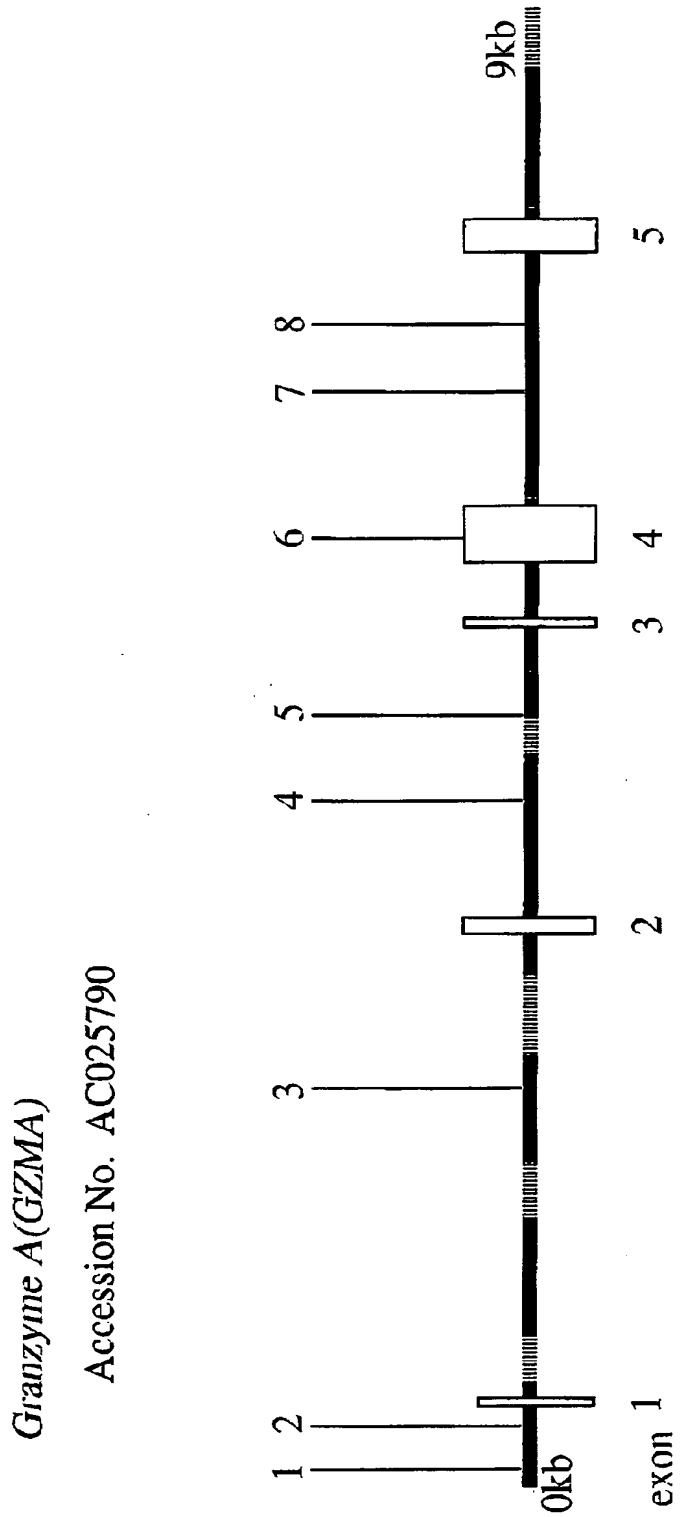
【図５０】


1.6kb
1
1
exon
0kb
N-acetyltransferase (NAT1)
Accession No. X17059

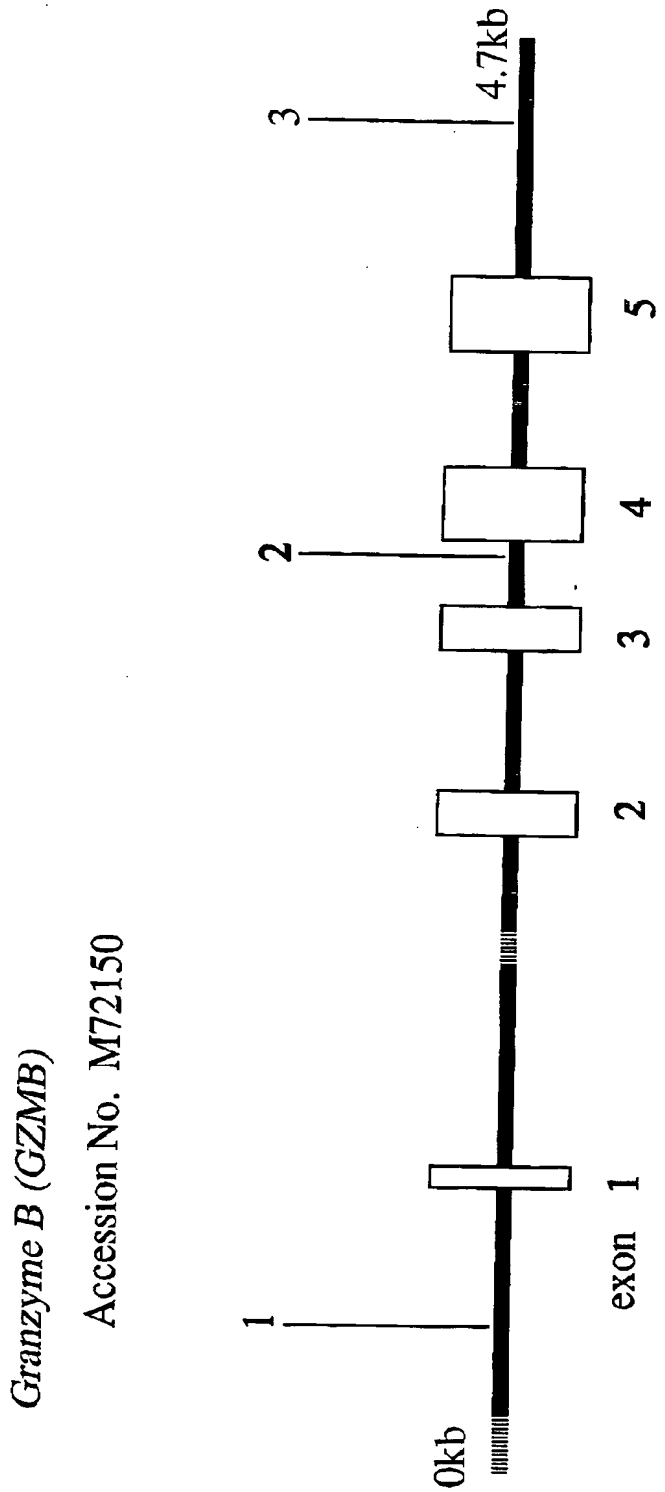
【図５１】


arylamine N-acetyltransferase (NAT2)
Accession No.: I22255, AC025062, AC025648, D10870
22 23~25 26 27
21 1 2 3 4 5 6 7 8 9 10~12 13~20
exon 1
2
ATG TAG
1kb

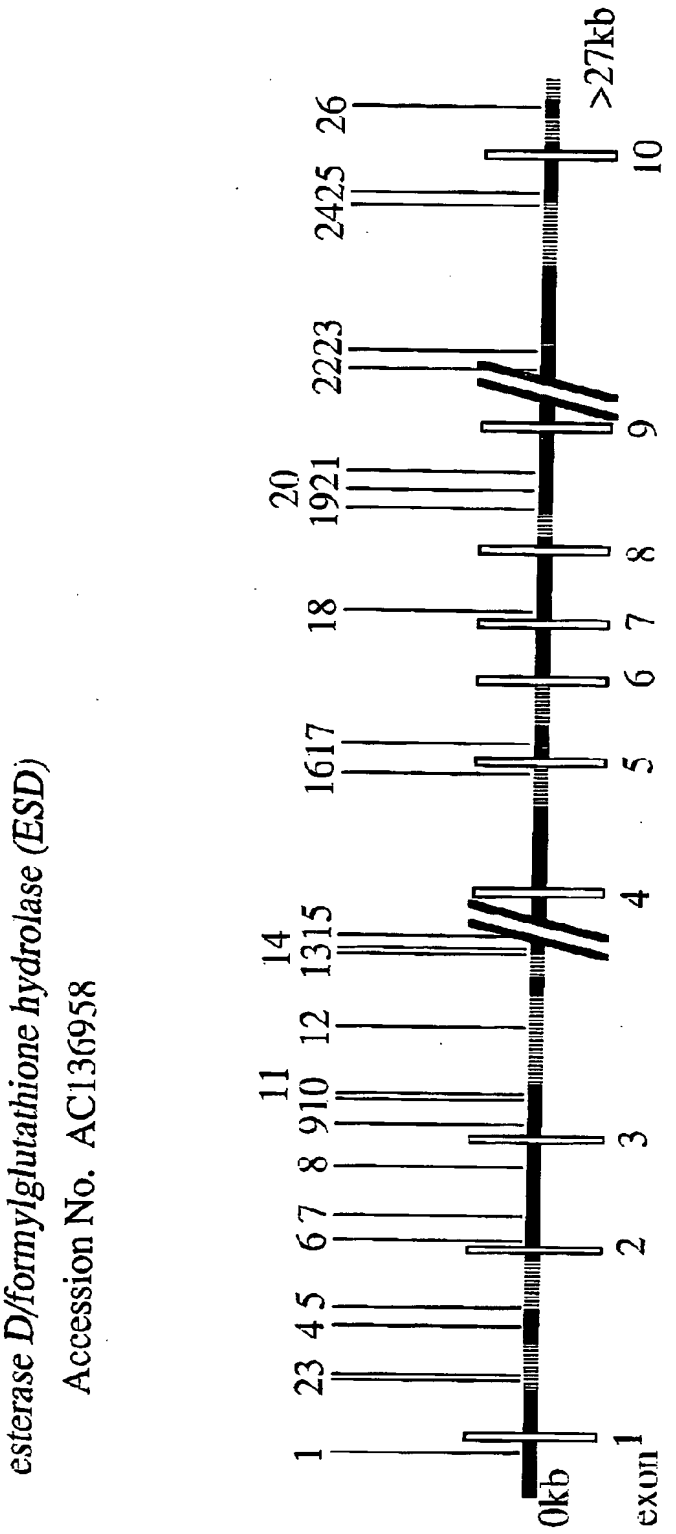
【図５２】


Granzyme A(GZMA)
Accession No. AC025790
9kb
0kb
exon 1
2
3
4
5
1
2
3
4
5
6
7
8

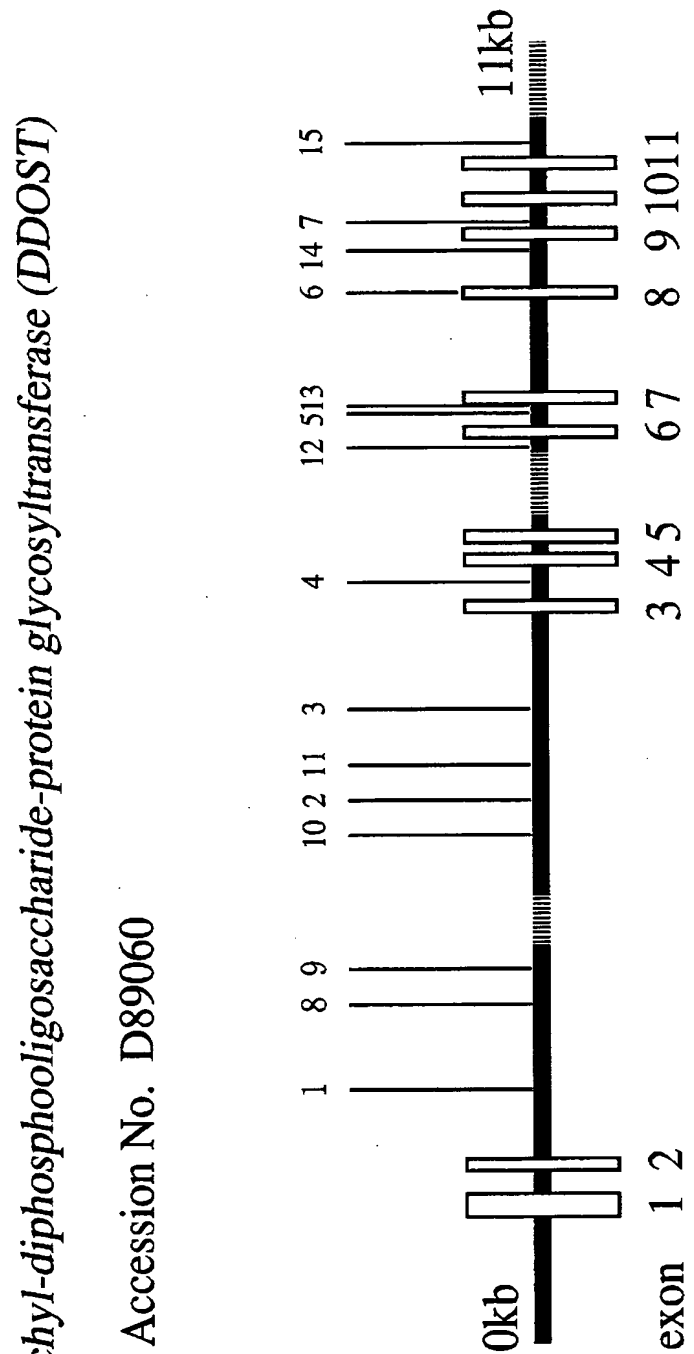
【図５３】



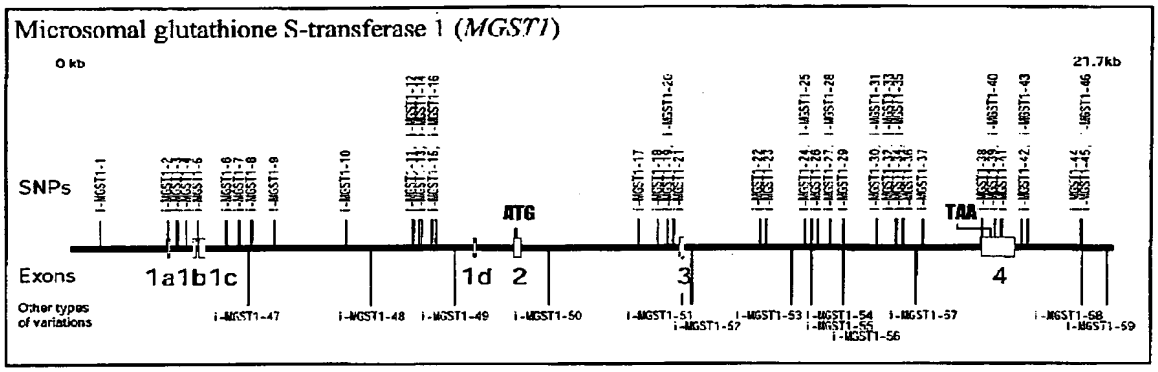
【図５４】


esterase D/formylglutathione hydrolase (ESD)
Accession No. AC136958
exon
0kb
>27kb
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26

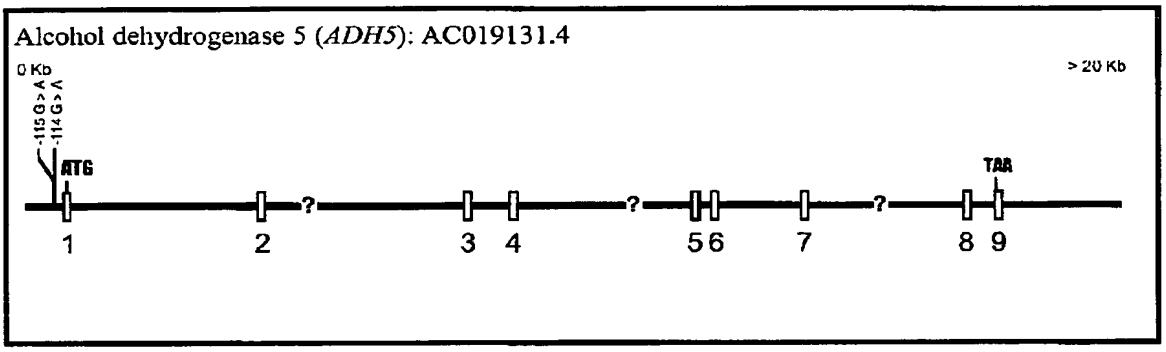
【図５５】


dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST)
Accession No. D89060
0kb
11kb
exon 1 2
3 4 5
6 7
8 9 10 11
1 8 9
10 2 11 3
4
12 5 13
6 14 7
15

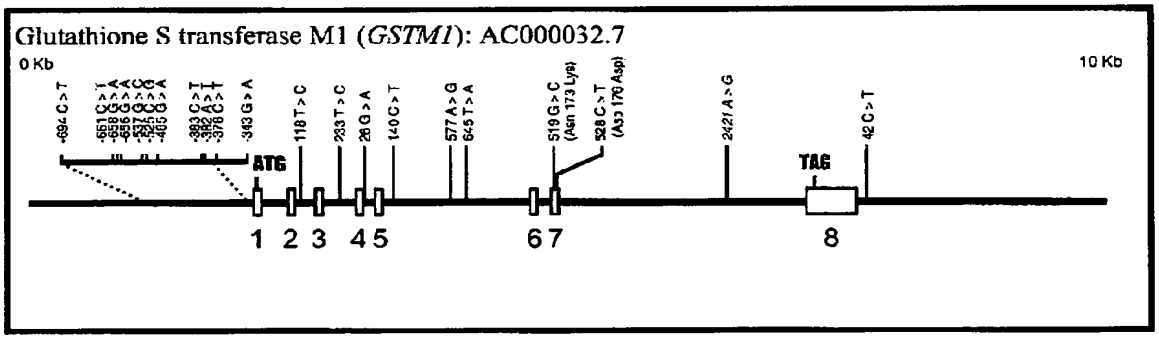
【図５６】



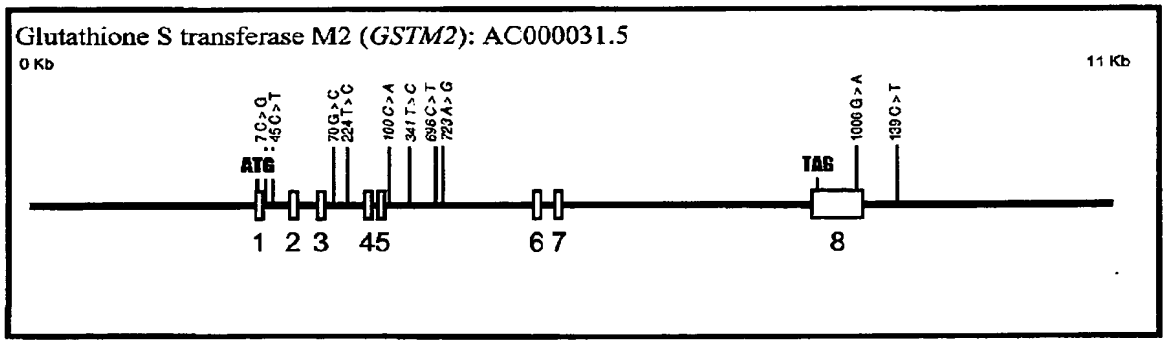
【図５７】



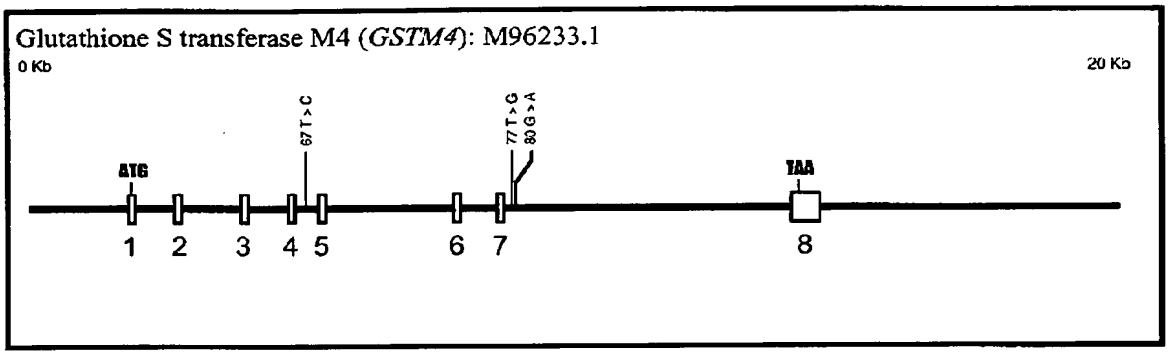
【図５８】



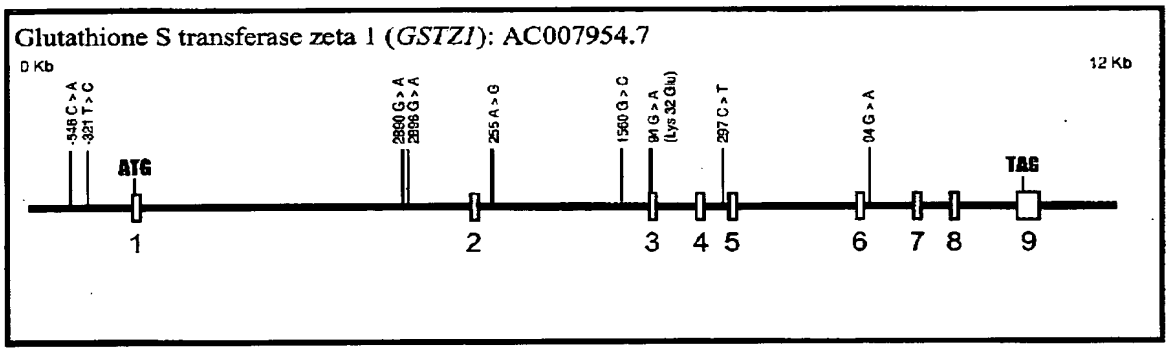
【図５９】



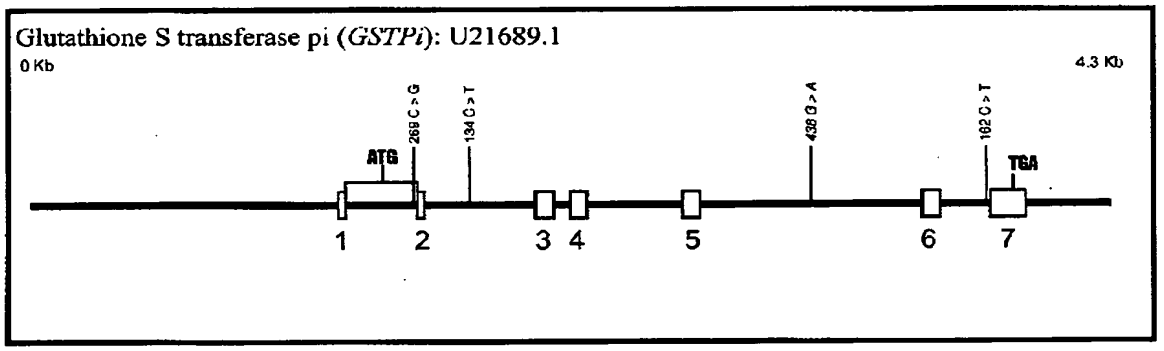
【図６０】



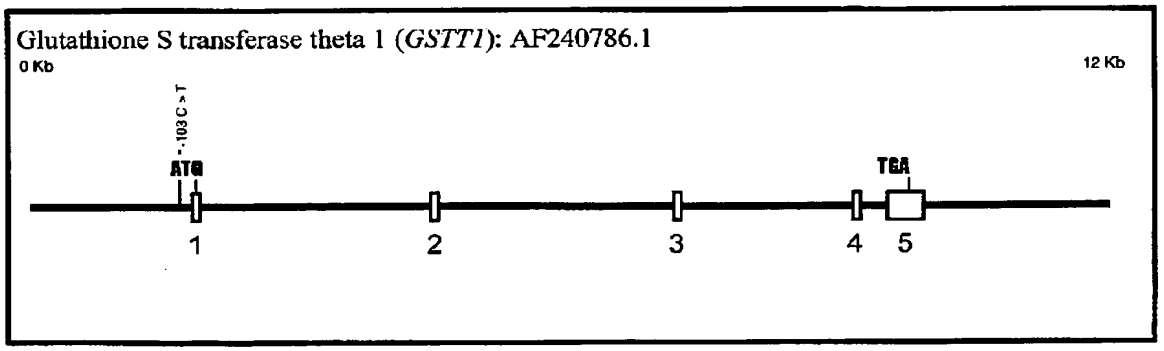
【図６１】



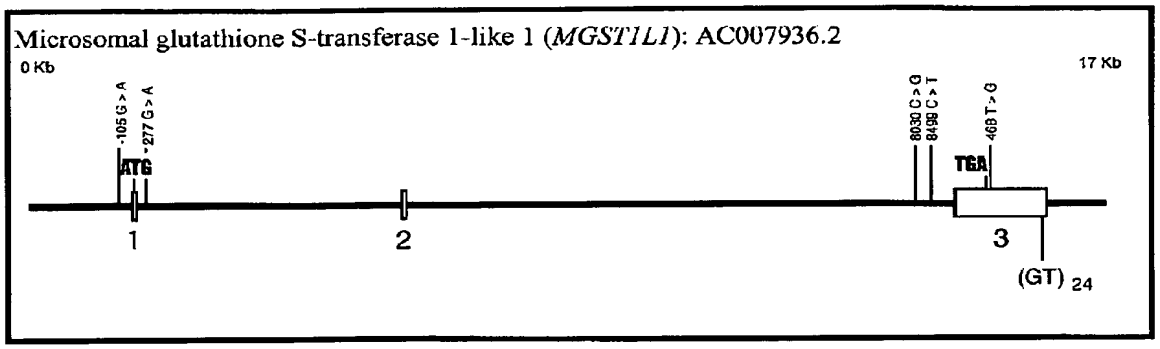
【図６２】



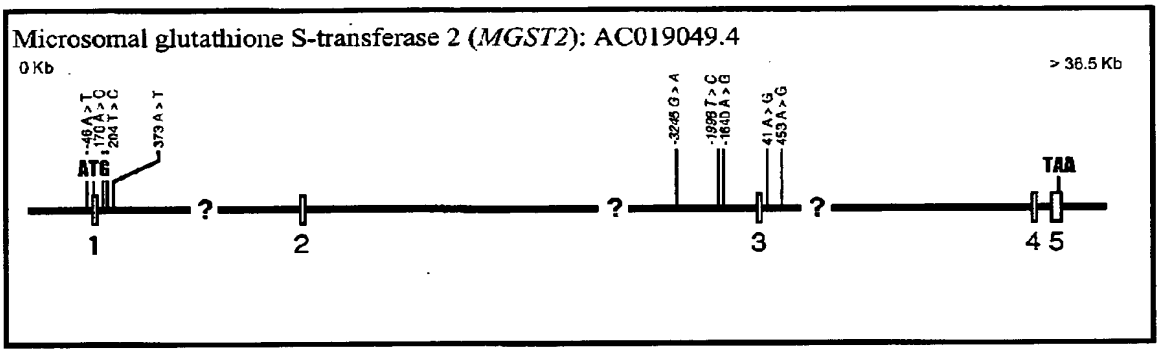
【図６３】



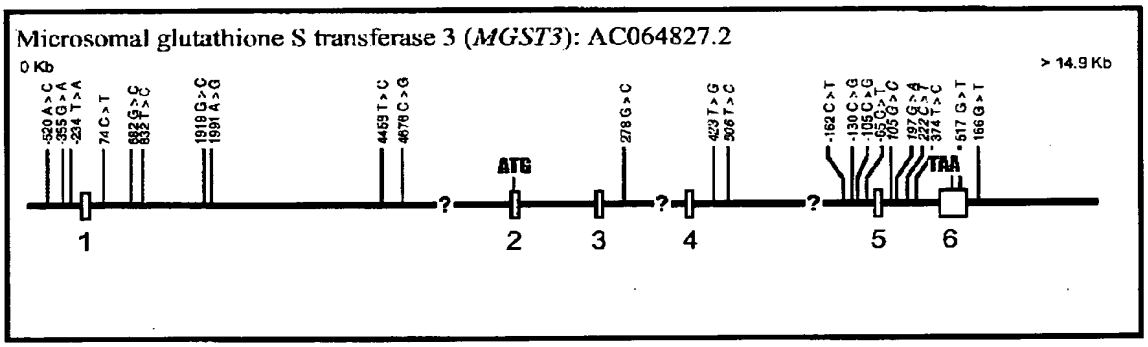
【図６４】


Microsomal glutathione S-transferase 1-like 1 (MGST1L1): AC007936.2
0 Kb
17 Kb
-105 G > A
-277 G > A
ATG
8030 C > G
8456 C > T
468 T > G
TGA
1
2
3
(GT) 24

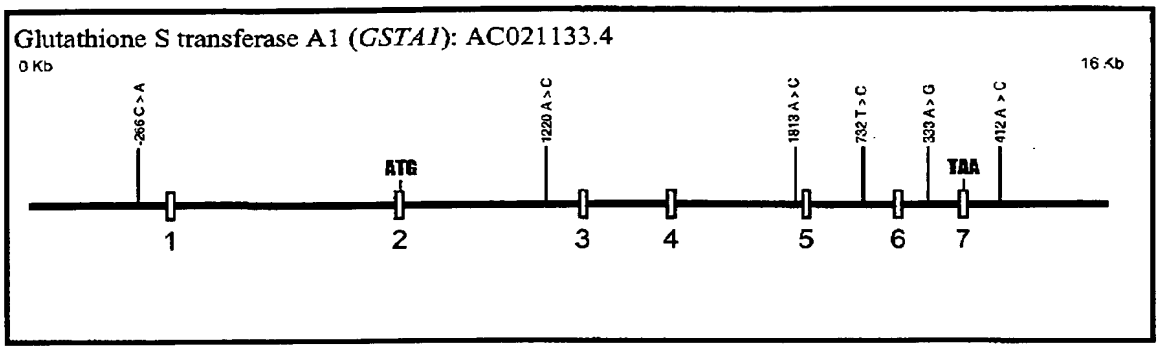
【図６５】


Microsomal glutathione S-transferase 2 (MGST2): AC019049.4
0 Kb
> 36.5 Kb
-46 A > T
-170 A > C
204 T > C
373 A > T
ATG
-3245 G > A
-1996 T > C
-1640 A > G
41 A > G
453 A > G
TAA
1
2
3
4 5

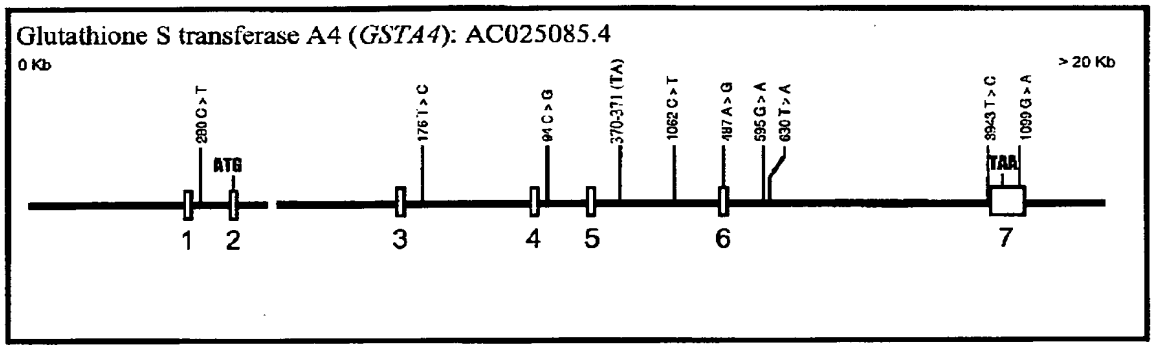
【図６６】


Microsomal glutathione S transferase 3 (MGST3): AC064827.2
0 Kb
> 14.9 Kb
-520 A > C
-355 G > A
-234 T > A
74 C > T
682 G > C
832 T > C
1919 G > C
1991 A > G
4459 T > C
4676 C > G
ATG
278 G > C
423 T > G
506 T > C
-162 C > T
-130 C > G
-105 C > T
-65 C > T
105 G > C
197 G > A
222 C > T
374 T > C
TAA
617 G > T
766 G > T
1
2
3
4
5
6

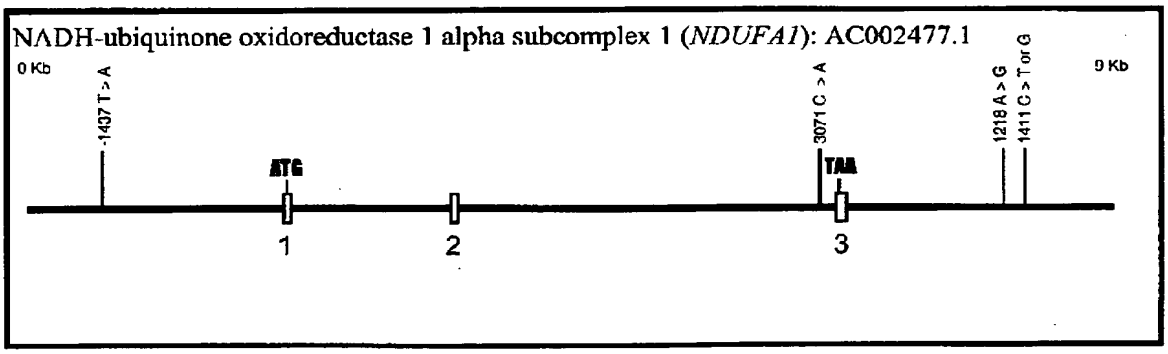
【図６７】



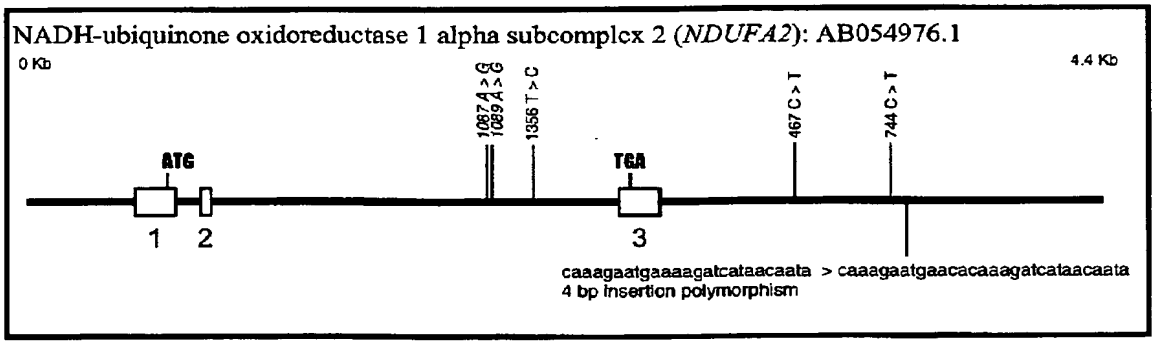
【図６８】



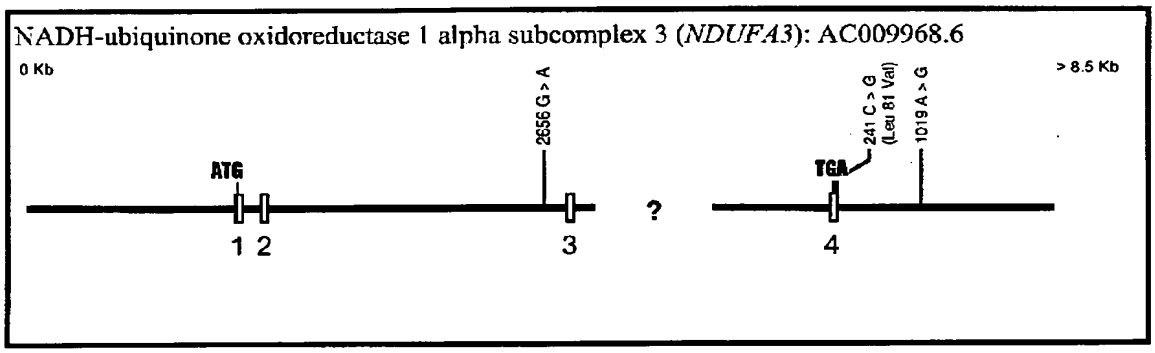
【図６９】



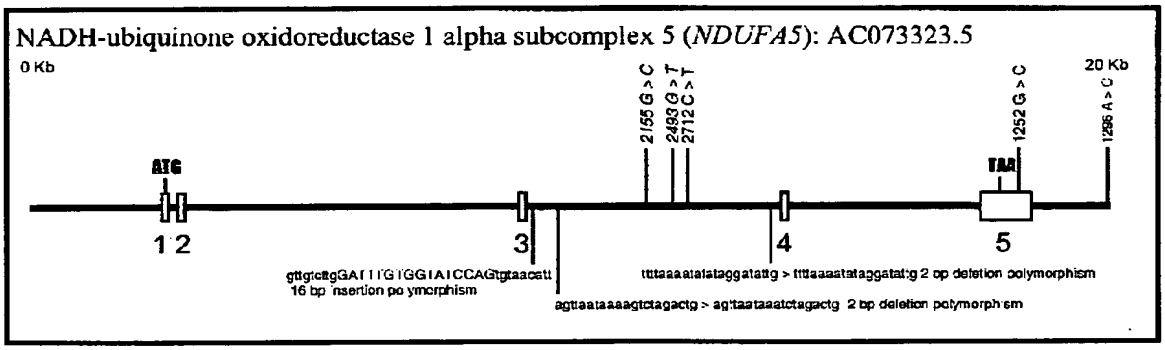
【図７０】



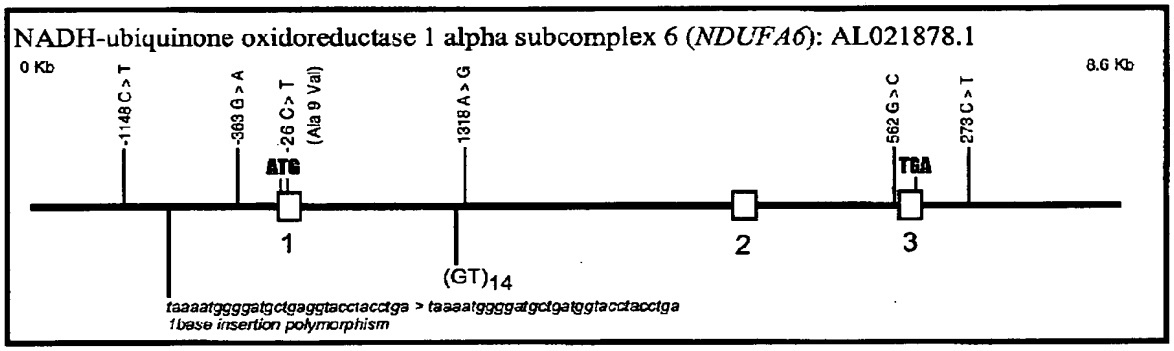
【図７１】



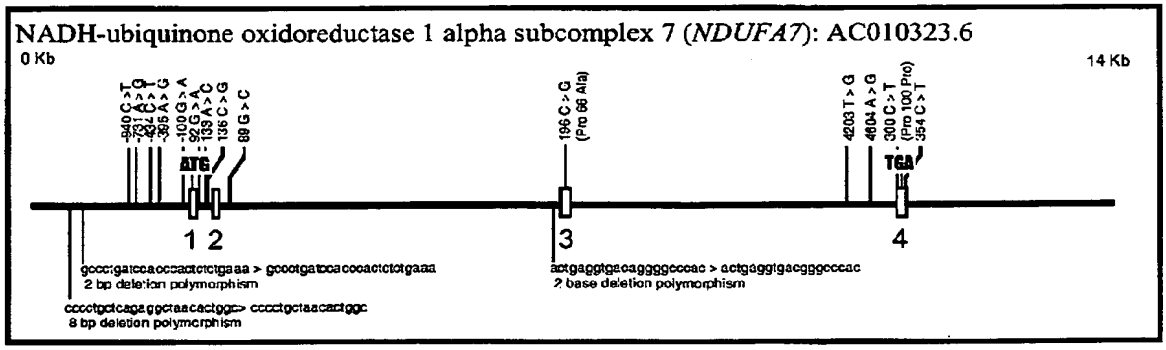
【図７２】



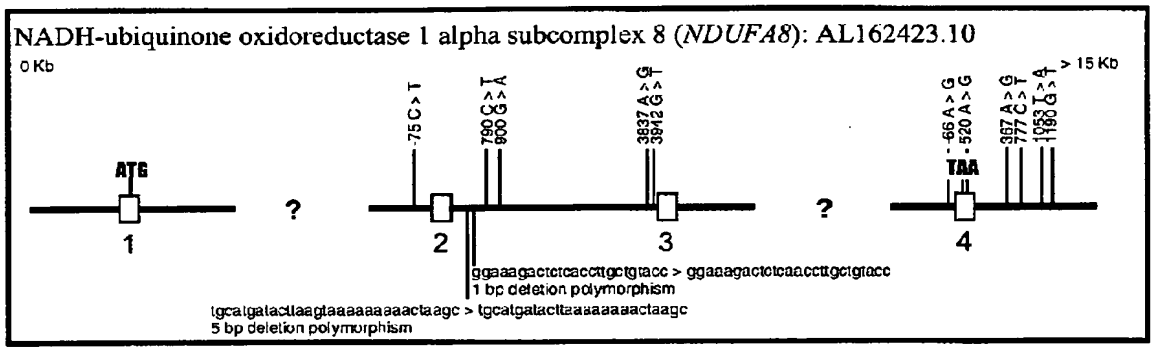
【図７３】



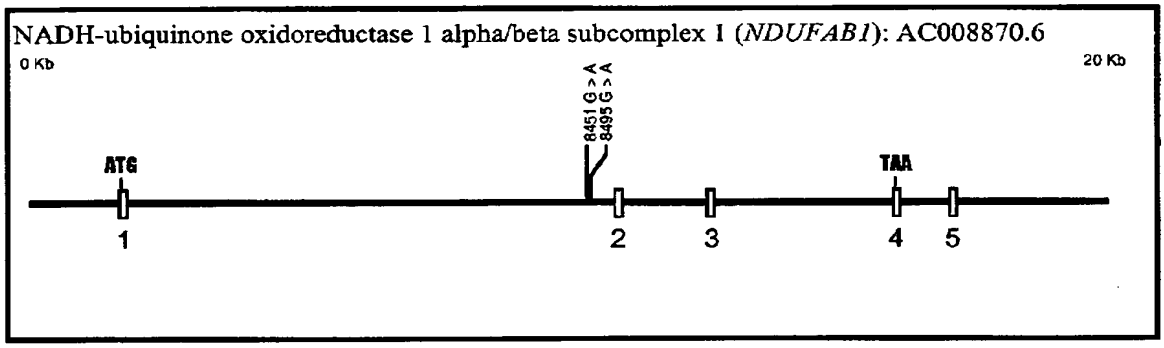
【図７４】



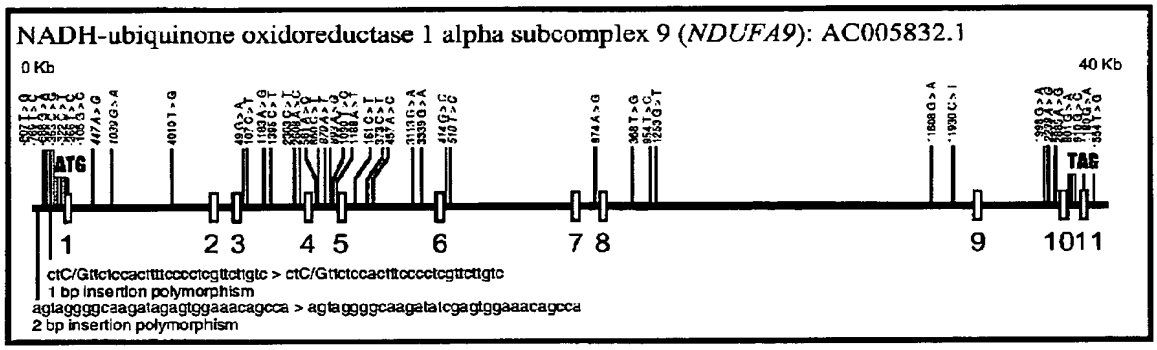
【図７５】



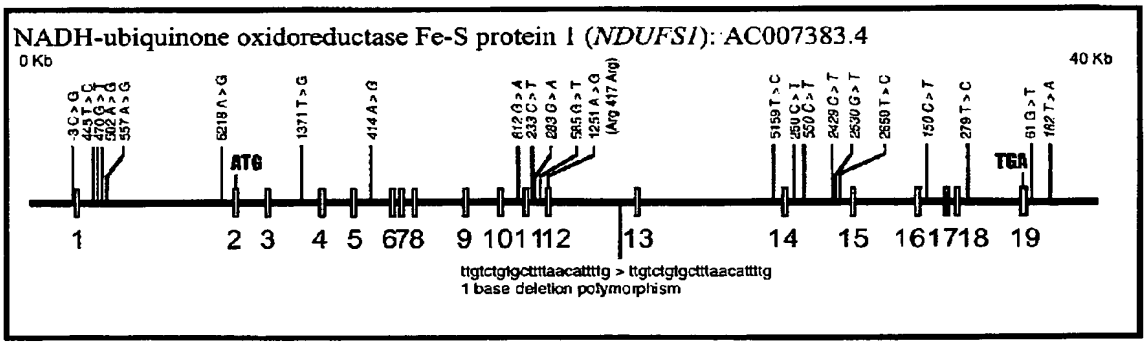
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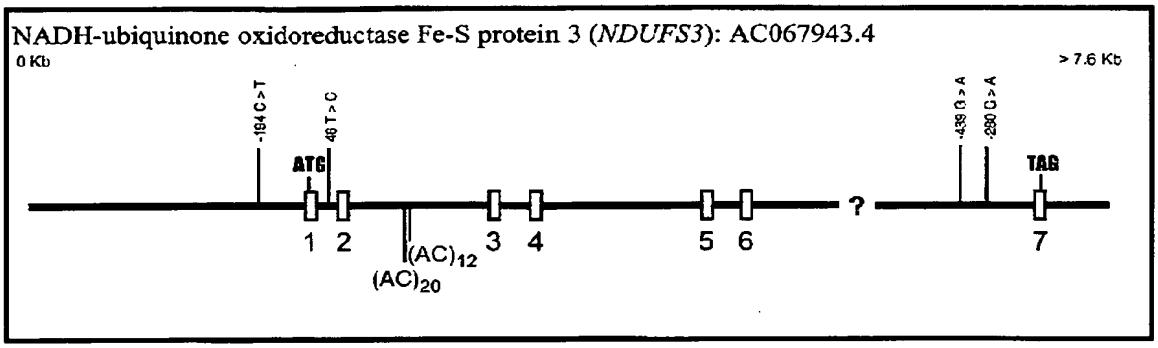
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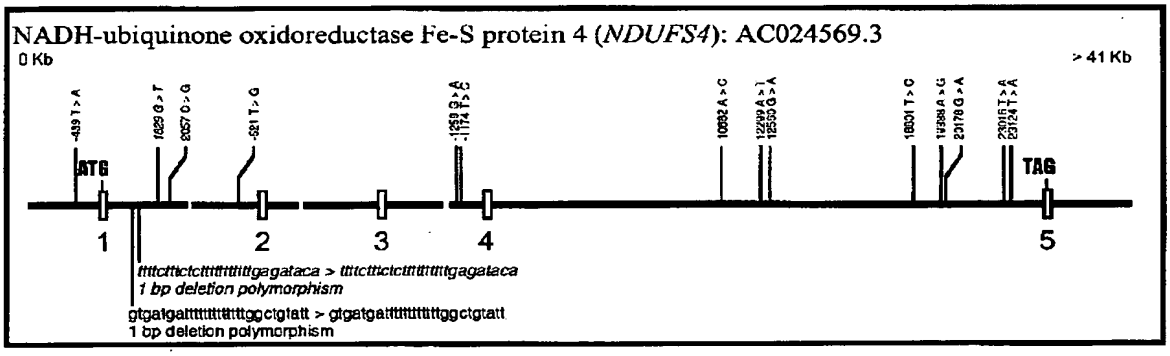
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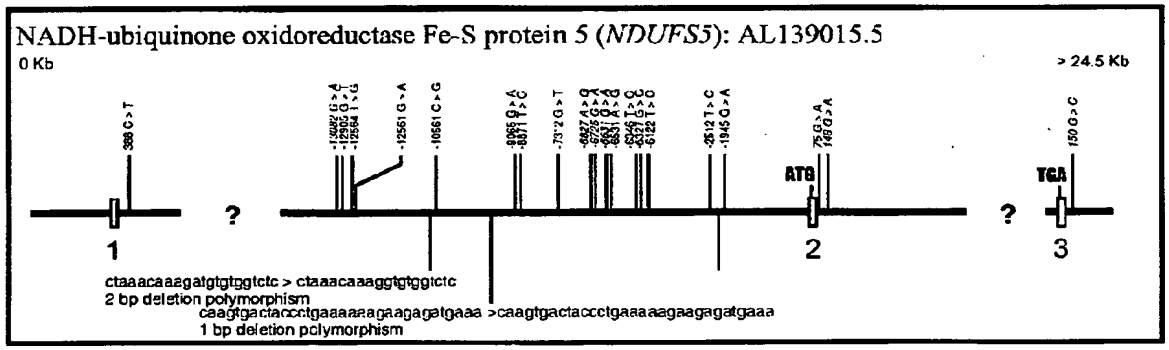
【図７９】



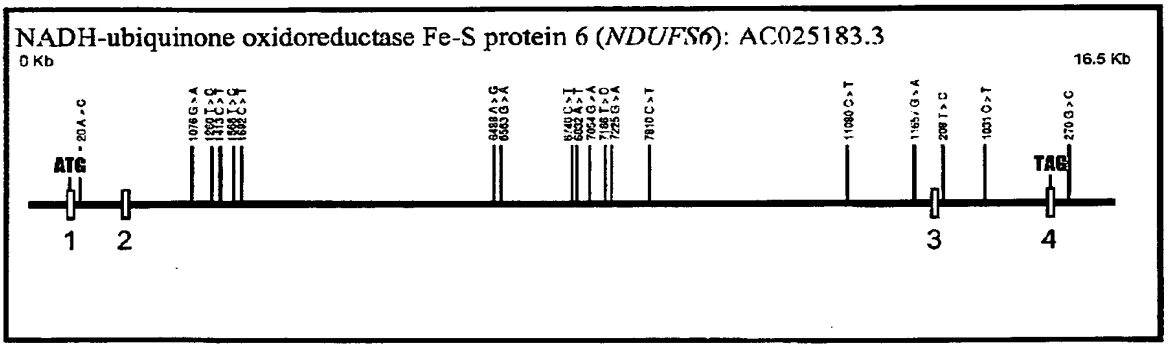
【図８０】



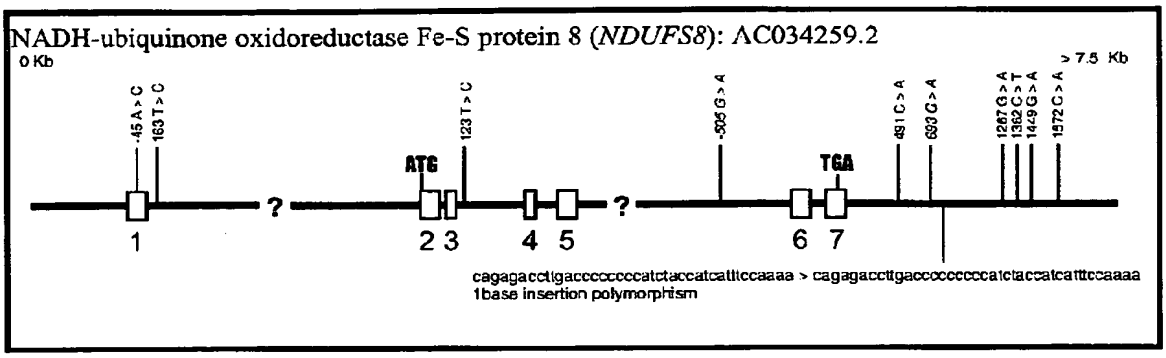
【図８１】



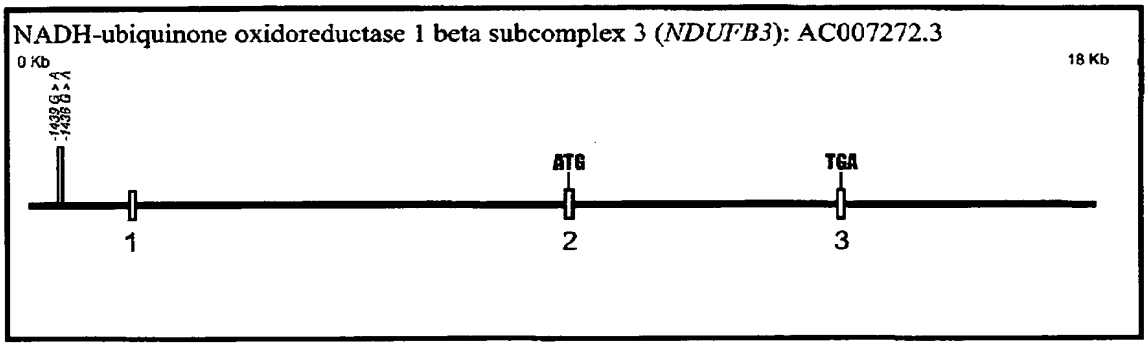
【図８２】



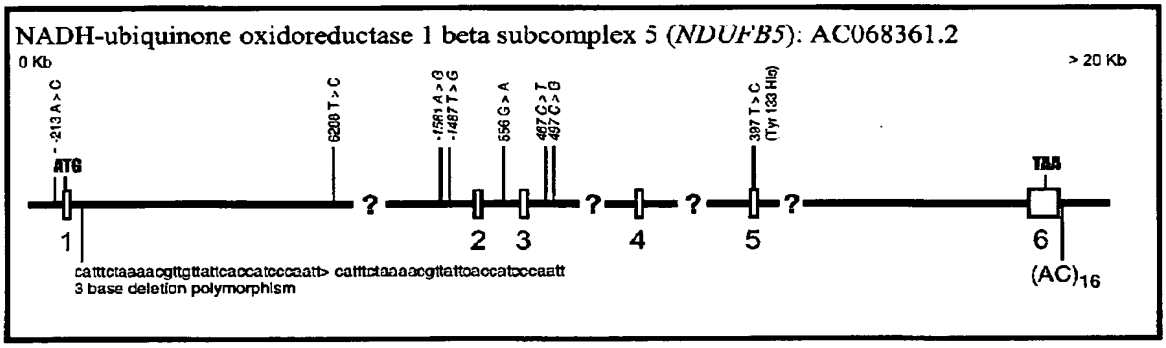
【図８３】



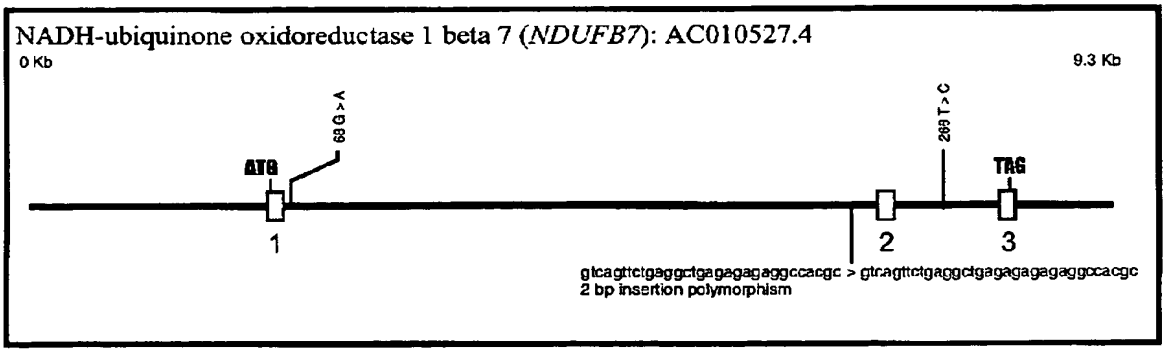
【図８４】



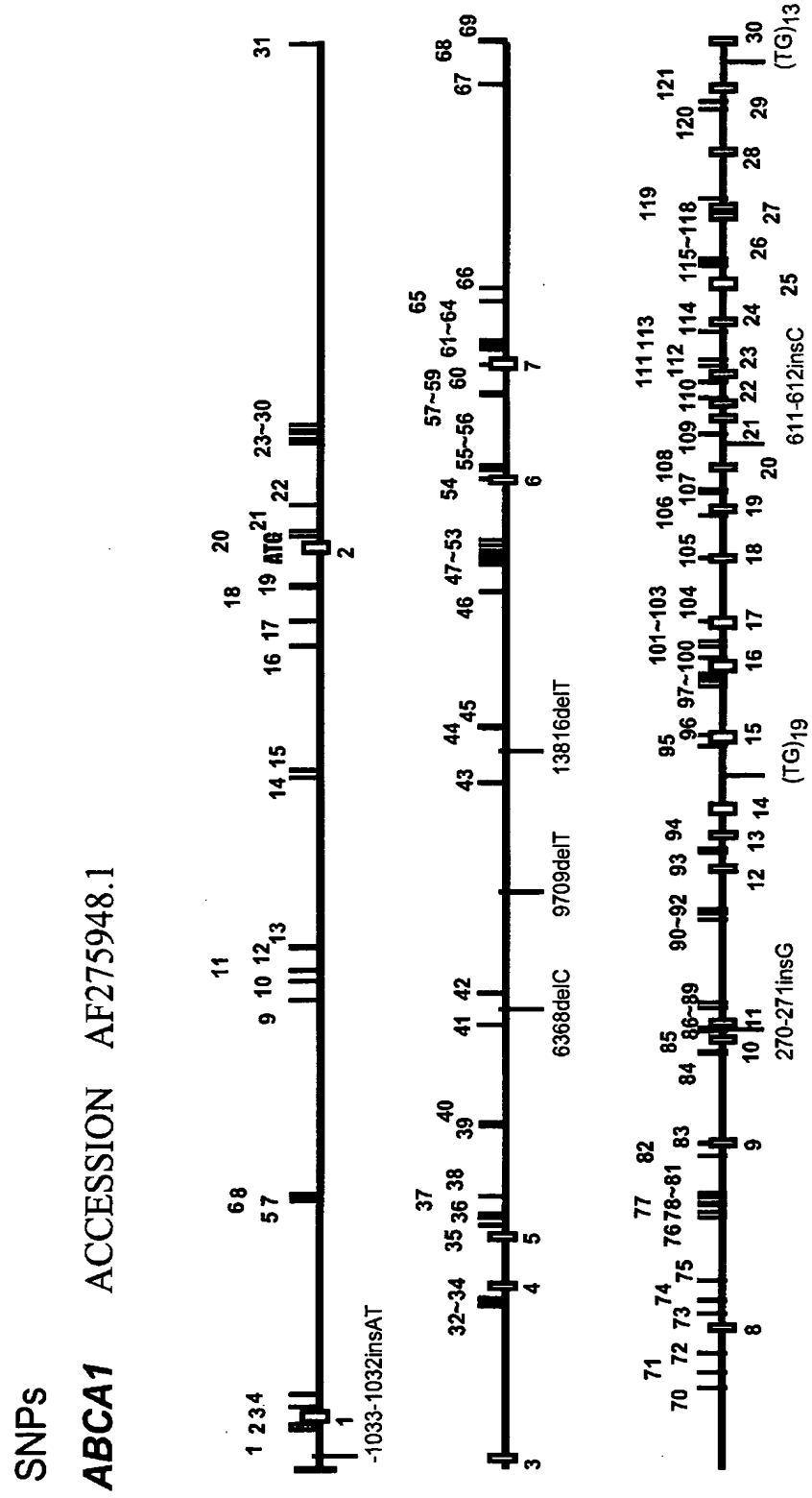
【図８５】



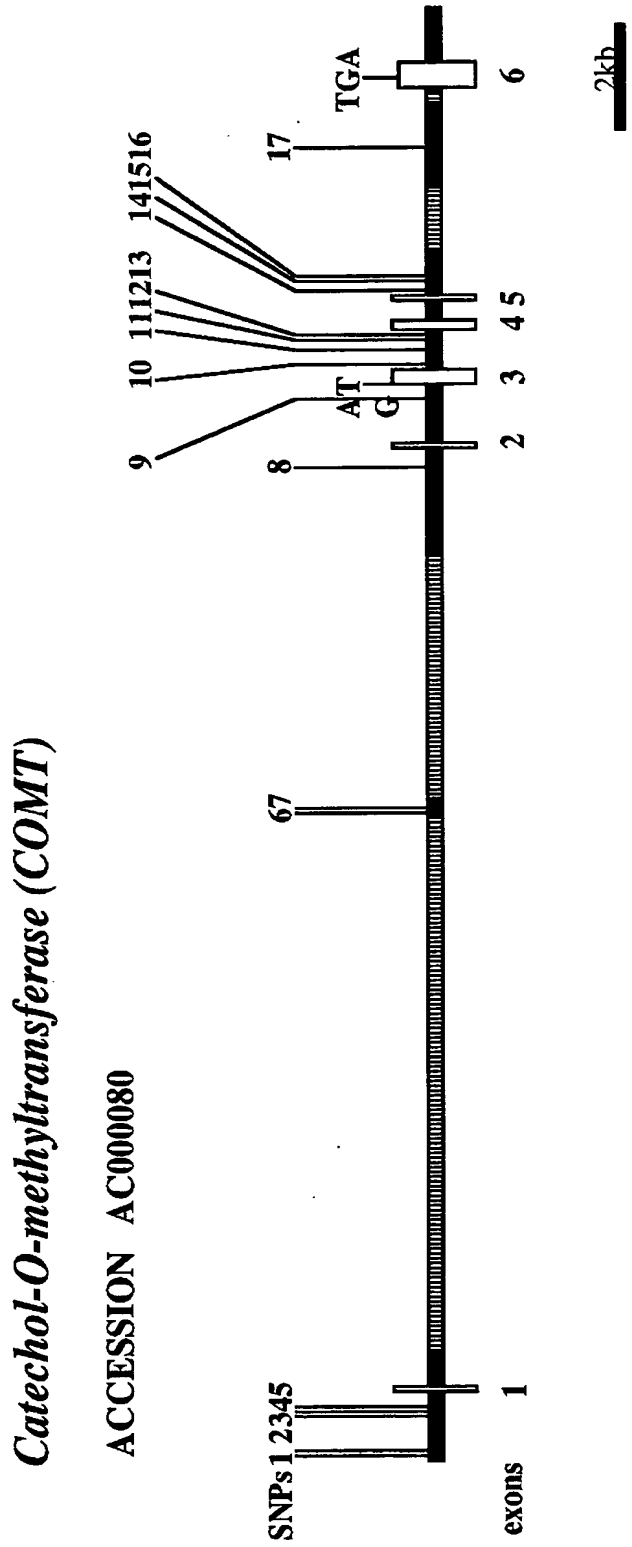
【図８６】



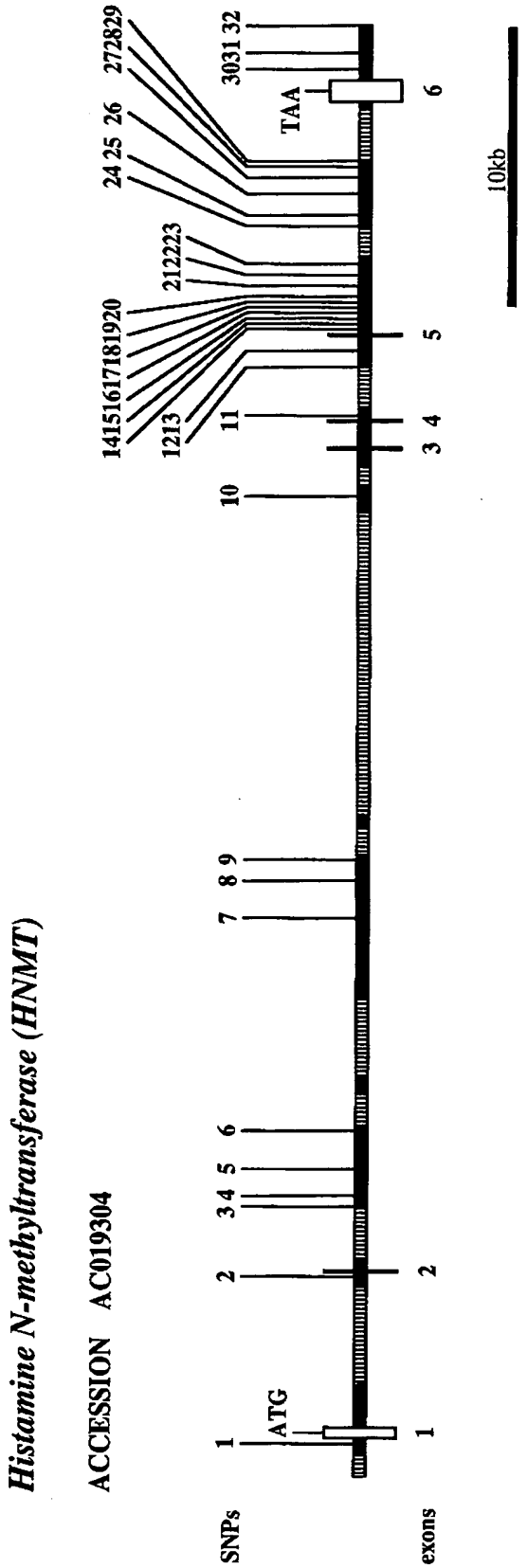
【図８７】


SNPs
ABCA1 ACCESSION AF275948.1
-1033-1032insAT
6368delC
9709delT
13816delT
270-271insG
(TG)19
611-612insC
(TG)13
391-392insT
847delC

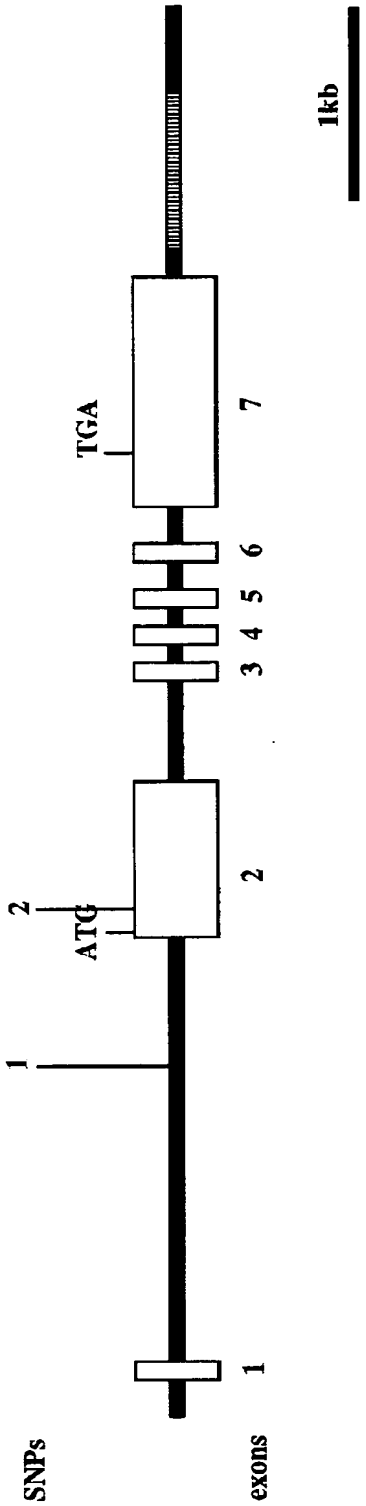
【図８８】


Catechol-O-methyltransferase (COMT)
ACCESSION AC000080
SNPs 1 2345
exons 1
67
8
9
10 111213 141516
17
A/T
G
2 3 4 5
TGA
6
2kb

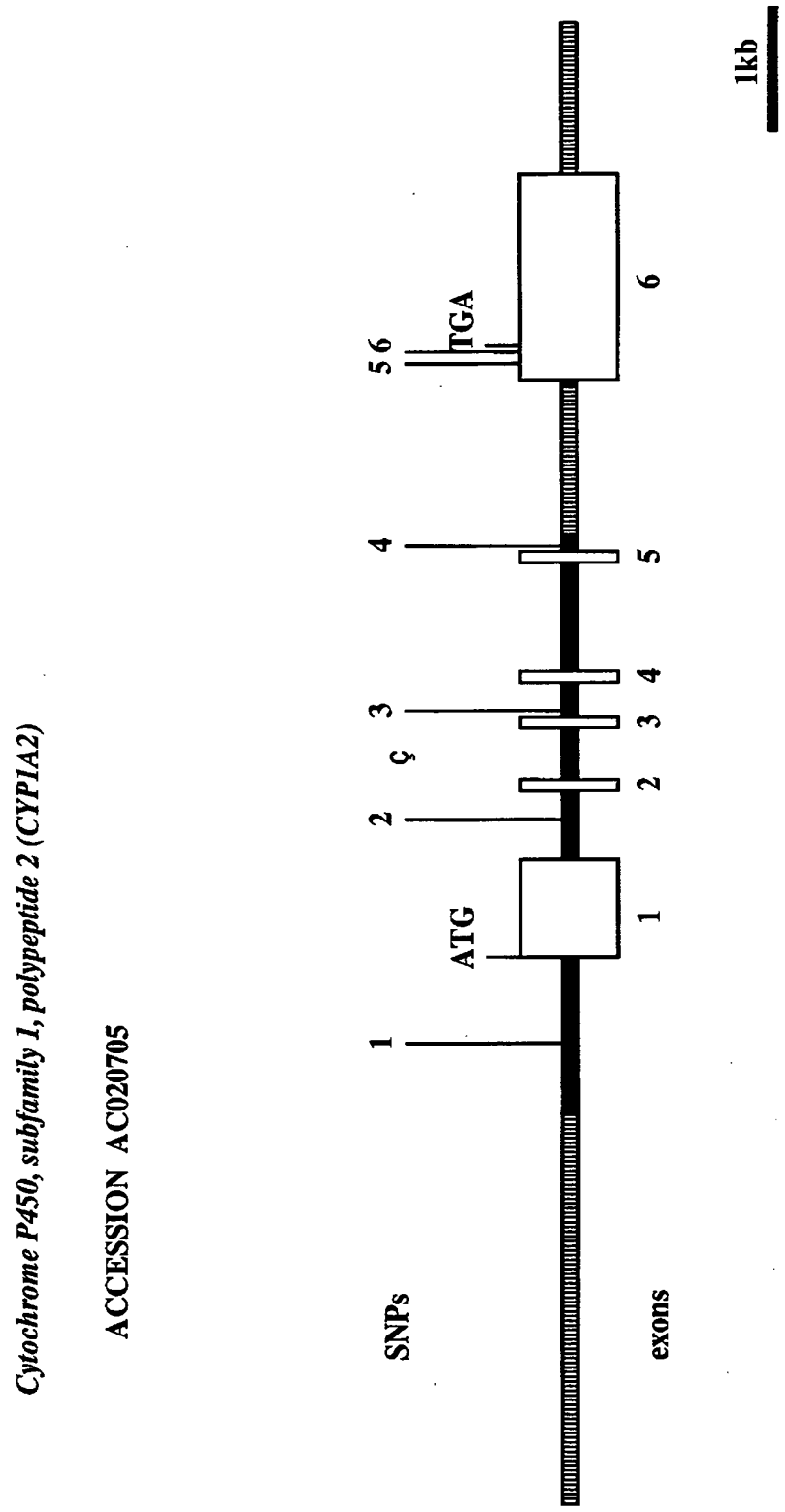
【図８９】


Histamine N-methyltransferase (HNMT)
ACCESSION AC019304
SNPs
exons
ATG
TAA
10kb
1
2
3 4 5
6
7 8 9
10
11
1213
14151617181920
212223
24 25 26
272829
3031 32
1
2
3 4
5
6

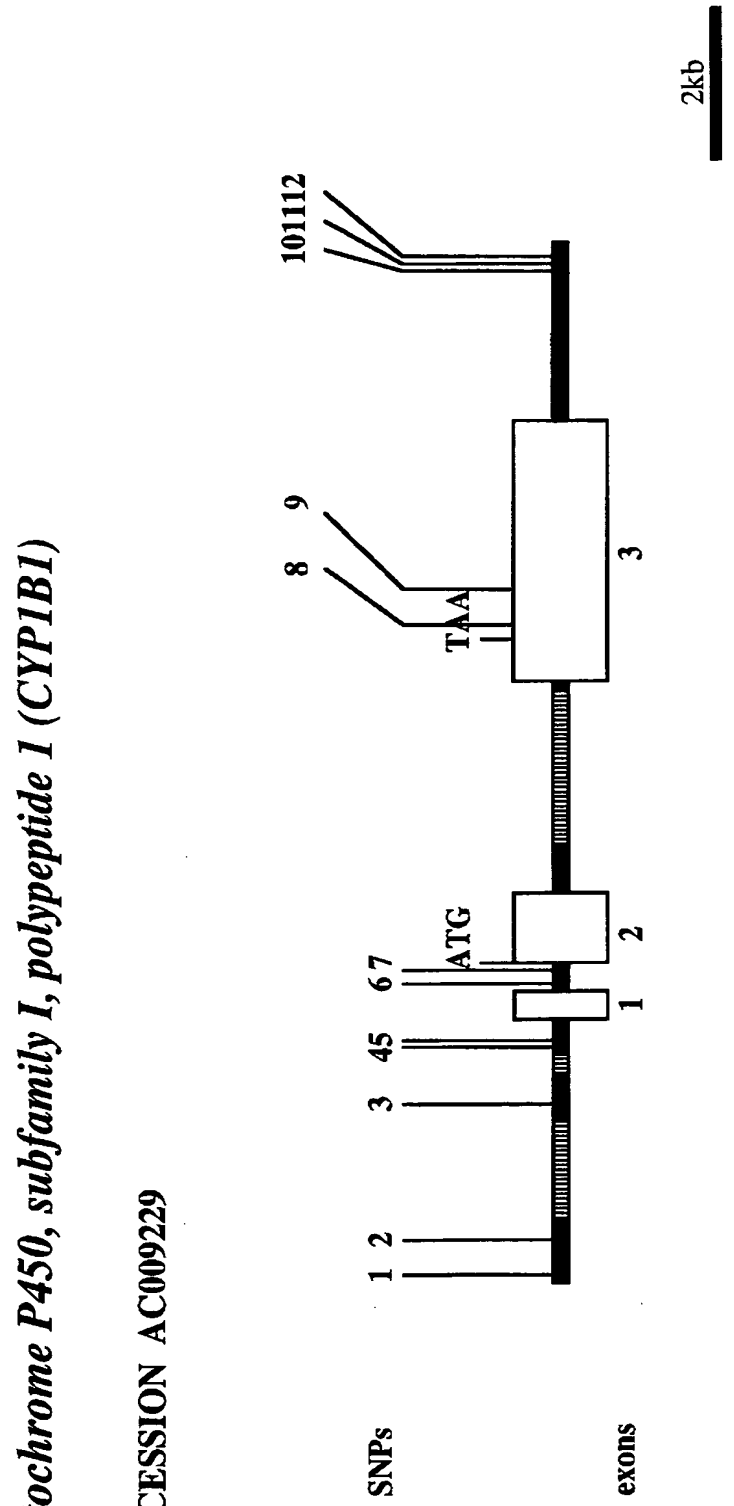
【図９０】


Cytochrome P450, subfamily I, polypeptide 1 (CYP1A1)
ACCESSION X04300
SNPs
exons
1
2
3
4
5
6
7
ATG
TGA
1kb

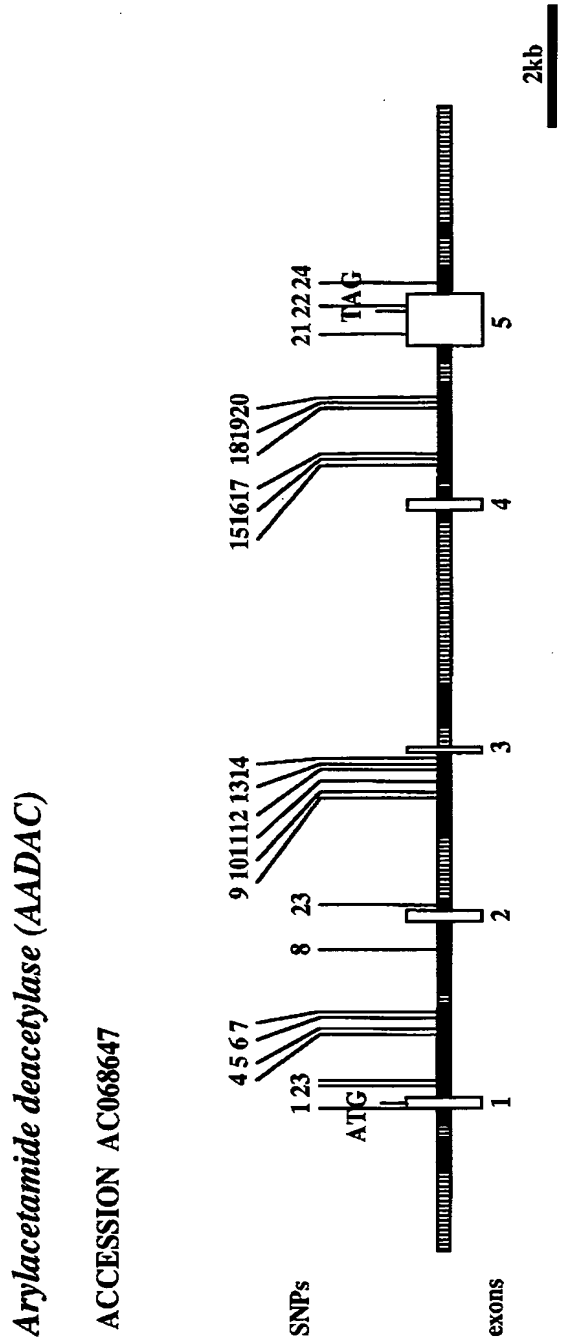
【図９１】


Cytochrome P450, subfamily 1, polypeptide 2 (CYP1A2)
ACCESSION AC020705
SNPs
exons
ATG
TGA
1kb
1
2
3
4
5
6
ç

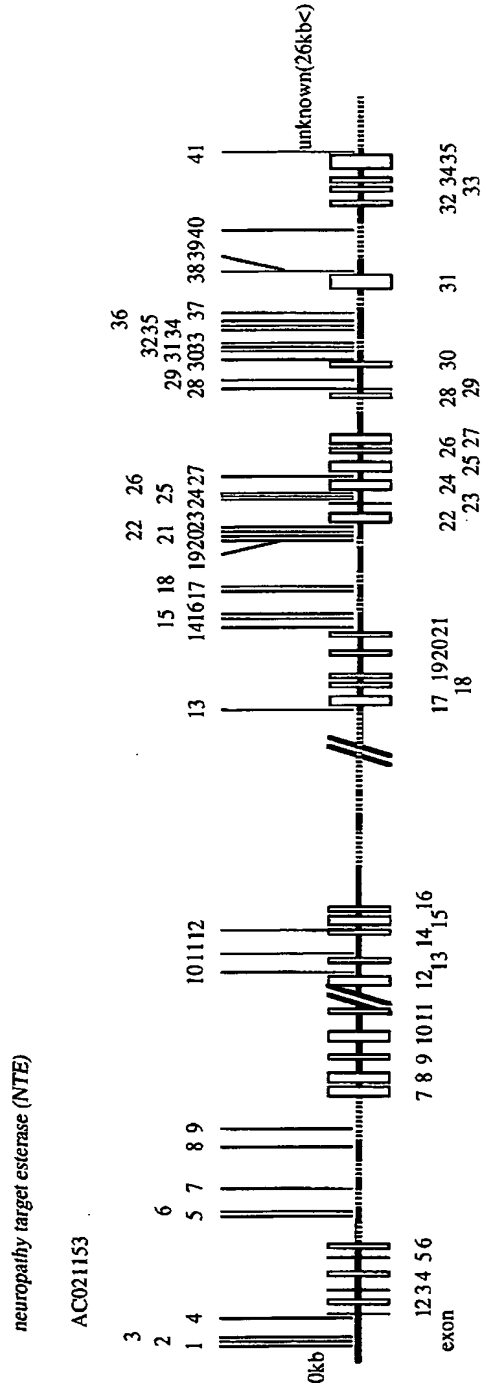
【図９２】


Cytochrome P450, subfamily I, polypeptide 1 (CYP1B1)
ACCESSION AC009229
SNPs
1 2
3
4 5
6 7
ATG
exons
1
2
3
TAA
8
9
101112
2kb

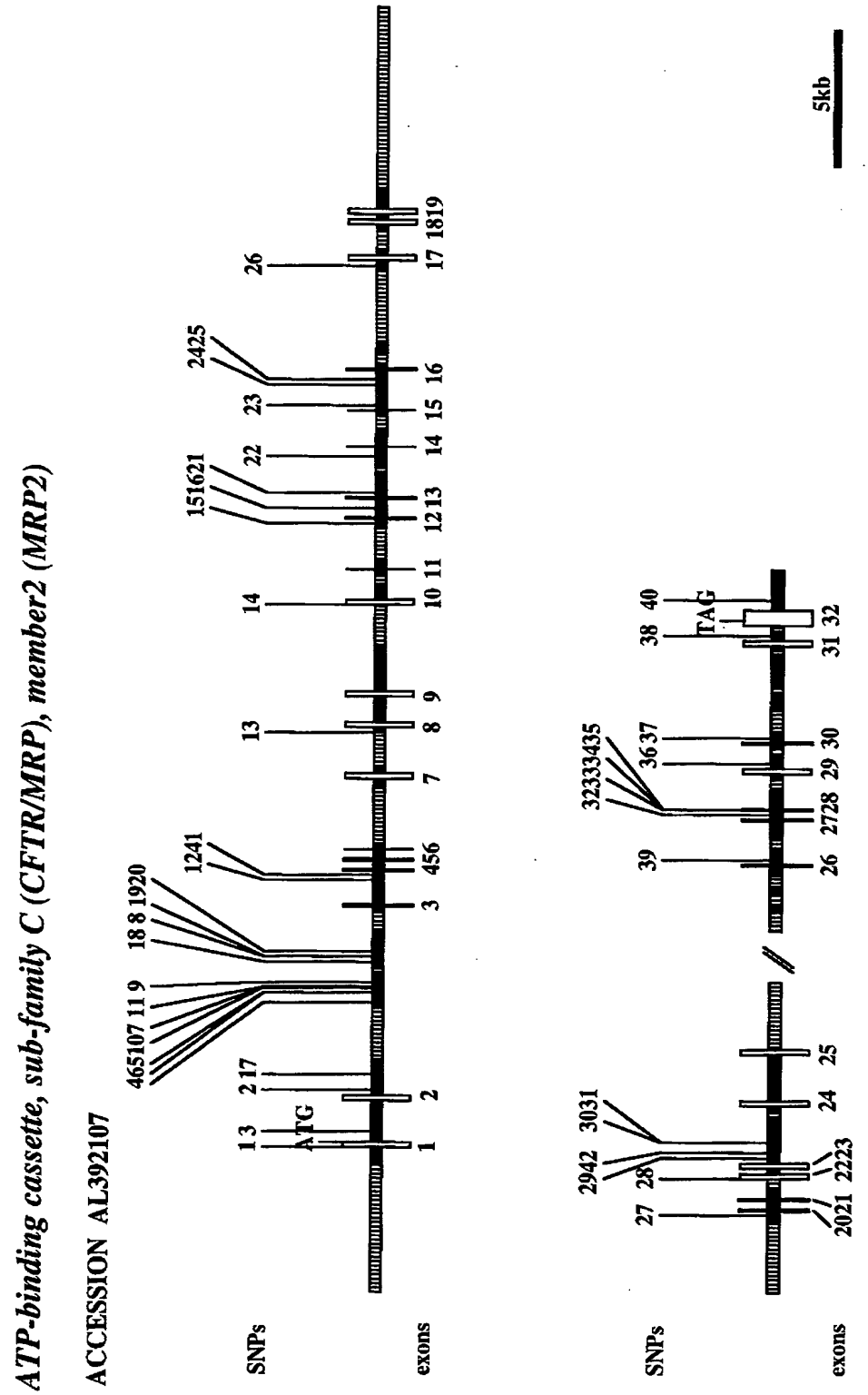
【図９３】


Arylacetamide deacetylase (AADAC)
ACCESSION AC068647
2kb
SNPs
exons
ATG
TAG
1 23
4 5 6 7
8
23
9 10 11 12 13 14
15 16 17
18 19 20
21 22 24
1
2
3
4
5

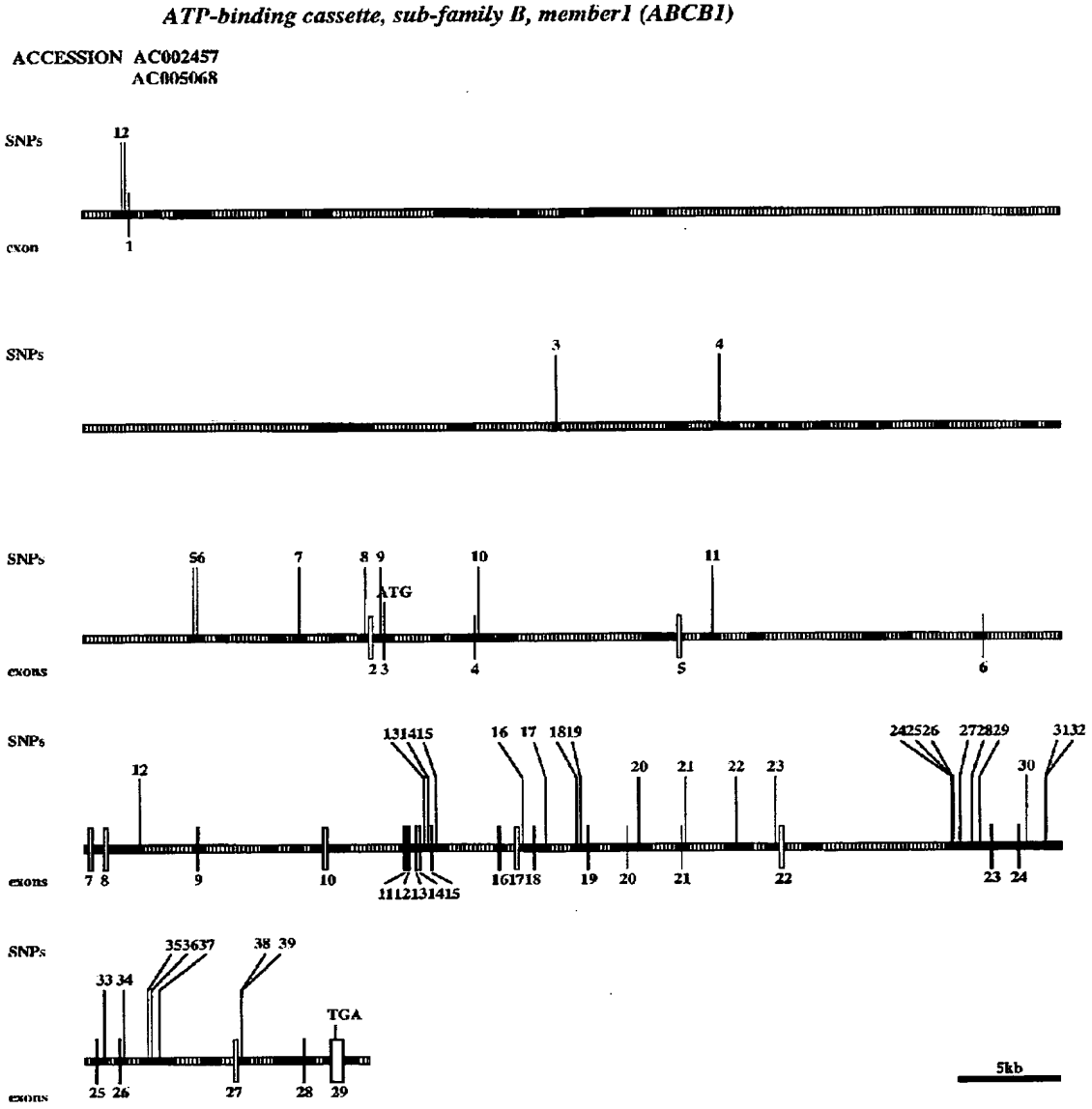
【図９４】


neuropathy target esterase (NTE)
AC021153
unknown(26kb<)
0kb
exon

【図９５】


ATP-binding cassette, sub-family C (CFTR/MRP), member2 (MRP2)
ACCESSION AL392107
5kb
SNPs
exons
ATG
TAG

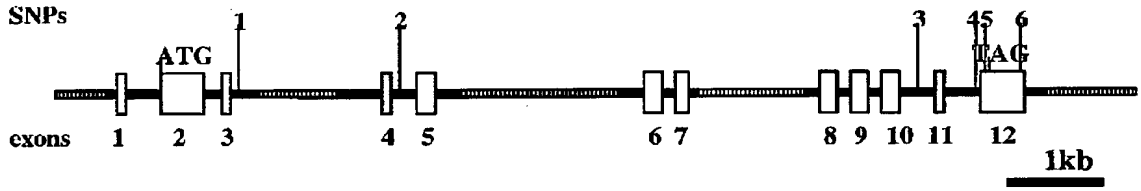
【図９６】


ATP-binding cassette, sub-family B, member1 (ABCB1)
ACCESSION AC002457
AC005068
SNPs
exon
ATG
TGA
5kb

【図９７】

ATP-binding cassette, sub-family B, member 3 (ABCB3)

ACCESSION X66401



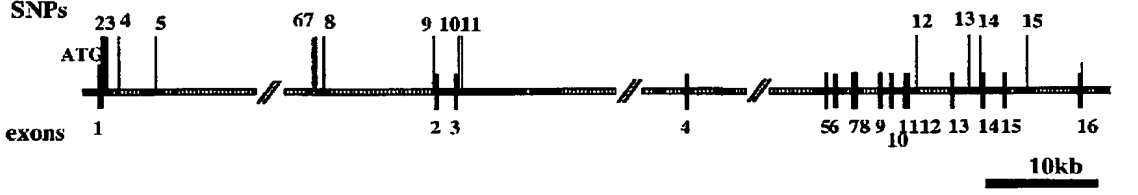
【図９８】

ATP-binding cassette, sub-family B, member 7 (ABCB7)

ACCESSION
AL360179

TAA

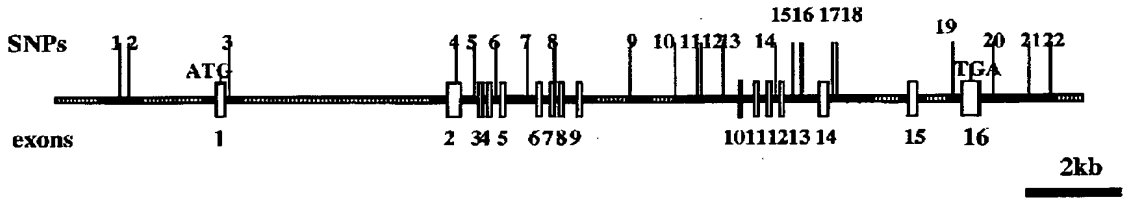
AC002417



【図９９】

ATP-binding cassette, sub-family B, member 8 (ABCB8)

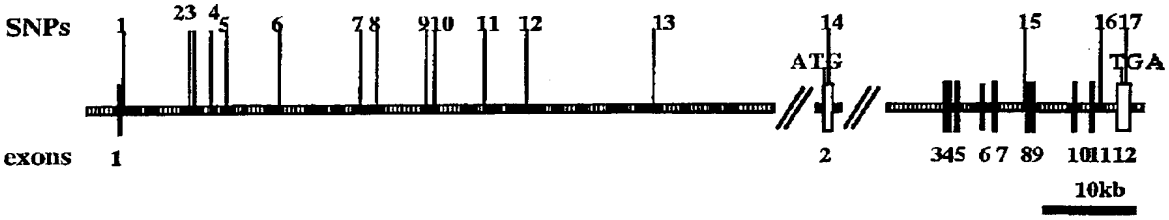
ACCESSION AC010973



【図１００】

ATP binding cassette, sub-family B, member 9 (ABCB9)

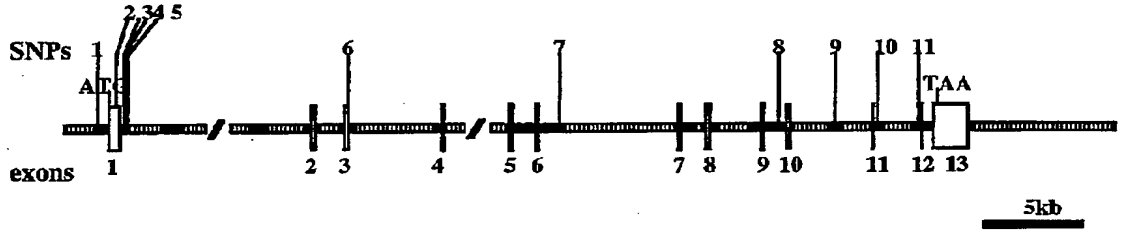
ACCESSION AC026362



【図１０１】

ATP binding cassette, sub-family B, member 10 (ABCB10)

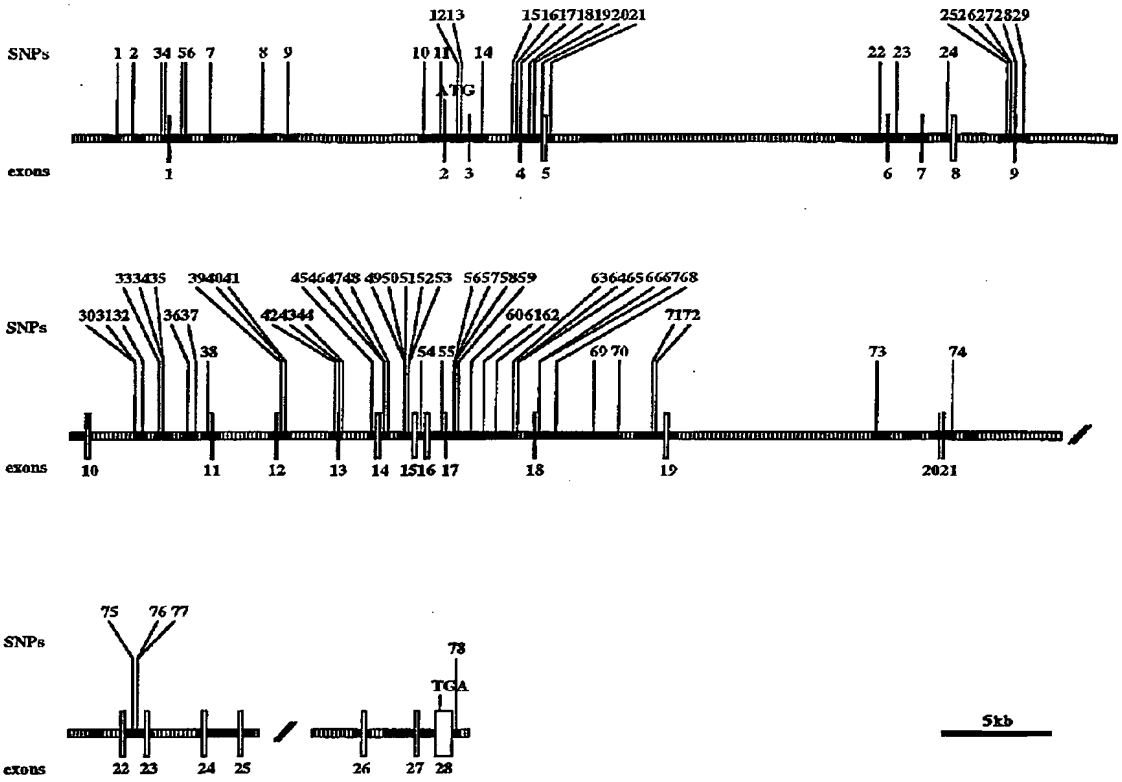
ACCESSION AL121990



【図１０２】

ATP-binding cassette, sub-family B, member 11 (ABCB11)

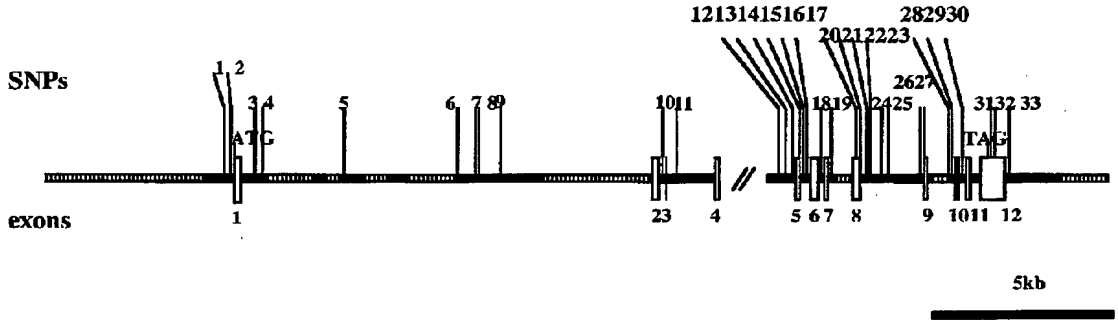
ACCESSION AC008177
AC069137



【図１０３】

Cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1)

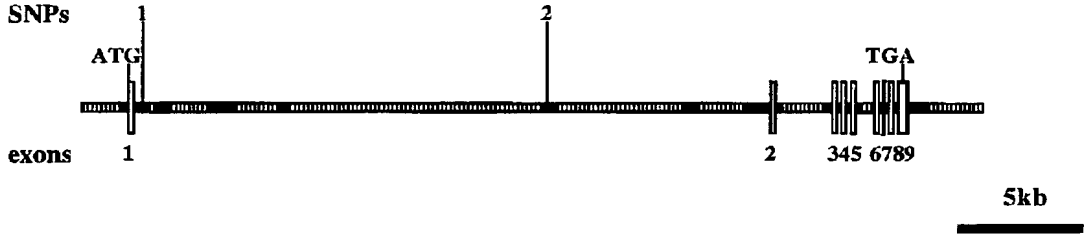
ACCESSION AL356793



【図１０４】

Cytochrome P450, subfamily XXVIIA, polypeptide 1 (CYP27A1)

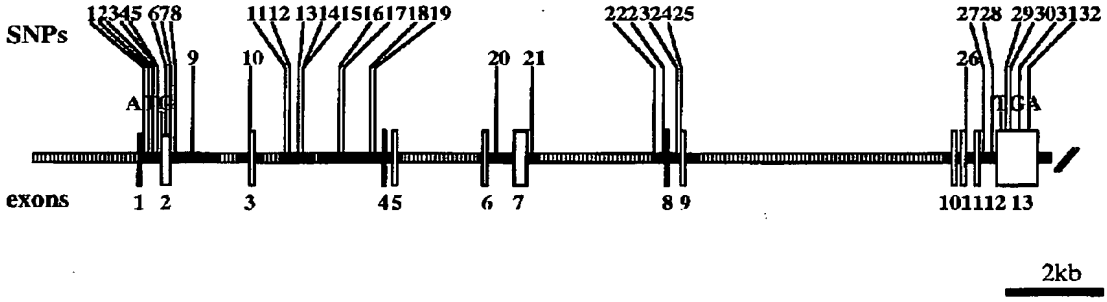
ACCESSION AC009974



【図１０５】

Cytochrome P450, subfamily IVF, polypeptide 2 (CYP4F2)

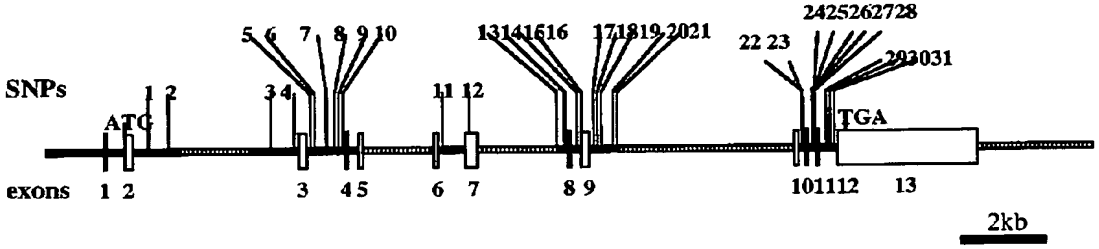
ACCESSION AC005336



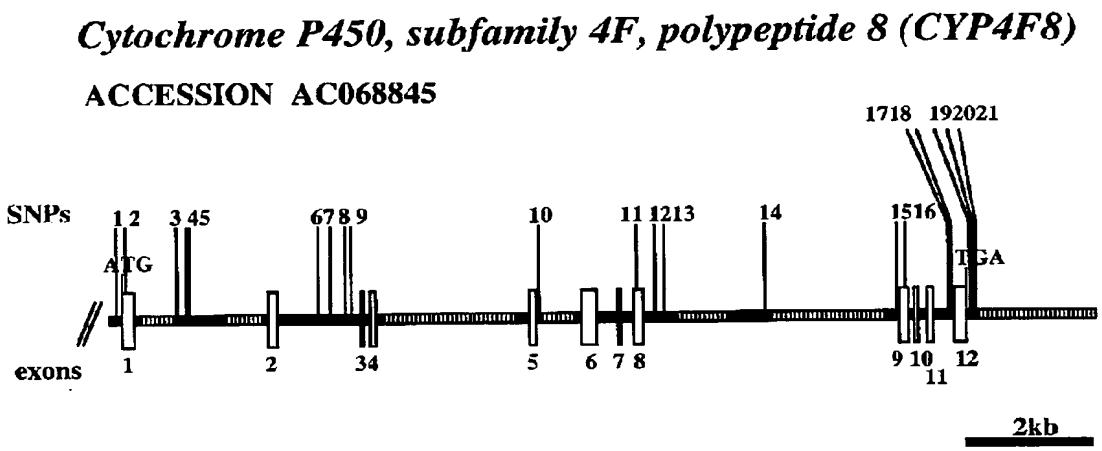
【図１０６】

Cytochrome P450, subfamily 4F, polypeptide 3 (CYP4F3)

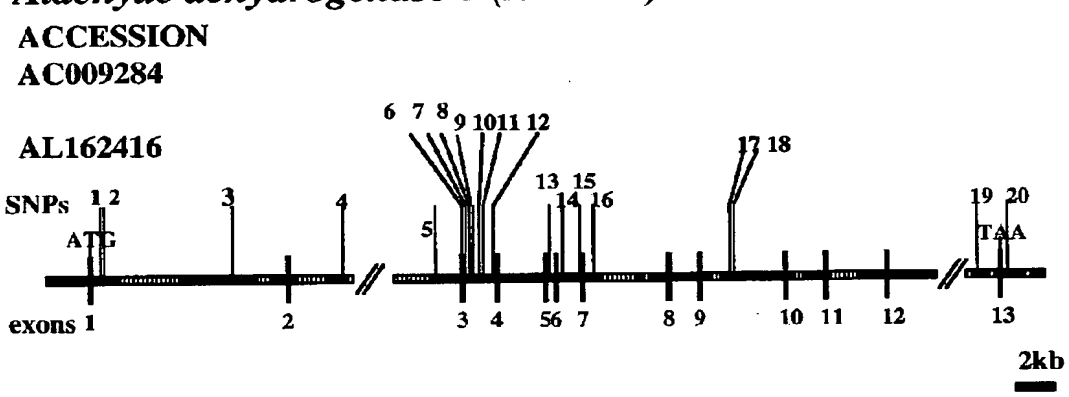
ACCESSION AD000685



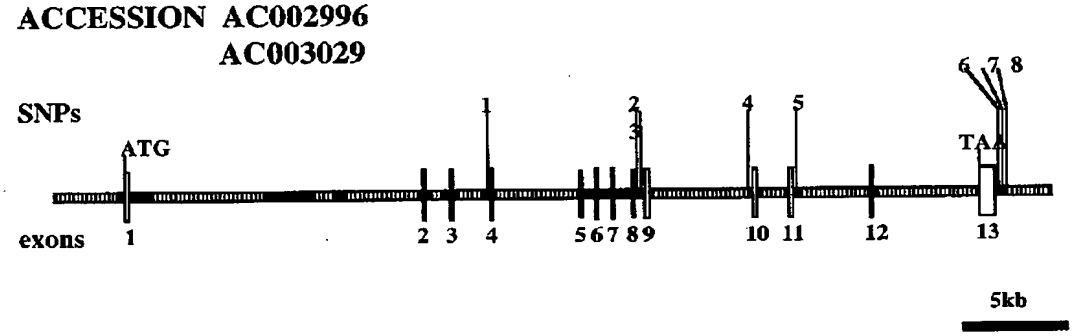
【図１０７】



【図１０８】



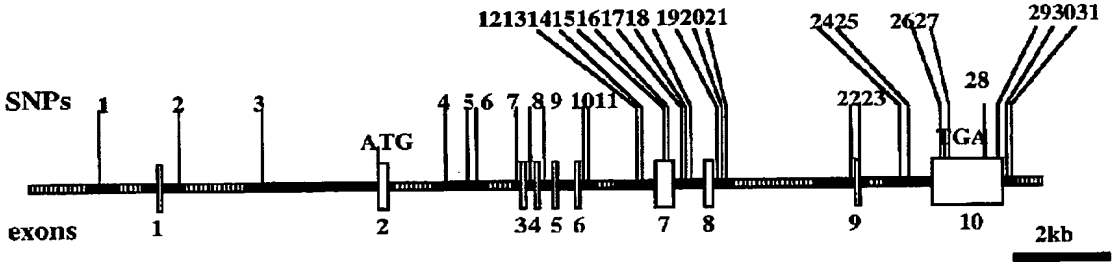
【図１０９】



【図１１０】

Aldehyde dehydrogenase 7 (ALDH7)

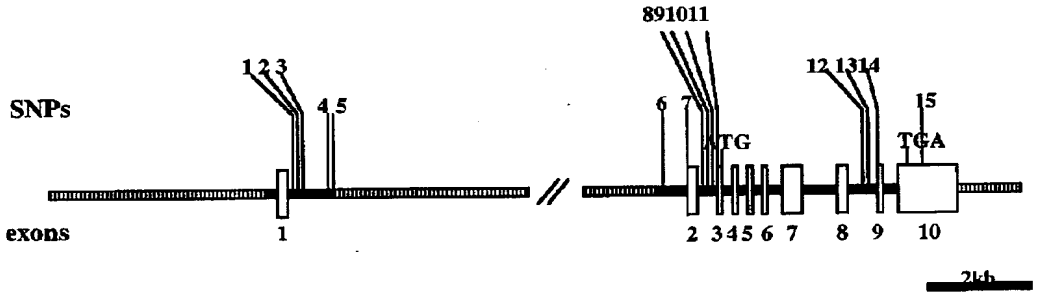
ACCESSION AC004923



【図１１１】

Aldehyde dehydrogenase 8 (ALDH8)

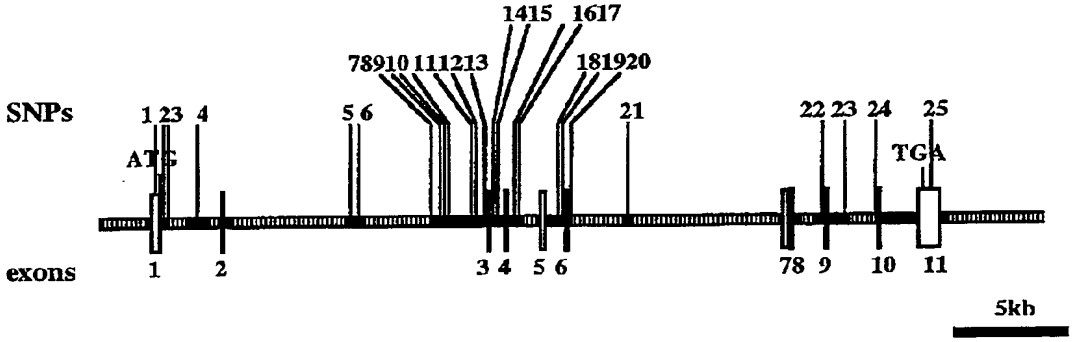
ACCESSION AC021987



【図１１２】

Aldehyde dehydrogenase 9 (ALDH9)

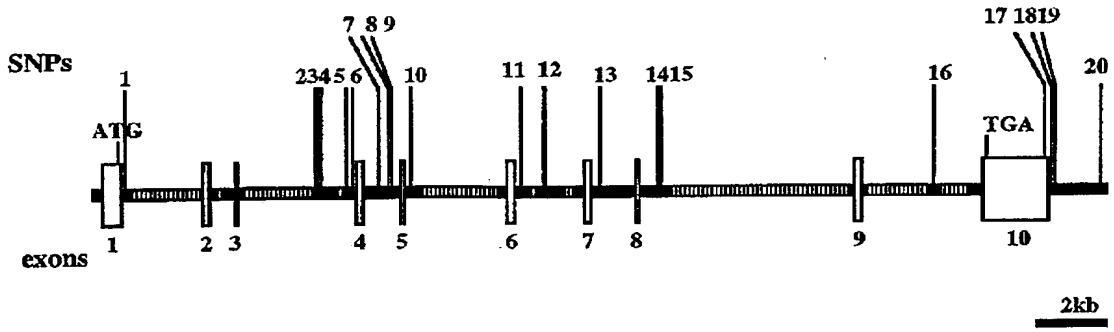
ACCESSION AL451074



【図１１３】

Aldehyde dehydrogenase 10 (ALDH10)

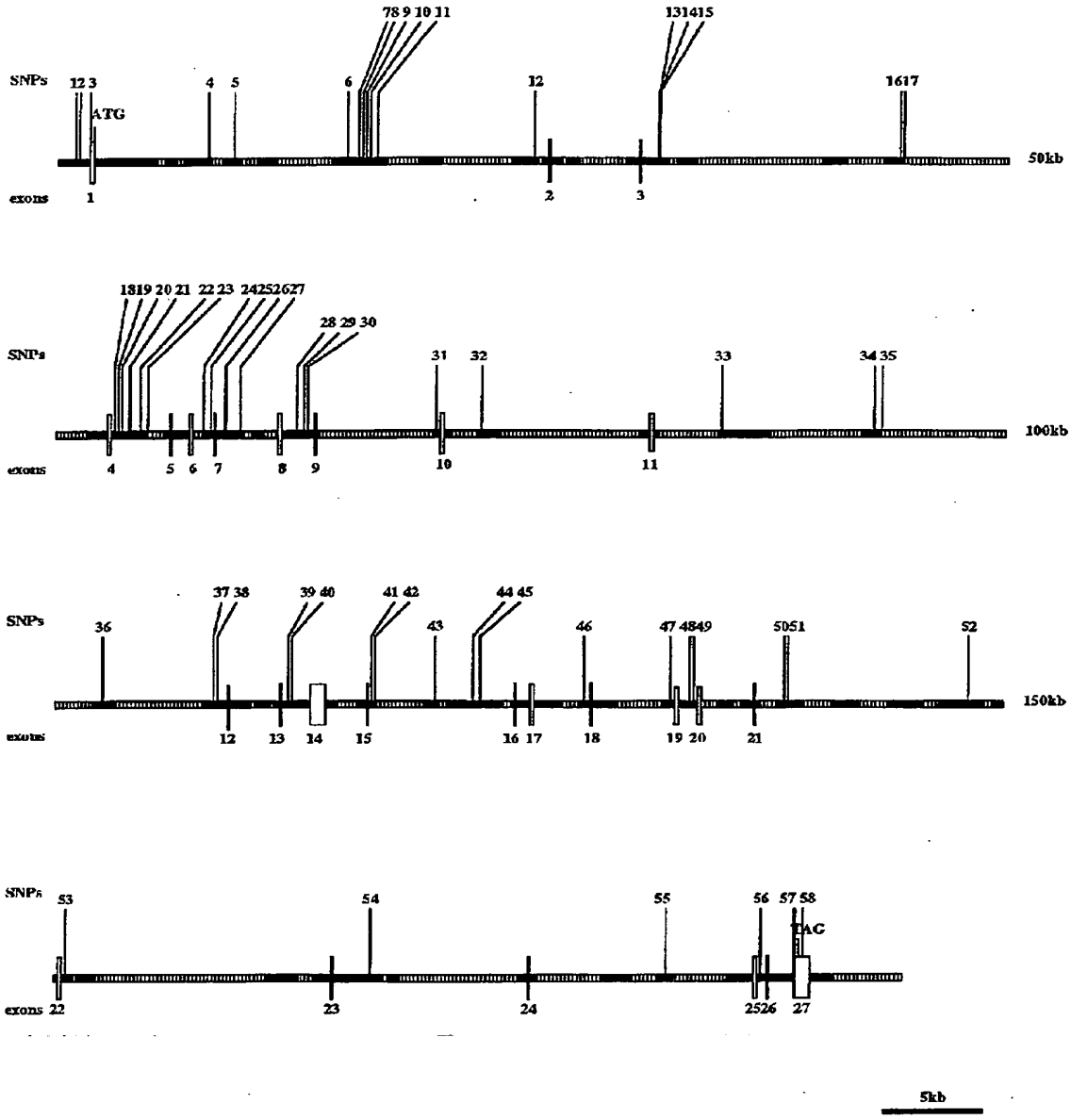
ACCESSION AC005722



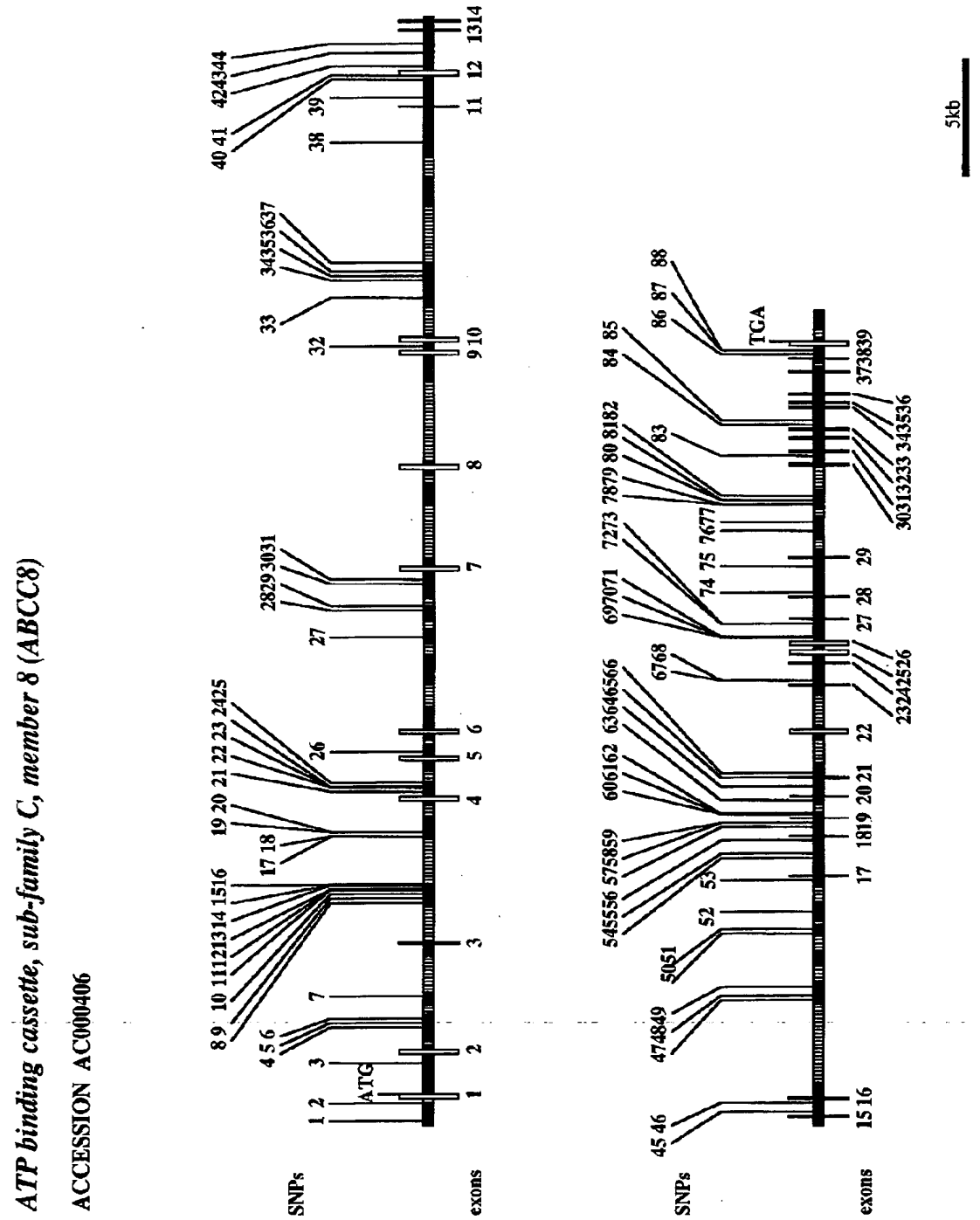
【図１１４】

ATP binding cassette, sub-family C, member 7 (ABCC7)

ACCESSION AC000111
AC000061



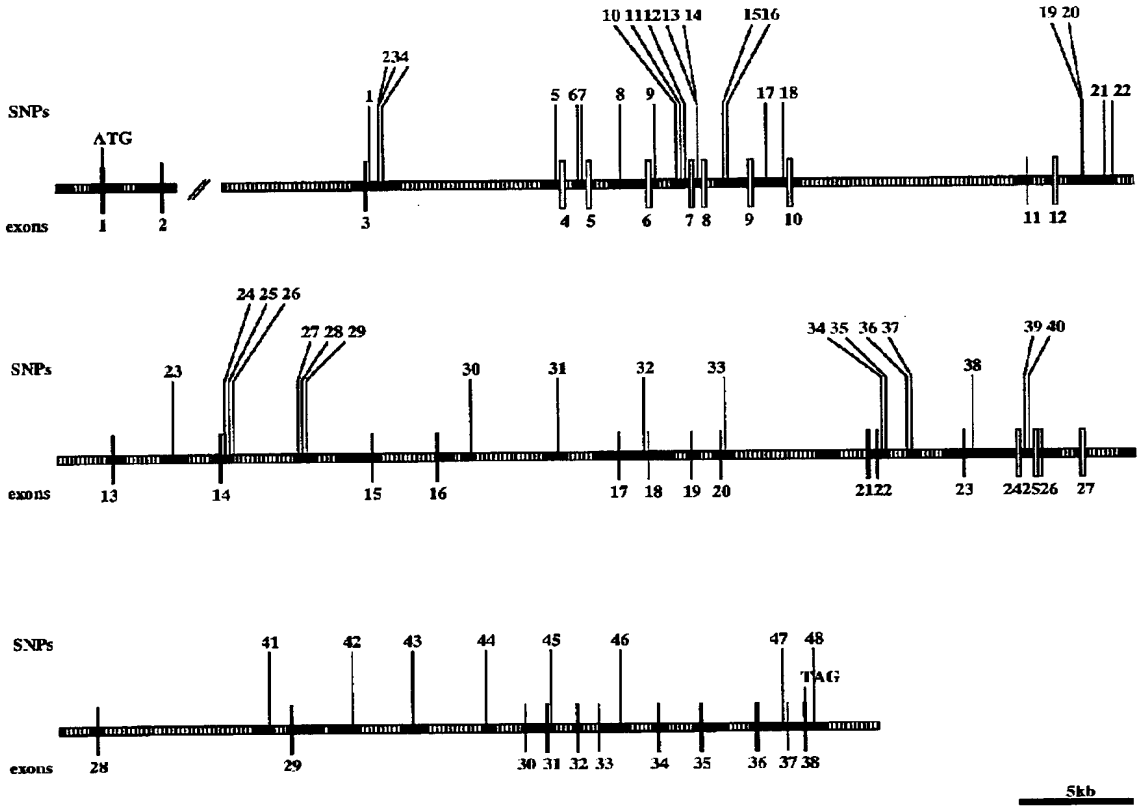
【図１１５】


ATP binding cassette, sub-family C, member 8 (ABCC8)
ACCESSION AC000406
ATG
TGA
SNPs
exons
5kb

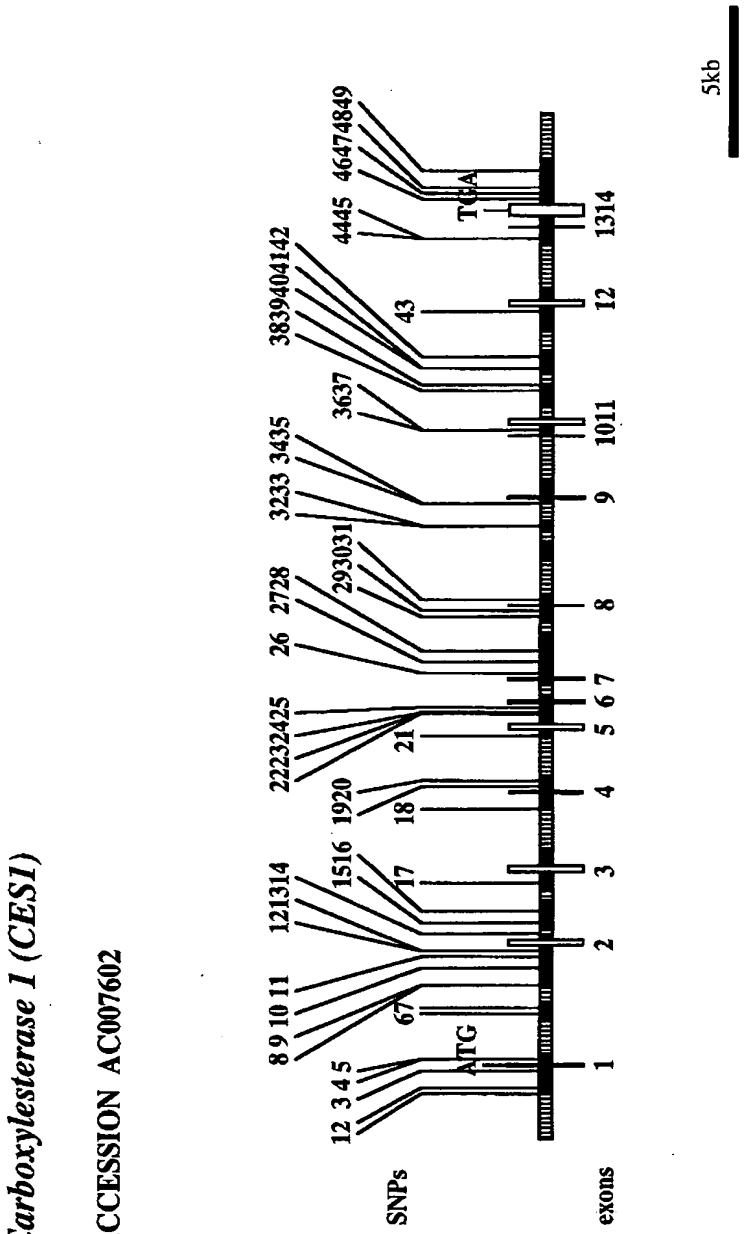
【図１１６】

ATP binding cassette, sub-family C, member 9 (ABCC9)

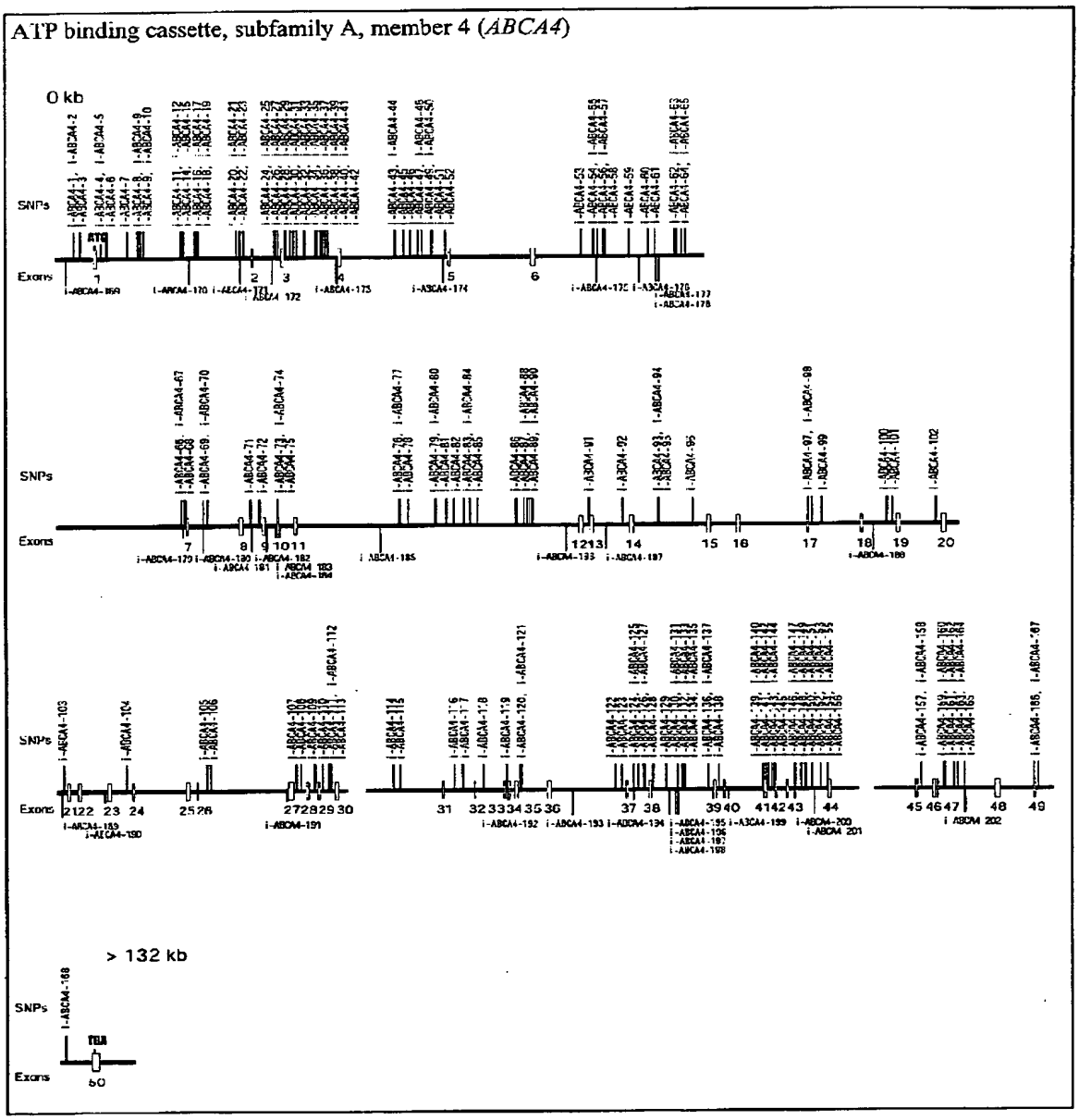
ACCESSION AC084806
AC008250



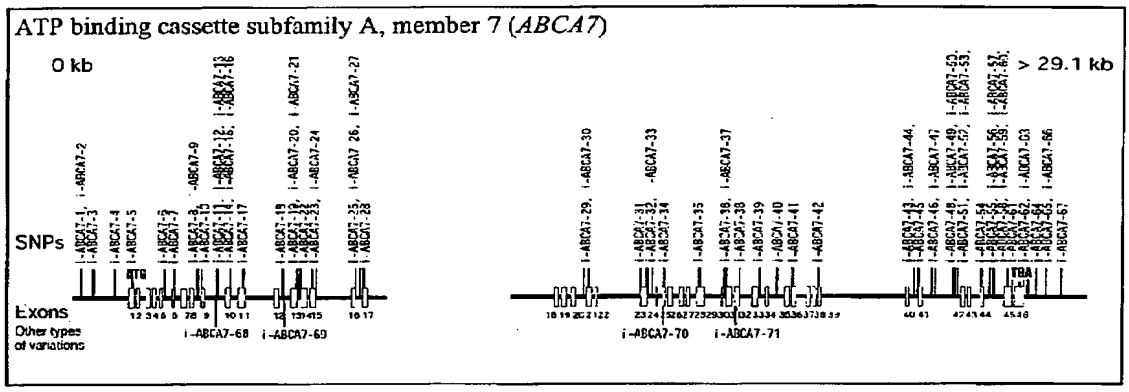
【図１１７】


Carboxylesterase 1 (CES1)
ACCESSION AC007602
5kb
SNPs
exons
ATG
TGA
12 3 4 5
8 9 10 11
67
121314
1516
17
1920
18
2223242 5
21
26
2728
293031
3233 3435
3637
383940 4142
43
4445
46474849
1
2
3
4
5 6 7
8
9
1011
12
1314

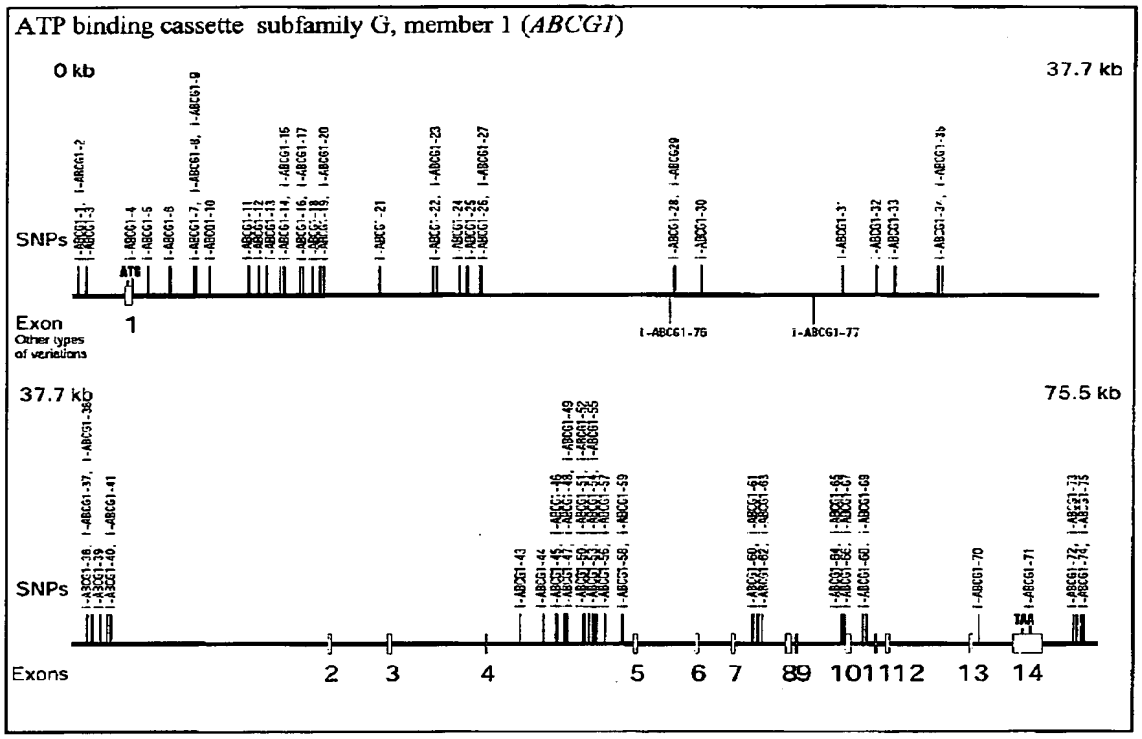
【図１１８】


ATP binding cassette, subfamily A, member 4 (ABCA4)
0 kb
SNPs
Exons
> 132 kb

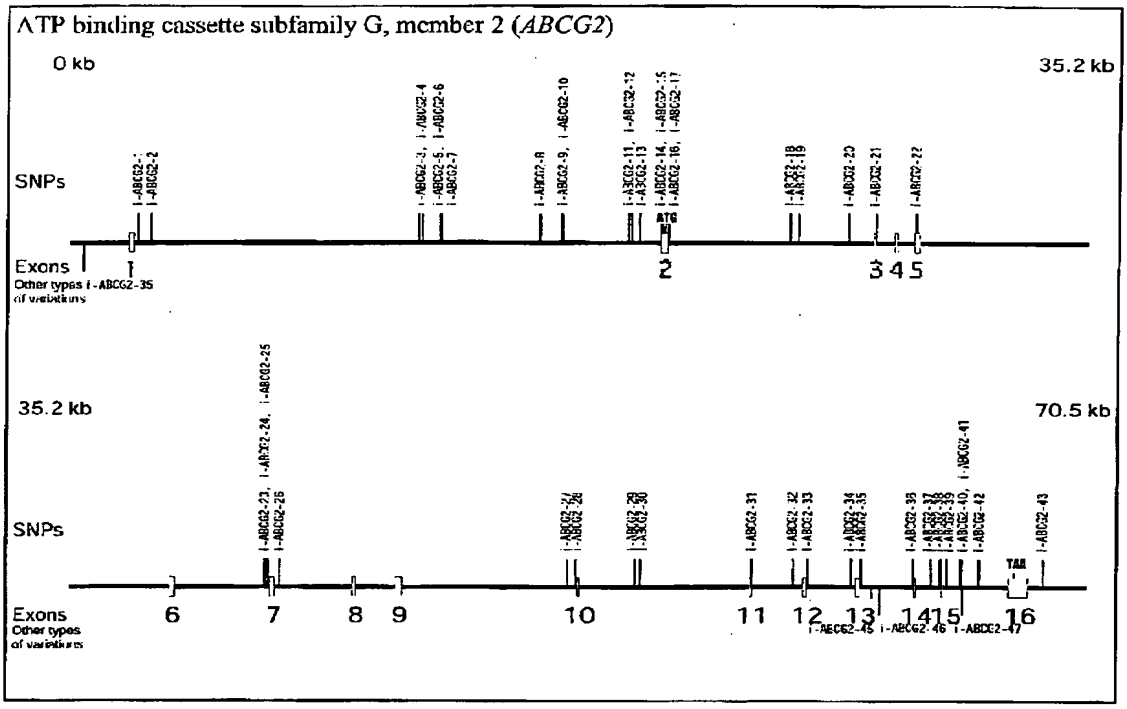
【図１１９】


ATP binding cassette subfamily A, member 7 (ABCA7)
0 kb
> 29.1 kb
SNPs
Exons
Other types of variations
i-ABCA7-68
i-ABCA7-69
i-ABCA7-70
i-ABCA7-71

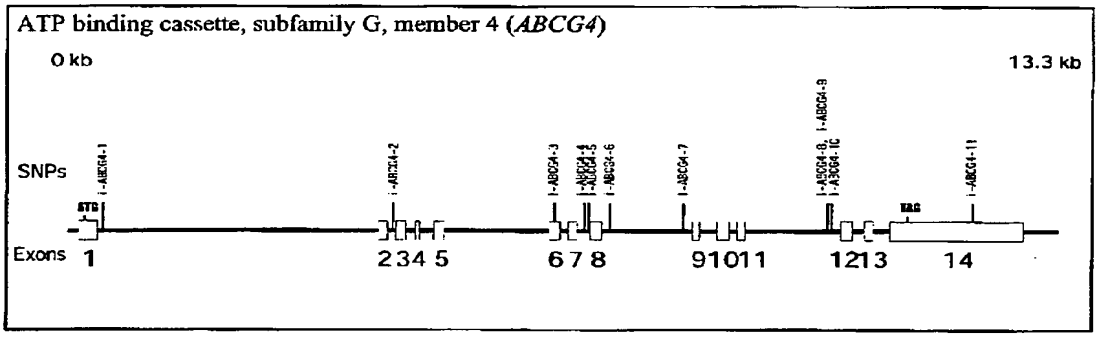
【図１２０】


ATP binding cassette subfamily G, member 1 (ABCG1)
0 kb
37.7 kb
SNPs
Exon
Other types of variations
i-ABCG1-76
i-ABCG1-77
37.7 kb
75.5 kb
SNPs
Exons
2 3 4 5 6 7 89 101112 13 14

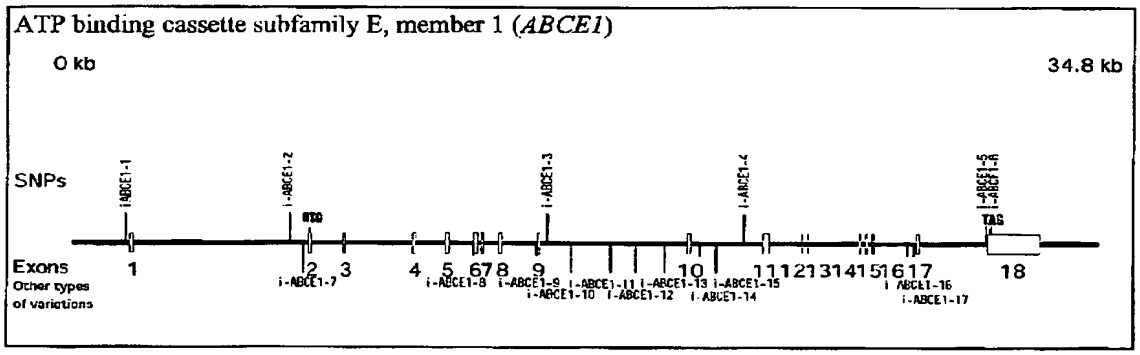
【図１２１】



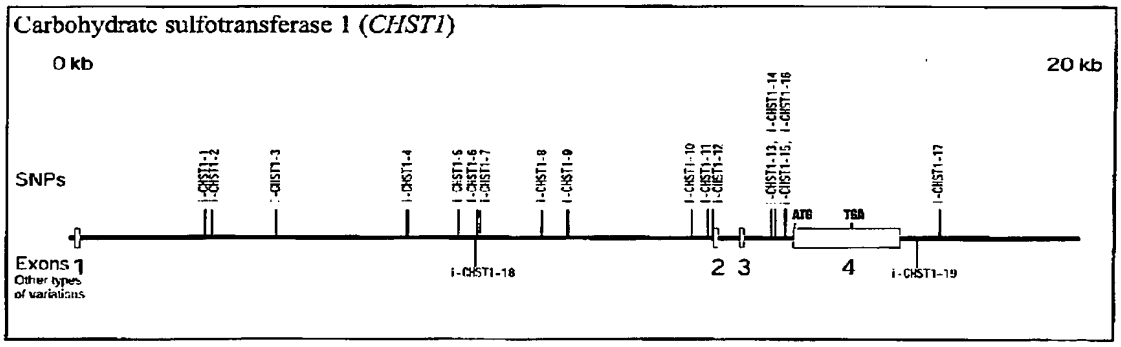
【図１２２】



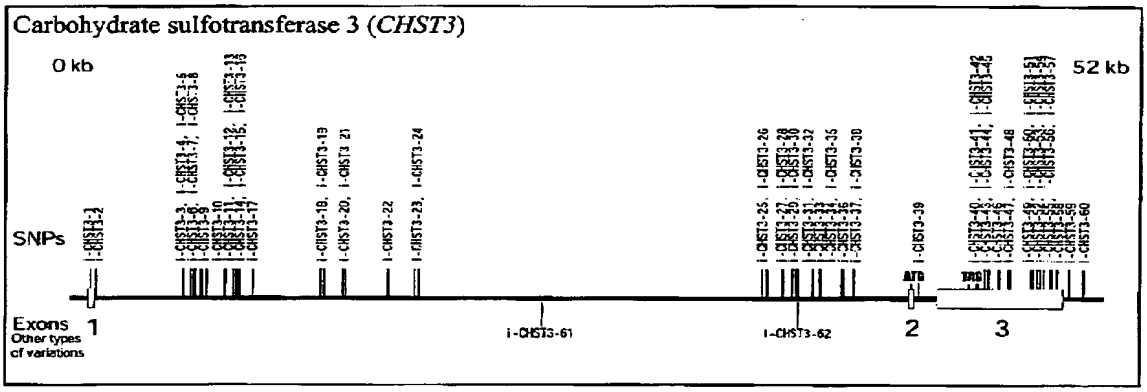
【図１２３】



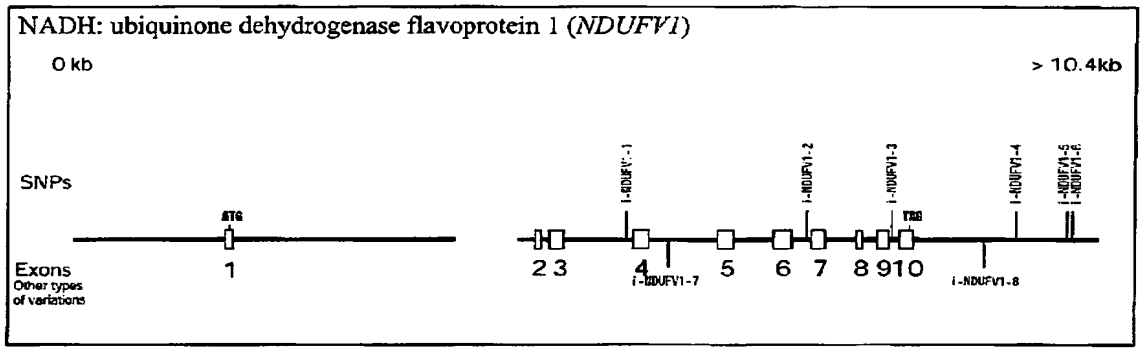
【図１２４】



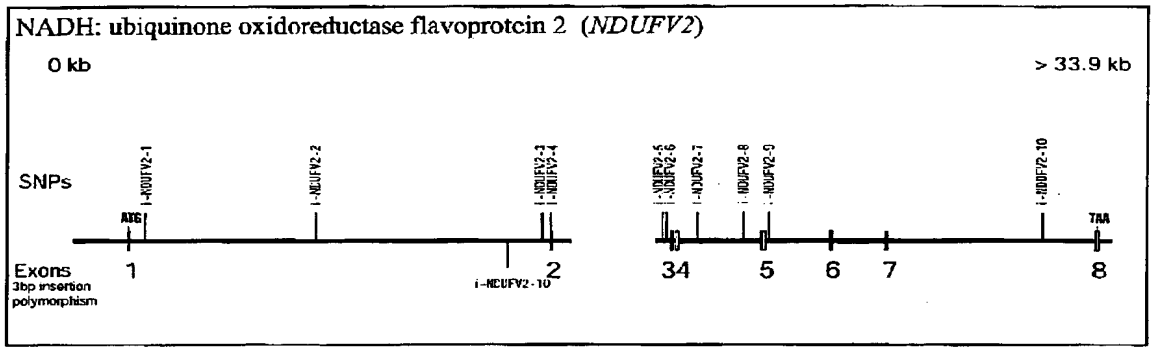
【図１２５】



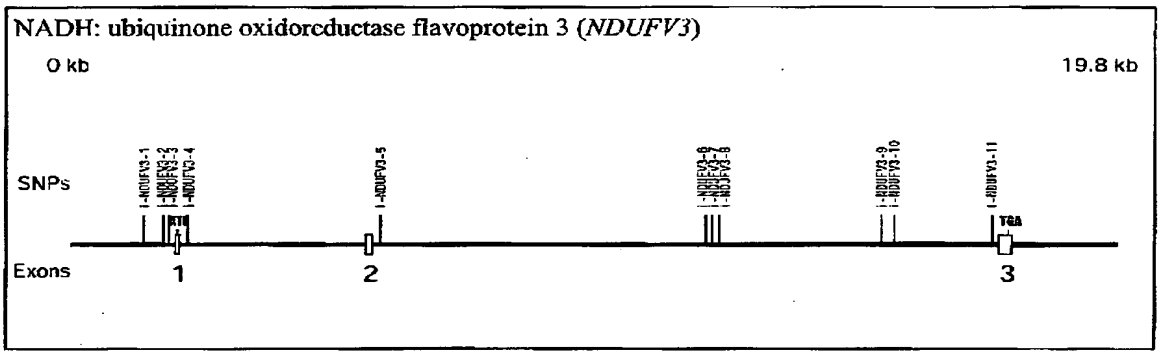
【図１２６】



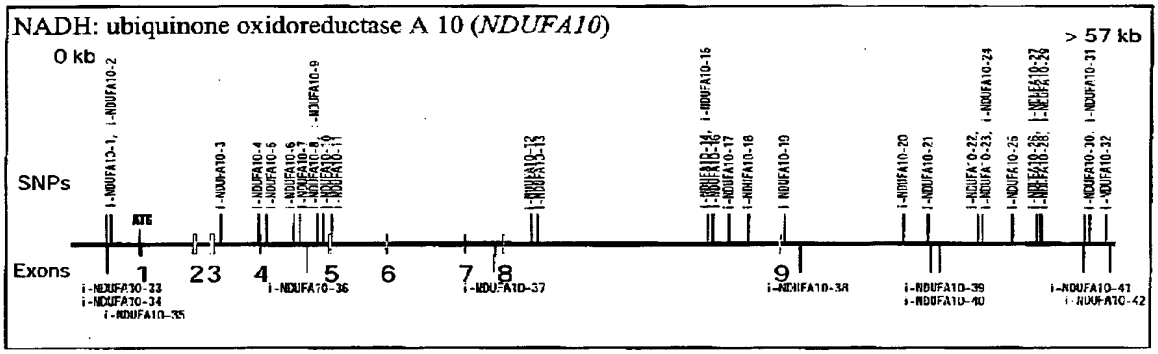
【図１２７】



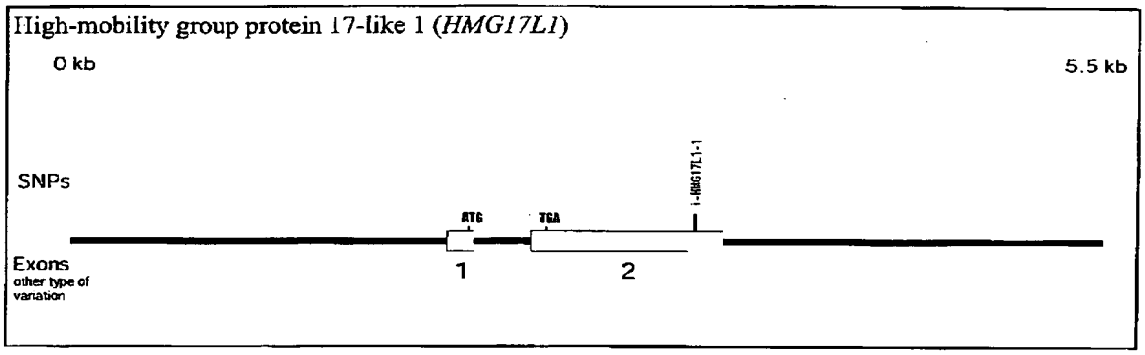
【図１２８】



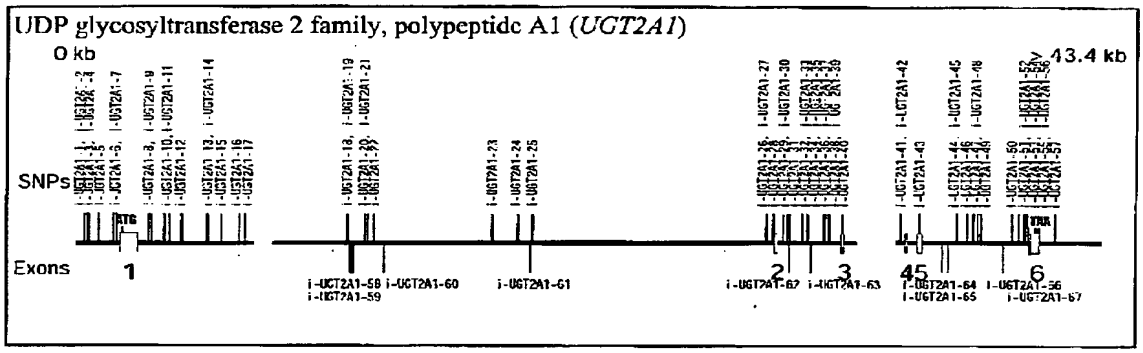
【図１２９】



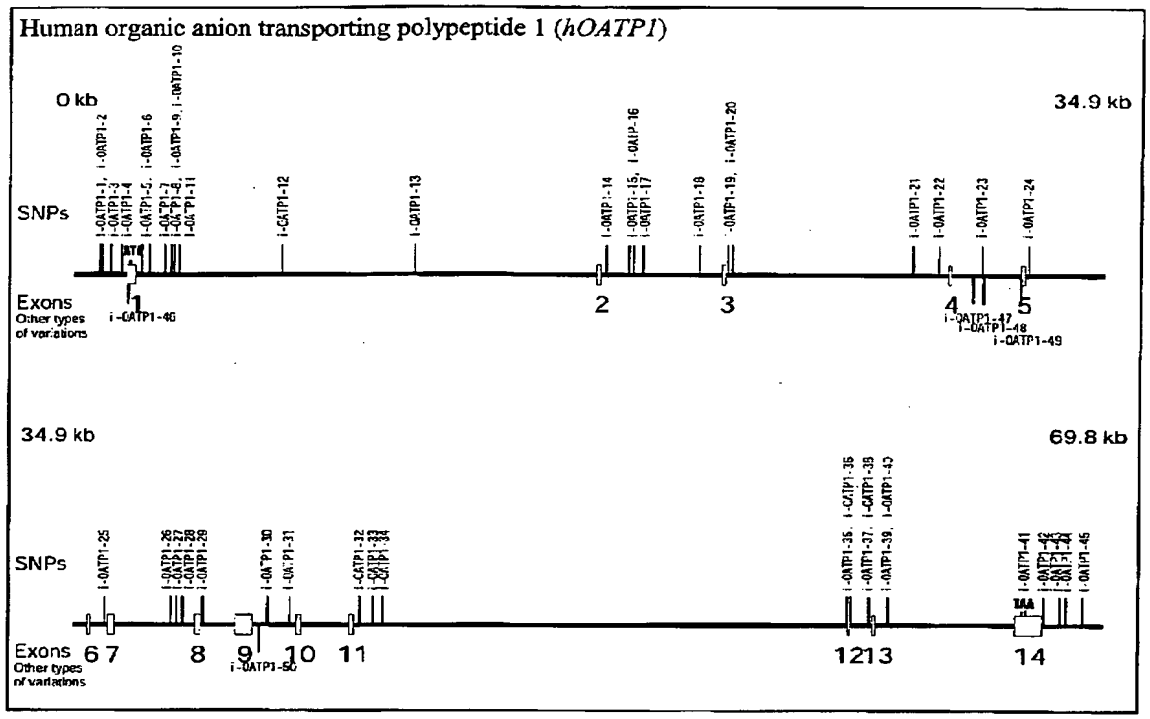
【図１３０】


High-mobility group protein 17-like 1 (*HMG17L1*)
0 kb
5.5 kb
SNPs
ATG
TGA
i-HMG17L1-1
Exons
other type of variation
1
2

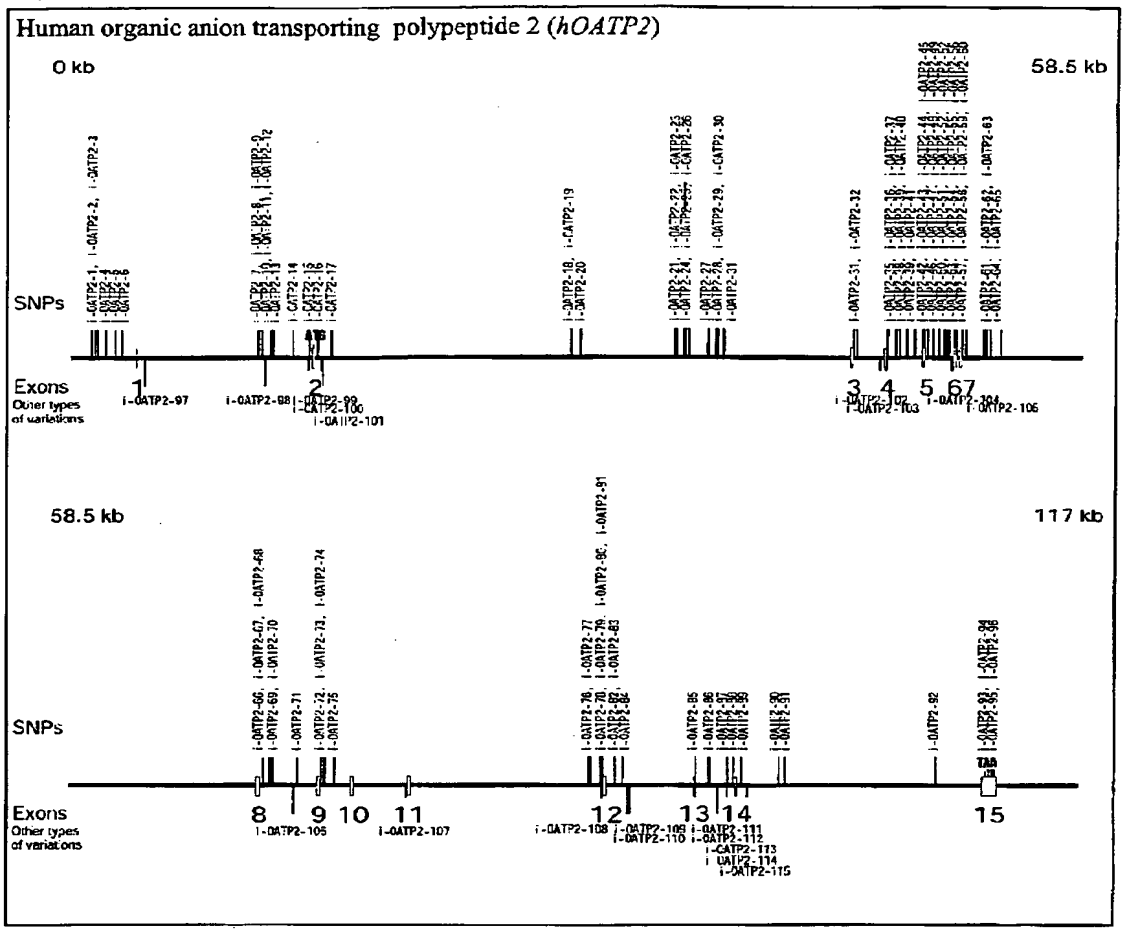
【図１３１】


UDP glycosyltransferase 2 family, polypeptide A1 (*UGT2A1*)
0 kb
43.4 kb
SNPs
Exons
1
2
3
45
6
i-UGT2A1-59
i-UGT2A1-60
i-UGT2A1-61
i-UGT2A1-64
i-UGT2A1-65
i-UGT2A1-66
i-UGT2A1-67

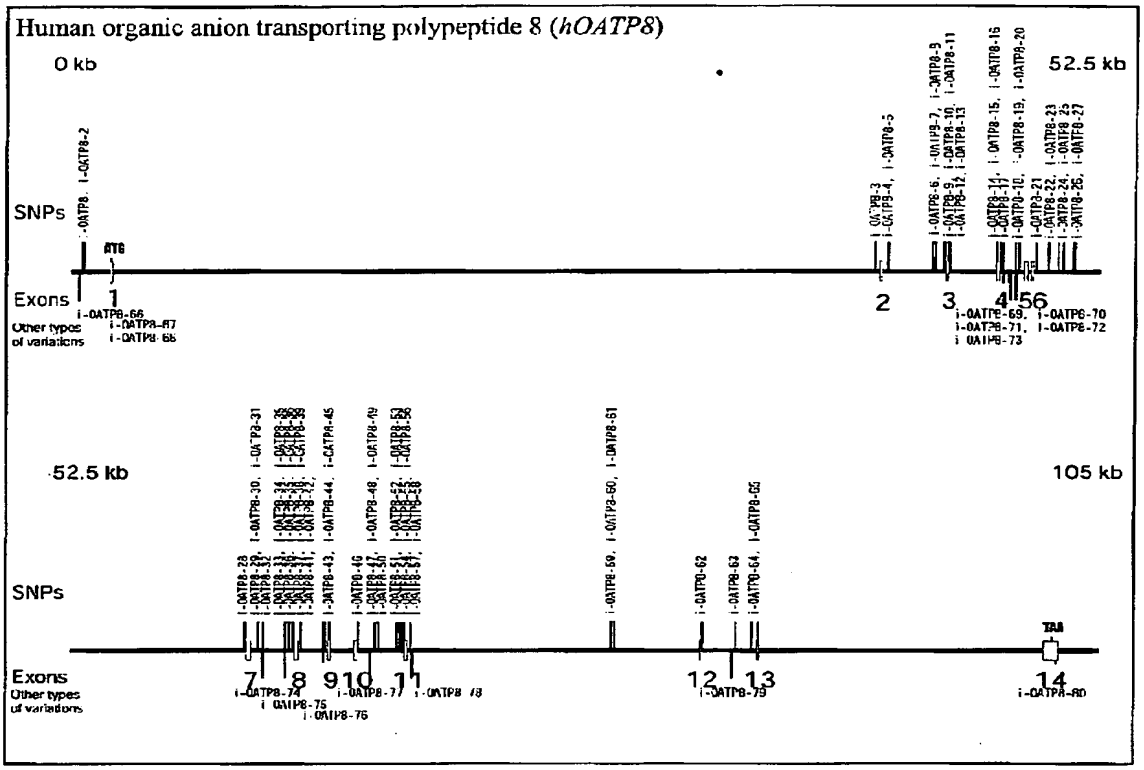
【図１３２】


Human organic anion transporting polypeptide 1 (hOATP1)
0 kb
34.9 kb
SNPs
Exons
Other types of variations
34.9 kb
69.8 kb
SNPs
Exons
Other types of variations

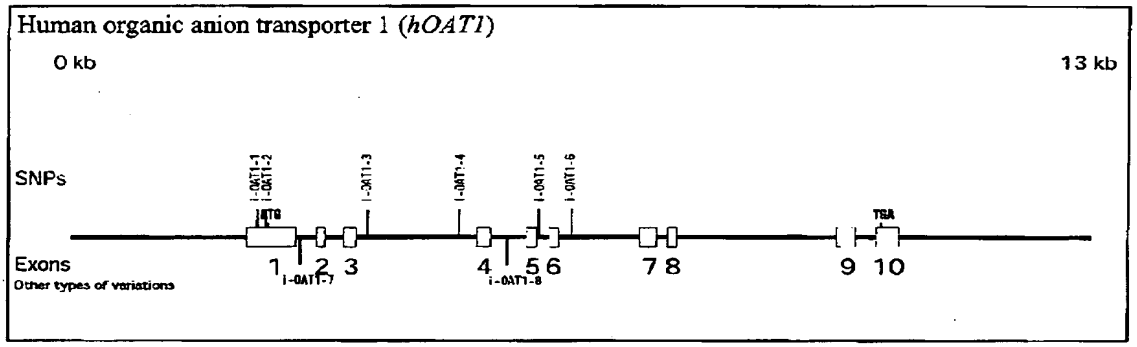
【図１３３】


Human organic anion transporting polypeptide 2 (hOATP2)
0 kb
58.5 kb
SNPs
Exons
Other types of variations
58.5 kb
117 kb
SNPs
Exons
Other types of variations

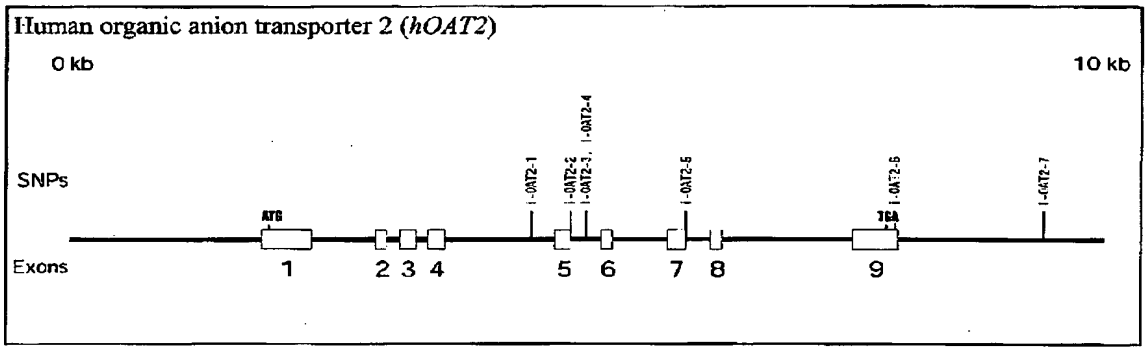
【図１３４】


Human organic anion transporting polypeptide 8 (hOATP8)
0 kb
52.5 kb
SNPs
ATG
Exons
1
2
3
4
5
6
Other types of variations
52.5 kb
105 kb
SNPs
TGA
Exons
7
8
9
10
11
12
13
14
Other types of variations

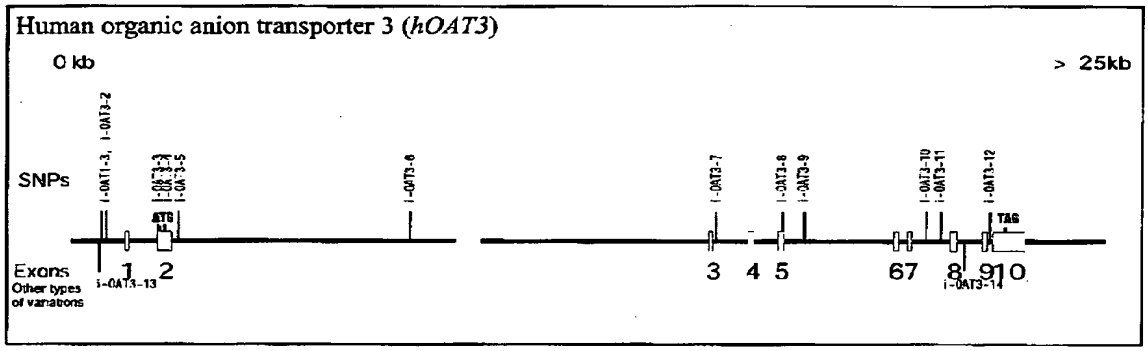
【図１３５】


Human organic anion transporter 1 (hOAT1)
0 kb
13 kb
SNPs
ATG
TGA
Exons
1
2
3
4
5
6
7
8
9
10
Other types of variations

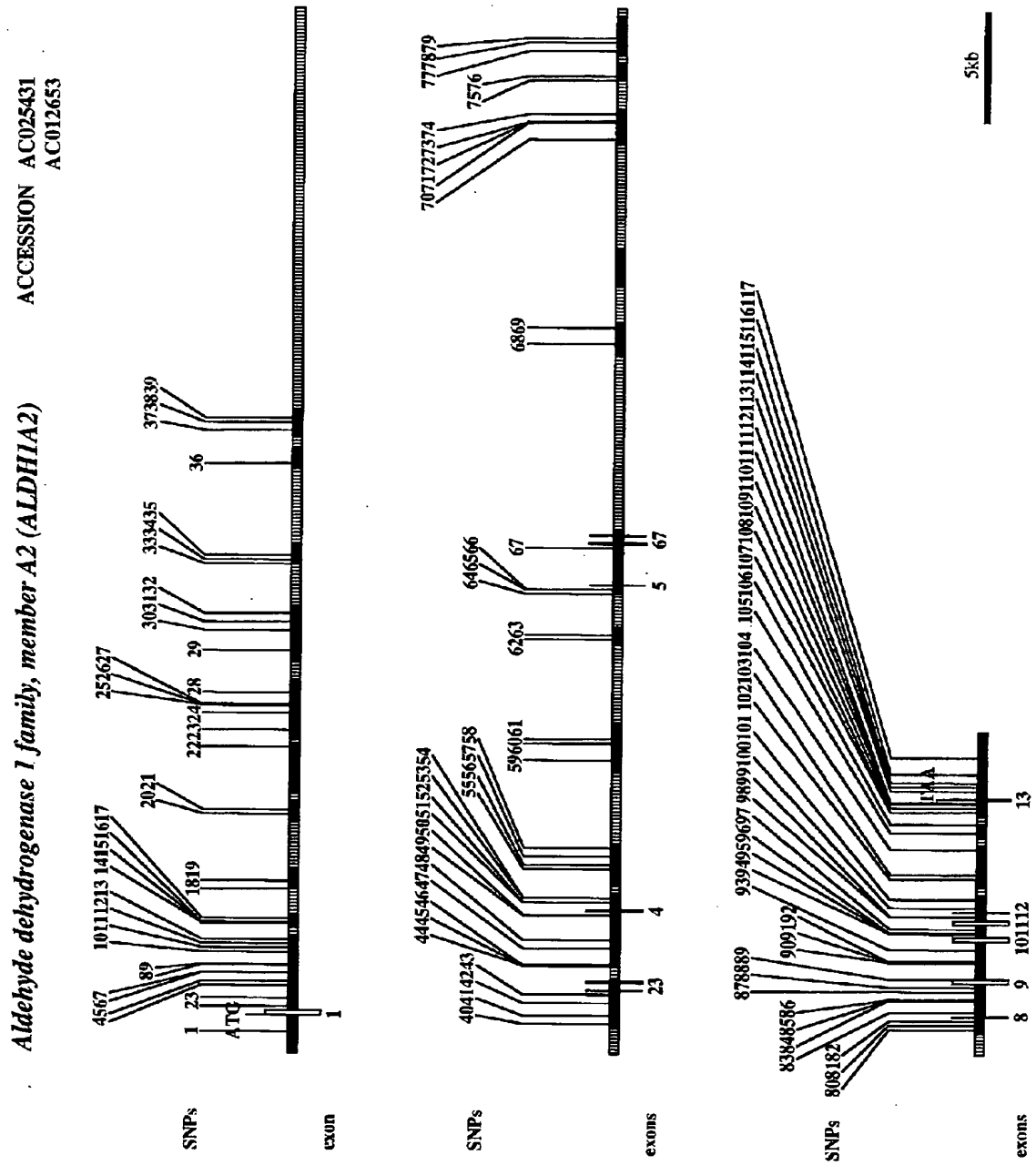
【図１３６】


Human organic anion transporter 2 (hOAT2)
0 kb
10 kb
SNPs
Exons
ATG
TGA
1
2 3 4
5
6
7
8
9

【図１３７】


Human organic anion transporter 3 (hOAT3)
0 kb
> 25kb
SNPs
Exons
Other types of variations
ATG
TAG
1
2
3
4 5
67
8
9
10

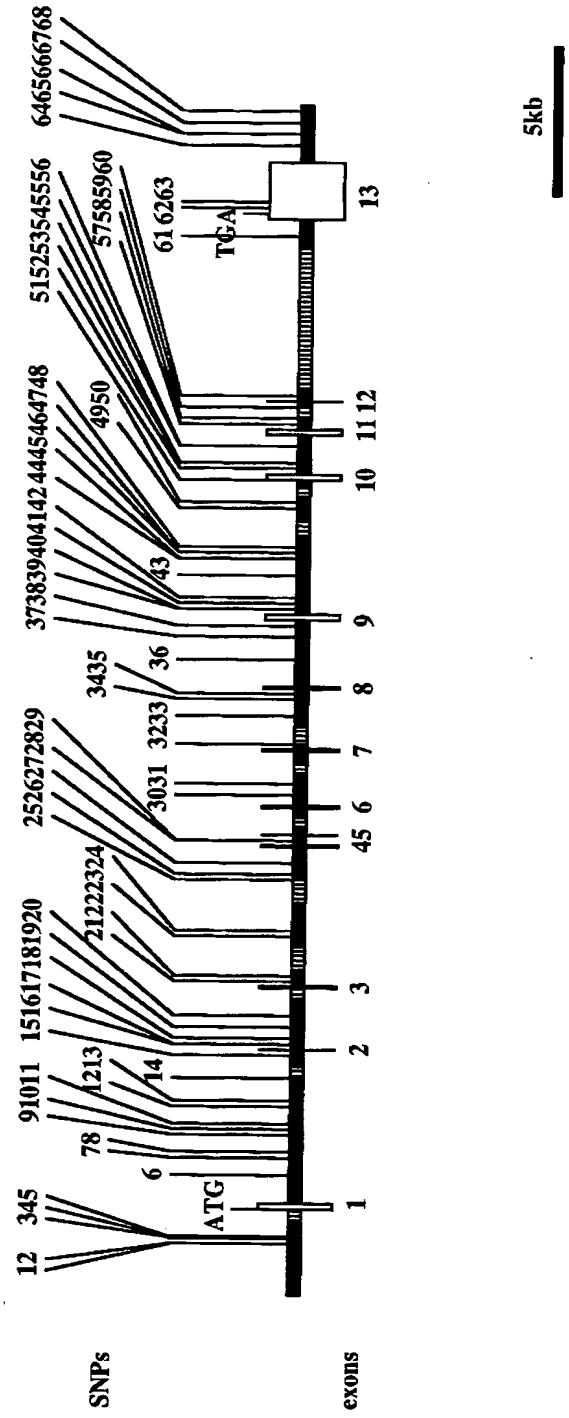
【図１３８】


Aldehyde dehydrogenase 1 family, member A2 (ALDH1A2)
ACCESSION AC025431
AC012653
SNPs
exon
SNPs
exons
SNPs
exons
5kb

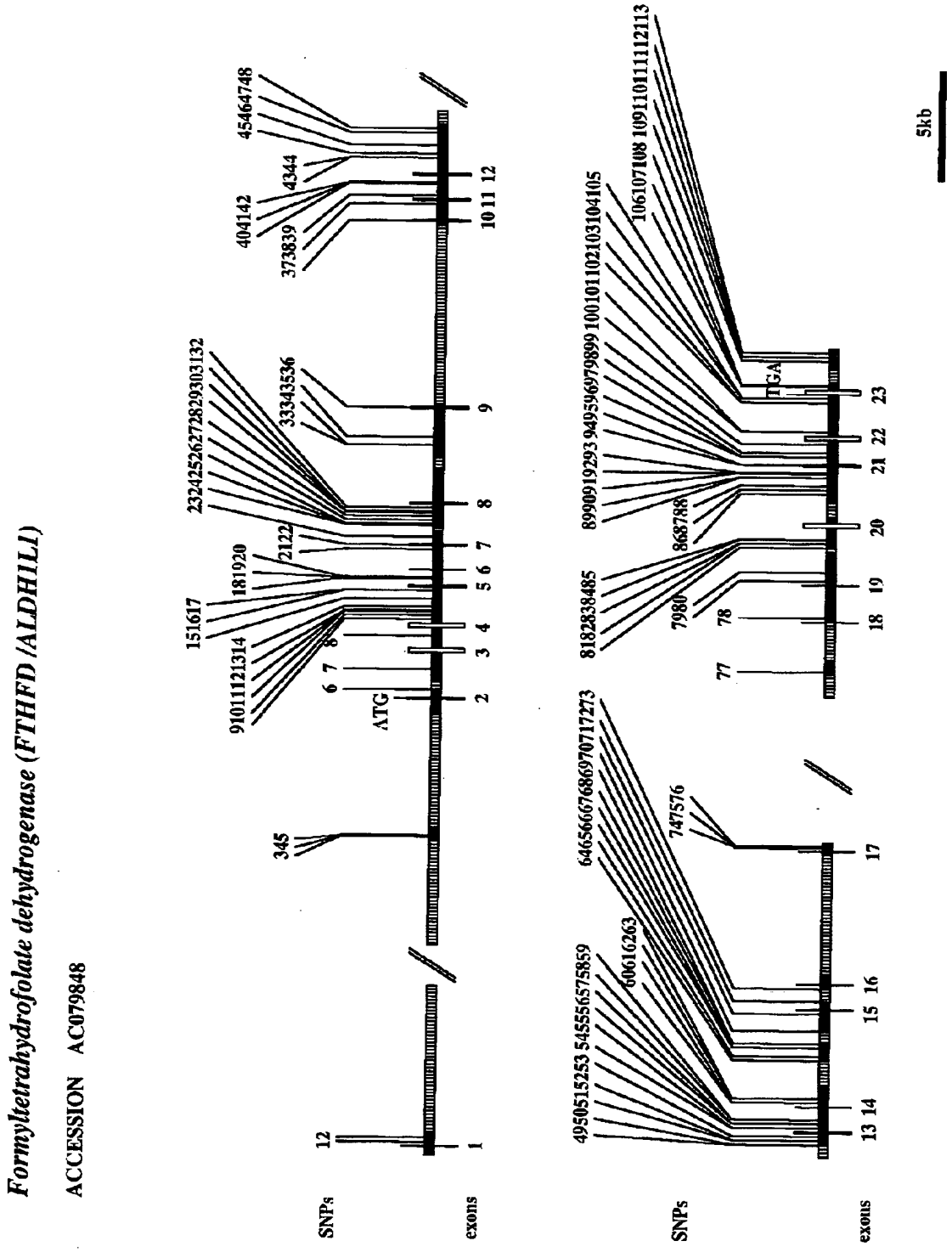
【図１３９】

Aldehyde dehydrogenase 1 family, member A3 (ALDH1A3)

ACCESSION　AC015712



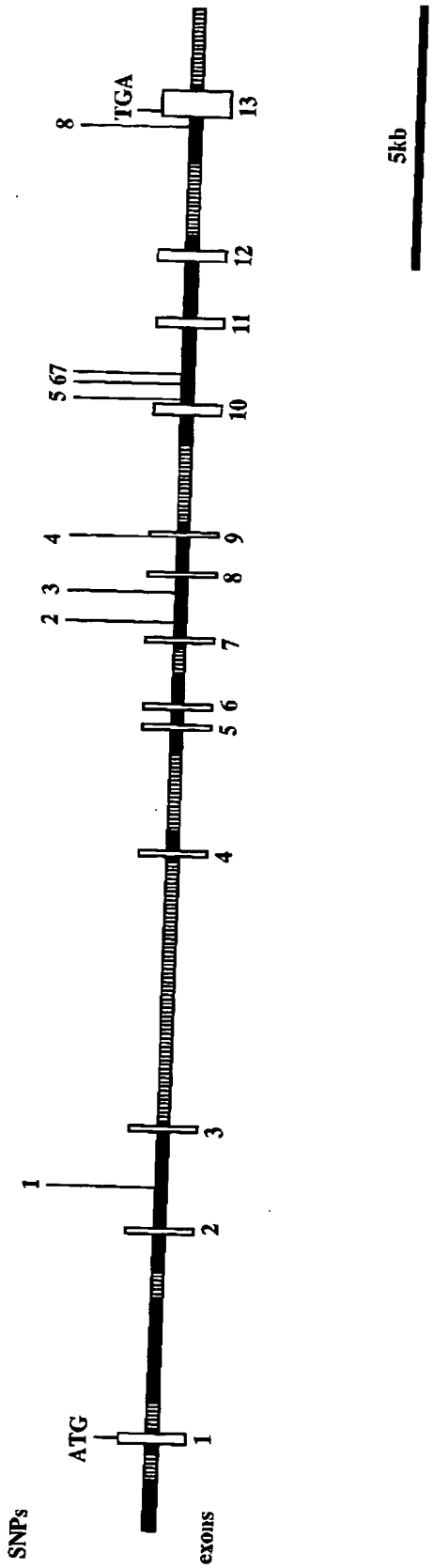
【図１４０】


Formyltetrahydrofolate dehydrogenase (FTHFD /ALDH1L1)
ACCESSION AC079848
SNPs
exons
ATG
TGA
5kb

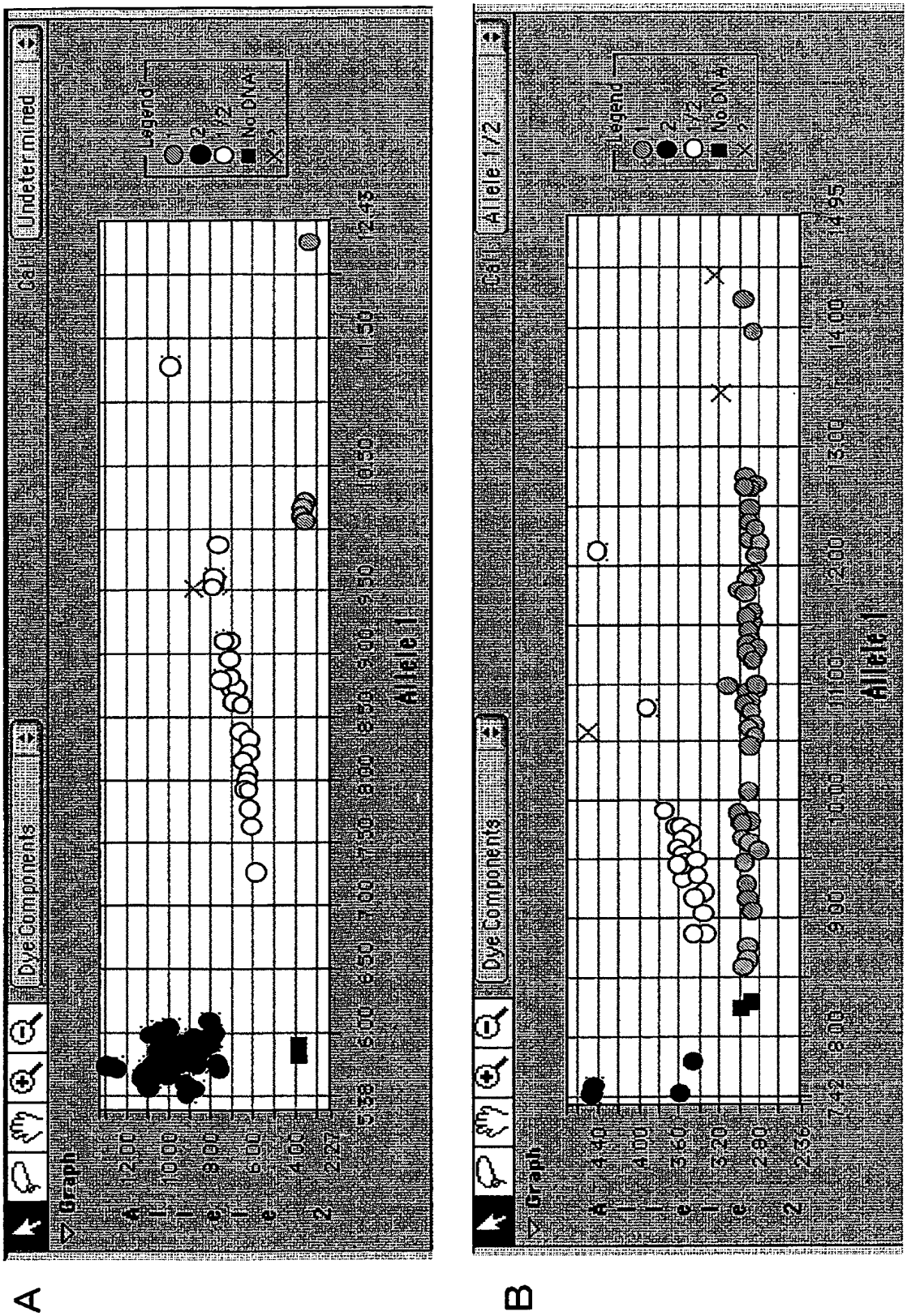
【図１４１】

Cytochrome P450, subfamily IIIA, polypeptide 4 (CYP3A4)

ACCESSION　AF280107



【図１４２】


Graph
Dye Components
Call
Undetermined
Legend
1
2
1/2
No DNA
X
Allele 1
Allele 2
A
B

【書類名】　要約書

【要約】

【課題】　遺伝子多型の検出方法の提供。

【解決手段】　薬物代謝酵素をコードする遺伝子中に存在する遺伝子多型情報から、該遺伝子多型部位を含むように、又は薬物代謝酵素をコードする遺伝子を増幅したときの増幅断片中に前記遺伝子多型部位が含まれるように、オリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーを作製し、得られるオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーを用いて、目的の薬物代謝酵素をコードする遺伝子中の少なくとも１個の遺伝子多型を検出することを特徴とする遺伝子多型の検出方法。

【選択図】　なし

特願２００１－２５６８６２

出　願　人　履　歴　情　報

識別番号　　［０００００６７９２］

１．変更年月日　　１９９０年　８月２８日
［変更理由］　　新規登録
住　所　　埼玉県和光市広沢２番１号
氏　名　　理化学研究所

特願２００１－２５６８６２

出　願　人　履　歴　情　報

識別番号　　［５００００５６７５８］

１．変更年月日　　２００２年　９月　９日
［変更理由］　　識別番号の二重登録による抹消
［統合先識別番号］５９８０３９６５５
住　所　　神奈川県横浜市青葉区あざみ野１－１７－３３
氏　名　　中村　祐輔

特願２００１－２５６８６２

出　願　人　履　歴　情　報

識別番号　　［５９８０３９６５５］

１．変更年月日　　２００２年　９月　９日
［変更理由］　　識別番号の二重登録による統合
［統合元識別番号］５０００５６７５８
住　所　　神奈川県横浜市青葉区あざみ野１丁目１７番３３号
氏　名　　中村　祐輔

特願２００１－２５６８６２

出　願　人　履　歴　情　報

識別番号　　［５０１００２４７１］

１．変更年月日　　２０００年１２月２７日
［変更理由］　　新規登録
住　所　　東京都国立市北１－１１－８
氏　名　　関根　章博

特願２００１－２５６８６２

出　願　人　履　歴　情　報

識別番号　　［５０１００２４８２］

１．変更年月日　　２０００年１２月２７日
［変更理由］　　新規登録
住　所　　神奈川県川崎市中原区田尻町２１
氏　名　　飯田　有俊

特願２００１－２５６８６２

出　願　人　履　歴　情　報

識別番号　［５０１００２４９３］

１．変更年月日　２０００年１２月２７日
［変更理由］　新規登録
住　所　東京都青梅市東青梅５－１０－６　河辺パークホームズ１０８
氏　名　斎藤　督